

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: February 22, 2005, 08:05:49 ; Search time 23.1073 Seconds

(without alignments)
3605.942 Million cell updates/sec

Title: US-10-817-423-2

Perfect score: 4491
Sequence: 1 MRNKGSGVVRLPNDLEDL.....LCDQWHSVAVSIKRIILH 866

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 9621673 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

1: PIR 79:*
2: PIR2:*
3: PIR3:*
4: PIR4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	3560.5	79.3	1713	2	A55347	adhesive ligand ep
2	1190	26.5	1816	1	S68960	laminin alpha-4 ch
3	948	21.1	3635	2	T10053	laminin alpha 5 ch
4	636.5	14.2	3712	2	S18253	laminin alpha-1 ch
5	600.5	13.4	3672	2	T23433	hypothetical prote
6	579.5	12.9	3704	2	T37316	probable laminin a
7	545	12.1	3084	1	MMMSA	laminin alpha-1 ch
8	531.5	11.8	1751	1	MMHUA	laminin alpha-2 ch
9	529.5	11.5	3075	1	S14458	laminin alpha-1 ch
10	516.5	11.5	3106	1	S53868	laminin alpha-2 ch
11	358.5	8.0	3102	2	T43281	laminin alpha ch
12	321.5	7.2	1530	2	A45944	neurexin I-alpha
13	320	7.1	1507	2	A40228	neurexin I-alpha
14	301.5	6.7	1438	2	A48216	neurexin III-alpha
15	301.5	6.7	1471	2	B48216	neurexin III-alpha
16	301.5	6.7	1578	2	I48216	neurexin III-alpha
17	288	6.4	1715	2	C40228	neurexin IV-alpha
18	261	5.8	1283	2	T13799	neurexin IV - trui
19	222.5	5.0	2823	2	F87908	protein T22A3.8 [i
20	222.5	5.0	2823	2	T23064	hypothetical prote
21	211.5	4.7	1264	2	T19565	hypothetical prote
22	195.5	4.4	3707	2	S18252	heparan sulfate pr
23	188	4.2	1722	2	E89753	protein FltC.4 [i
24	183	4.1	1385	2	T14158	neurexin IV - mous
25	183	4.1	4391	2	A58096	perlecan precursor
26	179.5	4.0	3097	2	T00021	DN-cadherin - trui
27	174	3.9	1381	2	T31083	parandrin - rat
28	169.5	3.8	3375	2	T19821	hypothetical prote
29	168.5	3.8	882	2	A39030	androgen-binding p

30	165.5	3.7	5147	1	IJPF7M	cadherin-related c
31	164.5	3.7	402	1	BOHUS	sex steroid-binding
32	163	3.6	403	2	A26371	sex steroid-binding
33	163	3.6	3034	2	T14119	seven-pass transme
34	161	3.6	1959	1	AGRT	agrin - rat
35	160	3.6	2325	2	A61208	chondroitin sulfate
36	156	3.5	1193	2	T21133	hypothetical prote
37	155	3.5	1955	1	AGCH	agrin precursor
38	154.5	3.4	367	2	A34436	sex steroid-binding
39	149	3.3	1328	2	T43060	agrin - electric r
40	148	3.3	281	2	T33466	hypothetical prote
41	146	3.3	757	2	T34362	hypothetical prote
42	146	3.3	4307	2	T20721	hypothetical prote
43	142	3.2	1523	2	T13953	MEGF5 protein - ra
44	140	3.1	2610	2	T20968	hypothetical prote
45	138	3.1	1025	2	T42626	secreted leucine-r

ALIGNMENTS

RESULT 1

A55347
adhesive ligand epiligrin, alpha-3 chain form A precursor - human
C:Species: Homo sapiens (man)
C>Date: 06-Feb-1995 #sequence_revision 06-Feb-1995 #text_change 09-Jul-2004
C/Accession: A55347
R:Ryan, M.C.; Tizard, R.; Vandevanter, D.R.; Carter, W.G.
J. Biol. Chem. 269, 22779-22787, 1994
A>Title: Cloning of the lam3 gene encoding the alpha3 chain of the adhesive ligand epi
A/Reference number: A55347; PMID:94357926; PMID:8077230
A/Accession: A55347
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-1713 <RVA>
A/Cross-references: UNIPROT:Q16787; GB:I34155; NID:9551596; PID:9551597
C/Superfamily: laminin alpha-4 chain; laminin G repeat homology; laminin-type EGF-like
C/Keywords: alternative splicing
F:67-114/Domain: laminin-type EGF-like homology <LE2>
F:192-1534/Domain: laminin G repeat homology <LG4>

Query Match	79.3%	Score 3560.5;	DB 2;	Length 1713;
Best local Similarity	78.4%	Pred. No. 1.1e-239;		
Matches 680;	Conservative 86;	Mismatches 98;	Indels 3;	Gaps 2;
QY	1	MRNKGSGVVRLPNDLEDKGYTSLFLQRPDLRENGSTEDMFVYTLGNKQASXDYIG	60	
DB	771	MRNKGSGVVRLPNDLEDKGYTSLFLQRPDLRENGSTEDMFVYTLGNKQASRDYIG	830	
QY	61	MAVVDGQLTCVNMIGREARVQIDVLTSESQBAVMDRKYRQRIYOPALNTYKATSN	120	
DB	831	MAVVDGQLTCVNMIGREARVQIDVLTSESQBAVMDRKYRQRIYOPALNTYKATSS	890	
QY	121	KPRAPVYDLEGGSSNTLNLDPEDAVFYGVGPDPDELRSRLRPPYKGCIELDNEN	180	
DB	891	KPRPGYDMDGSSNTLNLDPEDAVFYGVGPDPDELRSRLRPPYKGCIELDNEN	950	
QY	181	VLSLYNFKTFNNTTEVEBCRRRKRKESDKNYEGTGTYARIPTQPNAPFPNFIQTQTV	240	
DB	951	VLSLYNFKTFNNTTEVEBCRRRKRKESDKNYEGTGTYARVPTQPNAPFPNFIQTQTV	1010	
QY	241	DRGLLFFAENQDNFISLNTIDGNLMVRYKANSPPKRGKRDITINDGKHSILITIGKQ	300	
DB	1011	DRGLLFFAENQDNFISLNTIDGNLMVRYKANSPPKRGKRDITINDGKHSILITIGKQ	1070	
QY	301	KRAMINNVNERSVRIEIEIPFSTYVYGGIPAIAREFNISTPAPFGCMKRLKTSQVRL	360	
DB	1071	KRAMINNVNERTIIEIEIPFSTYVYGGIPAIAREFNISTPAPFGCMKRLKTSQVRL	1130	
QY	361	NDTVGVTKKCSSEDKLVRTASFSRGGQMSFTNLDVPSSTDFQUSFGQTFQPSGTLINHQ	420	
DB	1131	NDTVGVTKKCSSEDKLVRTASFSRGGQMSFTNLDVPSSTDFQUSFGQTFQPSGTLINHQ	1190	

6 = 350-566
4.1-566

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Oy 421 TRTSJLWTTEDGHEJLSTSDSNIPFSPGVMYDGLLHHVSVISDPSGLALLIDDOYL 480
Db 1191 TWNTLQVTTLEDGYTELSTSDSGPIFKSPQTMDELHAYSVISDMSGMLLIDDOQLR 1250
Oy 481 RNQRLPFSNMAQSLRLGGGHEGCI SNVLVQRPQSDBEVLDLASKSTYKDASLGGCSLN 540
Db 1251 NSKELKHMISSRQSLRLGGSNFEGCISNVFQRLSPLEVLDTLSNLSKRDVSLGGCSLN 1310
Oy 541 KPEPLMLFKSKRPFKGRIFVWYNQMLDQAPQAT-RSTANODGSLCLPEPLTKXSHRLQ 599
Db 1311 KPEPLMLKSGSTRFENKTKTFPRINOLQDTPVASSPSVSWQD--ACSLPEPTQANHGALQ 1368
Oy 600 FGDSPTSHLLKLPOELKLKPRSQESLDIQTTSPKGLVYAGTKDSFLMLVYADRVPAL 659
Db 1369 FGDIPTSHLLKRLPEGLKLKPRSQFPAVDWQTTSSRGLVYHTGTKSFMALYLSKRLVPAL 1428
Oy 660 GAGGKCLRLRKERYHDKRMTTVVFGLNGSKARLVYDGLRAQESGLPNSSTTSPREOYL 719
Db 1429 GTDKRKRLRKKEKKNDDKMTVVFGHDEKGRLLVVDGLRAREGSLPNSSTTISRAPYLL 1488
Oy 720 GLPLSRPKRSLPOHSFVGLCLDPOLNSKPLDPSPARFVSPICGSLSEKGIYFSGGGHV 779
Db 1489 GSPSGRKRKSLPTMSFVGLCLNFOJDSKPLTYTPSSSFVSSCLGGPLKGIYFSEGGHV 1548
Oy 780 ILANSVSLGPELKLTFSLRPSRLTGVLILHVSQSQGRSLVYMEAGKVTTSVSDAGSVT 839
Db 1549 VLASVLLGPEFKLVFSIRPSRLTGILLHISGQPKHLCVTLBAGKVTASDMSGAGGST 1608
Oy 840 SITPKQSLCDGQMSVANSIKORILHL 866
Db 1609 SVTPKQSLCDGQMSVAVTIKOHILHL 1635

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RESULT 2

laminin alpha-chain precursor - human

N/Alternate names: laminin A1

C/Species: Homo sapiens (man)

C/Date: 21-Aug-1998 #sequence revision 21-Aug-1998 #text_change 09-Jul-2004

C/Accession: S68960; S65926; S49149; S40150; I53516

R/Richards, A.; Al-Imara, L.; Pope, F.M.

Eur. J. Biochem. 238, 813-821, 1996

A/Title: The complete cDNA sequence of laminin alpha-4 and its relationship to the other

A/Reference number: S68960; MUID:96300249; PMID:8706685

A/Accession: S68960

A/Molecule type: mRNA

A/Residues: 1-1816 <RIC>

A/Cross-references: UNIPROT:Q16363; UNIPROT:Q14731; EMBL:X91171, NID:g1212962, PIDN:CAAG

A/Experimental source: tissue type heart

R/Riivanainen, A.; Sainio, K.; Sariola, H.; Tryggvason, K.

FEBS Lett. 365, 183-188, 1995

A/Title: Primary structure and expression of a novel human laminin alpha-4 chain.

A/Reference number: I53516; MUID:95300971; PMID:7781776

A/Accession: S65926

A/Molecule type: mRNA

A/Residues: 1-142, 'P', 144-177, 'P', 179-490, 'Y', 492-1056, 'P', 1058-1816 <ITV>

A/Cross-references: EMBL:S78569, NID:g1042081; PIDN:AA34635.1, PID:g1042082

R/Richards, A.O.; Al-Imara, L.; Carter, N.; Leversha, M.; Lloyd, J.C.; Pope, F.M.

submitted to the EMBL Data Library, December 1993

A/Description: Localization of the gene (LAMA4) to chromosome 6q21 and isolation of a p

A/Reference number: S49149

A/Accession: S49149

A/Molecule type: mRNA

A/Residues: 236-1816 <RI2>

A/Cross-references: EMBL:X76939, NID:g509805, PIDN:CAA50261.1, PID:g509806

R/Richards, A.J.; Al-Imara, L.; Carter, N.; Lloyd, J.C.; Pope, F.M.

submitted to the EMBL Data Library, February 1993

A/Description: Isolation of a partial cDNA encoding a protein homologous to laminin A. 7

A/Reference number: S40150

A/Accession: S40150

A/Molecule type: mRNA

A/Residues: 1403-1541, 'S', 1543-1816 <RI3>

A/Cross-references: EMBL:X70904; NID:g437804; PIDN:CAA50261.1, PID:g437805

C:Genetics:
A:Gene: GDB:LAMA4; LAMA3
A:Cross-references: GDB:203904; OMIM:600133
A:Map position: 6q21-6q21
C:Complex: laminins are trimers of an alpha-type, a beta-type, and a gamma-type laminin
A:Definition:
A:Description: Interact with cells and with other basement membrane proteins to promote
C:Superfamily: laminin alpha-4 chain; laminin G repeat homology; laminin-type Egf-like
C:Keywords: basement membrane; cell binding; coiled coil; extracellular matrix; glycoprotein
F:1-24/Domain: signal sequence #status predicted <SIG>
F:25-1816/Product: laminin alpha-4 chain #status predicted <MAT>
F:82-129/Domain: laminin-type EGF-like homology <LE1>
F:153-154/Domain: laminin-type EGF-like homology <LE2>
F:187-238/Domain: laminin-type EGF-like homology <LE3>
F:241-265/Domain: laminin-type EGF-like homology #status atypical <LE4>
F:717-719/Region: cell attachment (R-G-D) motif
F:862-1031/Domain: laminin G repeat homology <LG1>
F:1068-1223/Domain: laminin G repeat homology <LG2>
F:1252-1398/Domain: laminin G repeat homology <LG3>
F:1488-1636/Domain: laminin G repeat homology <LG4>
F:1665-1816/Domain: laminin G repeat homology <LG5>
F:1104, 215, 308, 450, 524, 550, 571, 574, 631, 633, 735, 751, 754, 780, 803, 1086, 1281, 1359, 1411/Bindin
F:266, 269/Dsulfide bonds: interchain #status predicted

Query Match

Best Local Similarity 33.2%; Pred. No. 3.6e-74;
 Matches 310; Conservative 161; Mismatches 372; Indels 90; Gaps 27

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0Y 1 MRPNKSGVETRLPNEDJEDKGYTSLFLP-----QRDLNENGSTBEMFMYLGNKQASK 56
Db 829 MMEFGQSAVEHASTSHDDLKAFSLSLYMKPPYKRELT--TADQFLYLLSSKNKAK 885
0Y 57 DYIGMAVVDQJLTCVNIJGDBREAEVQJDOVLTSESQZAVMDRYKFORIYQFANKLTYK 116
Db 886 EYMGJALIKNDLVVYVNIJTKDVEIPLDS--KPVSSWPAFYSIKJIBRGVGHKGVFLTP 943
0Y 117 ATSKRPAPAVYDLEGGSSNTLNTLDBEDAVFVVGCPRPBBLPSRLRPPRYGCIELDD 176
Db 944 SLSTAEKRLTKGEPFGSDSLDLDBEDVTFVYGVSPNFKPLPTSLNLTGPGCIELAT 1003
0Y 177 LNEVLSLYNFKTYLNTTEVEBERK-----EESDKNYFBSGTGYA--RIPTQPN--A 227
Db 1004 LNDVVISLYNFKHLYNMDPSTSVPCARDKLAFQTSRAASYFFPSSGAVYVRDITRBRKFG 1063
0Y 228 PFPNFQIOTQTYDRGLLFAENODNFIISNIEDGNLMRY-----KANSEPKKXCI 280
Db 1064 QVTFPDIKVRTPADNGILTLNVNGSMFRLKEMRGYLAHYVDFFGSSGRVHLEBTLKKA- 1122
0Y 281 RDTINDGKNSILTTIGKLOKMMINVERSVRI---EGEIPDSTYYLGGIP-----I 331
Db 1123 --QINDAKYHEISL-IYHNDKRMILVDRHRYVSMDBEKKCIPTDIIYIGAPBEILQSR 1179
0Y 332 AIRERFNISTPFAFGKMKNL---KKTSGVYRLNDTVGVTKKCSHDMVLVTTASFSRGOM 388
Db 1180 ALRAHLPLADI-NFGCKKKGFQFGKDFNLLQETTLTGVGCPEDSLISRAYFN--GQS 1236
0Y 389 SFTMLD-VPSIDRRQSLRFGQTPQPSGTLNHCORTSSLVLTLEDGHIELSTBNSNPIR 447
Db 1237 FIASIQIKISFPDGEFGGNFRTLOPNGLLFFYASGSVFSISLNGTVIMDKV--GIKVO 1294
0Y 448 KSPSTYMDGLLHNHVSISDTSGLR--LLID-DQVLRNRQRLPSPSNAQOSLR--LGS-- 499
Db 1295 SVDQNYMDGLSHF--VISSVSPTRTELIVDKSRGNSNPKKGIKELQQAEBKKKPYFGGSP 1352
0Y 500 -----GHPEGCTISAVLVORFSQSPETVLDAKSTKQDASIGGCSLKNPPLMLFKSPXR 554
Db 1353 ISAGYANFTGCTISAVYETRVDRDVEVEDFORYTEKATSLYBCEPIESSPFLMLKKKKNL 1412
0Y 555 NKGRIFMVNQ--LMQDAPQATRSTEAQDQDSCLPLNT-----KASHRLQOF 600
Db 1413 SKPQASQNKKGKSKDAP-----SMDPVALKLPERKNTPRNSCHLSNSPRLAEHAYQY 1465
0Y 601 GDSPTSHLLKLPQBLKLPKRSQFSLDIQTSSPKGLVFAAGTKD--SFLALVYVADGRVVA 658

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Db      1466 GGNANRQREPEHLKQDPRGASQSFISRLRTSSHGMIFFYDGDQENDPMLFLAHGRLYVM 1525
Qy      659 LGAGKKLRLRSRERHDKWHTVVPGLNGKARLVVDGLRAQEGSL-PGNSTISPREQV 717
Db      1526 FNVGHKKLRISQEKYNDGLMHDVIFIRERSGGLVIDGLRVLEESLPPEATWTKIKGPI 1585
Qy      718 YLGLPLSRKESLPQ-----HSPVGLADPQLNKGKLPDPSARFGVSPCLDGLSEKGIYFS 773
Db      1586 YLDGVAPEGKAVKAVQINSIYFSGCLSNQLQNGASITSASQTSVTFCEFGMEHTGYFS 1645
Qy      774 QGGGVILANSVSLGPELKTFSIRPSRLTGVLIVHVSQSGORLSVYMEAGKYTTSVSD 833
Db      1646 TBGGVYVLDSEFNIGLKEFLAFPRPSSSGTLVHGHSVNGEYLVNVMKKGQYIVKKNNG 1705
Qy      834 AGGSVTSITPKQSLCDGQMSVAVSIKORLIHL 866
Db      1706 IRDFTSVTPKQSLCDGRMHRITVIRDSNVVQL 1738

RESULT 3
T10053
laminin alpha 5 chain - mouse (fragment)
C/Species: Mus musculus (house mouse)
C/Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 09-Jul-2004
C/Accession: T10053
R/Miner, J.H.; Lewis, R.M.; Sane, J.R.
submitted to the EMBL Data Library, November 1997
A/Reference number: Z16923
A/Accession: T10053
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: mRNA
A/Residues: 1-3635 <MIN>
A/Cross-references: UNIPROT:Q61001; EMBL:U37501; NID:g2599231; PID:g2599232
C/Genetics:
A/Gene: lama5
C/Keywords: basement membrane; cell binding; extracellular matrix
P:1888-1939/Domain: laminin-type EGF-like homology <LBS>
P:1942-1970/Domain: EGF homology <EGF>

Query Match      21.1%; Score 948; DB 2; Length 3635;
Best Local Similarity 30.6%; Pred. No. 8.9e-57;
Matches 285; Conservative 167; Mismatches 360; Indels 120; Gaps 37;

Qy      1 MRNNGSGVRLPNLIDELKGYTSLFLQRPDLRENG--TEDMFVMTLGNKDAKDY 58
Db      2656 MKEFGSGVRLPRPRDLADLAAYALFKHISPVPADEPGKTDGDFLVYMGSRQATGDY 2715
Qy      59 IGMAVVDGQLTCVYNTGDR-BARVQIDQVLTSSSQAVMDRVKFORIYPAKLNTYKKA 117
Db      2716 MGVSRLRQKVMWYRLDKAGPTTISIDENIGEQ-----PAVSIDRTLPGHNSVTV- 2768
Qy      118 TSNPKAPAVYDLEGS-----SNTLNLDPEDAVFYGVYPPDELPRLFPYKGCIE 173
Db      2769 -----KQMHKIKGDTVAQGSBELNLHDDPFFYGVGSPSNTPPRLPFPYLGIE 2822
Qy      174 LDDINENVLSLYNFKTTFNNTTEVEBCRRRKEE-----SDKNYFEGTGAFLPTQDNAP 228
Db      2823 METINEVSLYNEQTFMLDITAVDKCARSKATGDPWLTGSGYLDGSGFARISFEQO-- 2880
Qy      229 FPN---FIQITQTVVDGLFPRANQNFISINLEDNLMRYKLN-----EPPK- 276
Db      2881 FSNKRRDQELRLVSYNGIIFFLQDSQFLCLAVQEGTLVLFYDFGGLKKADLPQQA 2940
Qy      277 -----EKGIPTINDGKHSILITGKQKRMIVNRSVRIEGLFDFSTYUUGT--- 329
Db      2941 LTAASKAIQVFLAANKRVLV---RYERATVFSVDQDNL---EMAD--AYLGVPRP 2992
Qy      330 --PLAIBERNISTPAFQGCNKLN---KTSGVRLADTYGVTKKCSBDMKLVTPASPSR 384
Db      2993 QLPFLSLKQLFP-SGGSVSGCKIGKALGKYVDLKRNL-TTGISFGCTADLLVGRTRWTHG 3050
Qy      385 GCGMSFPNLDV-PSTDFQLSFGQTQPSGTLNLHQRTSSLVTLLEDHIELSTDSN 443

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Db      3051 HGFPLALPDVAITVAVVSGFGRGTQDNNLLYRTSPDGPYQVSLREGHVTLRENNQE 3110
Qy      444 IPIFKSPGYTMGLLHVSVISPTSGRLIIDP-QVLRNQNLBFSNSNQ-----QSLR 497
Db      3111 V---ETQRFADAPFVAVFYSNVTVVVDQQLVSHKHTTPTMLQLOPEPSRL 3167
Qy      498 GG-----GHFPGCISNVLYVQFSSPEVLDLASKTKKDAISGCSLNKPPPLMFKS 550
Db      3168 GGLPVSGTFRNSGCLSNVFPVQRLRGPRVFDLHQMGSNNVSV-GCT-----PAQLIETS 3222
Qy      551 PKRPNKRIFFNVNQLMDAPQATRSYEA-----QDGRCLPPLNTKASHRALQF-GDSP 604
Db      3223 RATAQK-----VERSRQSPQDLACTTPMLPGTIQAYQGGPLPS-----YLQFVGI 3272
Qy      605 TSHLLKLPOELKPKSPQSLDIQTTSPKGLVYVYAGTKGSLFALYADGNNVVALAGK 664
Db      3273 SHNRRLHLSM-LVRPFAASQGLLSTAP-----MSGRSPS-LVLFNHHGFVQTEGPGP 3325
Qy      665 KLRLSKERYHDKWHTVVPGLNGKARLVVDGLRA-QEGSLPQNSTISPREQVYL---- 719
Db      3326 RLQVQRQSHSRAGQMRVSVYRWGMQOQLVVDGSSQTMQKALHRRVPRARPPITLSVG 3385
Qy      720 GLPLSRKPKSLP-QHSFVGLARDFOLNSKPLDPSARFGVSPCLGSLKGIYFSQGGH 778
Db      3386 GLPASGVSSKLPVSVGSGCLKTLQDKQPLRTPTQVGVTPCVSGPLDGLFFPGSEGV 3445
Qy      779 VILANSVSLGPELKTFSIRPSRLTGVLIVHVSQSGORLSV-YMEAGKYTTSV---SSDA 834
Db      3446 VTLELPKAKPVPVLELEMRPLAAGLIFHL-----GQALATPYMQLKVLTEQVLLQAND 3501
Qy      835 GGSVTSITPKQSLCDGQMSVAVSIKORLIHL 866
Db      3502 AGESFTWVTPYKLCDRMHRVAVIMGDTURL 3533

RESULT 4
S18253
laminin alpha-1 chain precursor - fruit fly (Drosophila melanogaster)
C/Species: Drosophila melanogaster
C/Date: 16-Sep-1992 #sequence_revision 24-Jul-1997 #text_change 09-Jul-2004
C/Accession: S28399; S18253
R/Kusche-Gullberg, M.; Garrison, K.; Mackrell, A.J.; Fessler, J.H.
EMBO J. 11, 4519-4527, 1992
A/Title: Laminin A chain: expression during Drosophila development and genomic sequence
A/Reference number: S28399; NID:93049203; PMID:1425586
A/Accession: S28399
A/Status: preliminary
A/Molecule type: nucleic acid
A/Residues: 1-3712 <KUS>
A/Cross-references: UNIPROT:Q00174; GB:M96388; NID:g157799; PID:AAA28662.1; PID:g15780
R/Garrison, K.; Mackrell, A.J.; Fessler, J.H.
J. Biol. Chem. 266, 22899-22904, 1991
A/Title: Drosophila laminin A chain sequence, interspecies comparison, and domain struc
A/Reference number: S18253; NID:92078147; PMID:1744083
A/Accession: S18253
A/Molecule type: mRNA
A/Residues: 1762-3712 <GAR>
A/Cross-references: EMBL:M75882; NID:g157797; PID:AAA28661.1; PID:g157798
C/Genetics:
A/Gene: FlyBase:lana
A/Cross-references: FlyBase:FBgn0002526
C/Supfamily: laminin alpha-1 chain; laminin G repeat homology; laminin-type EGF-like
C/Keywords: basement membrane; cell binding; coiled coil; disulfide bond; extracellular
P:273-330/Domain: laminin-type EGF-like homology <LEG>
P:333-400/Domain: laminin-type EGF-like homology <LEG>
P:541-584/Domain: laminin-type EGF-like homology <LEG>
P:1776-2115/Domain: III <DOM3>
P:1776-1806/Domain: laminin-type EGF-like homology #status atypical <LE1>
P:1809-1856/Domain: laminin-type EGF-like homology <LE2>
P:1859-1914/Domain: laminin-type EGF-like homology <LE3>
P:1917-1967/Domain: laminin-type EGF-like homology <LE4>
P:1970-2014/Domain: laminin-type EGF-like homology <LE5>

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QY 498 GGGH-----PEGCISNVLVORFSGPEVLDAKSTKQASLGCSL 539
 DB 3184 DQSNPDASFLSAFPGKSGSTFVGCIGDVTL-----NGKLDPAN-SEIKELSLNGCSL 3237
 QY 540 ---NKPFLMLFKSPKPKNGRI FVNVQIMODAPQATST-----EAMQDRSGCL 586
 DB 3238 SDDENISTTTTAAKPTDDSDVAVLPIDEEESTTTTTTTTTTEPTERPAEPADHGCSL 3297
 QY 587 P--PLATKASHRLAQGDSTSHLLKLPOELLKPSQSPLDQTSPPKLVYAGTK-D 643
 DB 3298 PEDPMVQFEDAEFGNSQOYSRIEYDILPEALDKSGEFTFKRPTSDMGIPIANTKRT 3357
 QY 644 SFPLATVADGRVYFALGAGGKRLRSKERYHDGKMTVFGNLGKARLVV-DGLRAOE 702
 DB 3358 DRIATVLEHGRVFTYDTGSGQVITKSDKSIDGRMHTIKVSRGKSAHLIVDNGSYSE 3417
 QY 703 GSLPGN-STISPREQVTLG---LPLSRKPKSL---POHSFVGCILDPOLNSKPLDPSAR 755
 DB 3418 GAANQMBDLIETPPFVYGVADLAGFARNLVVGRSQSGCIKOPKLNKSLDN-GKE 3476
 QY 756 FGVSPLCGSLKGIYFSGCGHYLLANSVSLPELKLTFSTRPSLTGVLHVGSQSG 815
 DB 3477 FGTEOCOSFS-BPGMYFGKDGAYAIQKDYEVGLTGLBVEKRPKMKNGILFSGVYL--E 3533
 QY 816 RLSTVMEAGKVTTSVSDAGSVTSITP--KQSLCDGQMSVAVSIKORIL 864
 DB 3534 YITVEFVNGSIKTIVSGSGBELMHPDIENQYCDGQMSFKISKRNLL 3584

RESULT 6

T37316
 probable laminin alpha chain - Caenorhabditis elegans
 C/Species: Caenorhabditis elegans
 C/Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
 C/Accession: T37316
 R/Joh, K.; Zhu, K.; Hedgecock, E.M.; Inoue, T.; Horii, K.
 submitted to the EMBL Data Library, August 1998
 A/Description: Laminin alpha chain gene in the nematode C. elegans.
 A/Reference number: Z21681
 A/Accession: T37316
 A/Status: preliminary; translated from GB/EMBL/DBJ
 A/Molecule type: DNA
 A/Residues: 1-3704 <JOH>
 A/Cross-references: UNIPROT:P91904; EMBL:AB016806; PIRN:BA32347.1
 A/Experimental source: strain N2
 C/Genetic: A:Gene: epi-1
 A:Map position: IV
 A/Intons: 66/1; 284/3; 563/1; 1187/3; 1248/3; 1300/1; 1460/1; 1623/3; 2361/3; 2988/3; 3
 C/Superfamily: Laminin alpha-1 chain; laminin G repeat homology; laminin-type EGF-like h

Query Match 12.9%; Score 579.5; DB 2; Length 3704;
 Best Local Similarity 23.7%; Pred. No. 4.9e-31;
 Matches 237; Conservative 155; Mismatches 388; Indels 215; Gaps 40;
 QY 3 FNGKSGVYRLPNLDELKGYTSLSLFQRPDLRENGSTDMFVYIGKDA----- 54
 DB 2696 FEKGSGLDINIPORVTRSAHADISFYFRT--QEHG-----IPLFGNEETAVGSRAP 2748
 QY 55 SKYIGMAVVDGQLTCVYNIGDEARVQIDQVLTSSQSAWMDRVFQGIYPAKLANTY 114
 DB 2749 TADYVALEIYEGPKTVDJADPAVAKD-----TPVNGLMRLRLIERI-----GKT 2797
 QY 115 KEATSNKPKAPAVYDLE---GGSSNTLNLNDPEDAVFYVGYGPPDEFLPSRLRPPYKGC 171
 DB 2798 VSTYTLKSNPVETAEKSSVAGNGKSVTLNNGQISRLFVGVFTSARISDILNRPDVG 2857
 QY 172 IEEDDLNENVLSTYNFTTNLNTTEVEPKRRKESDKY--FEGTGYA-----R 220
 DB 2858 IESLKHGEPIGLWNSREKNTVNGAKKPKITTDNADBLVSLDGGYTSYKPSHNPFR 2917
 QY 221 IIPQNPAPFNFIQTIGTITVDRLGLPAENQDPFISINIDGNLMVRYKLNSEPKPKGI 280

DB 2918 KATKISLSELT-----SPHGLFVVGKDKDPMALIELSDGVKSLVDLGS-----GV 2964
 QY 281 RDTI-----NGKHSILITIGKQKRMIVNNESSVRIEGERI-----EDFSF---YIIG 327
 DB 2965 GQWTESSNVNDGKMT--VSTVERKHVKIMIDGETEVLGVPCKDSMTSTFLYIG 3022
 QY 328 GPIAIRERFNISTPAFOGCMKRLKKTSGVRLND---TVGVKKCSBDMLKVRASPF-S 383
 DB 3023 GTPSGLSVATTI--VLRGCIKSVKLGSDNVLDLSEHAKGVRSQC--PLHSRTVYSFLS 3078
 QY 384 RGGQMSFTNLDPVSTDRFQLSFEGPOT--FQSGTLLNHQRTSLSLVTL-EDGHEILST 439
 DB 3079 DRTTASFNNAATERSED-VSGTFKFTKRSIRQSSSLFTVNDDEDSVLSINEDGILTVTS 3137
 QY 440 RD--SNIPFKSPGYMDGLHVSISTPSGLRLIDQVLRNRRLSPFSNAQOSL 497
 DB 3138 GEDIAITELIASP---DEKMHVSTIRKTYIIRIDADD-----SFSREVARKHA 3183
 QY 498 GGGH-----PEGCISNVLVORFSGPEVLDAKSTKQASLGCSL 539
 DB 3184 DQSNPDASFLSAFPGKSGSTFVGCIGDVTL-----NGKLDPAN-SEIKELSLNGCSL 3237
 QY 540 N-----KPPFLML 547
 DB 3238 SDDENISTTTTAAKPTDDSDVAVLPIDEEESTTTTTTTTTTEPTERPAEPADHGCSL 3297
 QY 548 -----FKSPKPKNGRI FVNVQIMODAPQATSTEAQDRSGCLP--PLATKASHR 586
 DB 3298 NAKRBSSTFEFEDHP-----ESVLSAPRDPGHCSPLEDPMVQFEDAE 3341
 QY 597 ALQFGDSPSHLLKLPOELLKRSQFSLDIQTSKGLVYAGTK-DSPLATVYADGRV 655
 DB 3342 GNFPSQOYSRIEYDILPEALDKSGEFTFKRPTSDMGIPIANTKRTDHIAVLEHGRV 3401
 QY 656 VFALGAGKRLRSKERYHDGKMTVFGNLGKARLVV-DGLRAQEGSLPGN-STISF 713
 DB 3402 VFTYDVGSGQVITKSDKSIDGRMHTIKVSRGKSAHLIVDNGSYSEGAANQMBDLIET 3461
 QY 714 REQVTLG---LPLSRKPKSL---POHSFVGCILDPOLNSKPLDPSARFVSGSLG 767
 DB 3462 QPFFYVGVADLAGFARNLVVGRSQSGCIKOPKLNKSLDN-CKEFTEOCOSFS-E 3519
 QY 768 KGIYFSGCGHYLLANSVSLPELKLTFSTRPSLTGVLHVGSQSGORSLVMEAGKVT 827
 DB 3520 PGMYFGKDGAYAIQKDYEVGLTGLBVEKRPKMKNGILFSGVYL--EITVEFVNGSIK 3577
 QY 828 TSVSDAGSVTSITP--KQSLCDGQMSVAVSIKORIL 864
 DB 3578 TTVSGSGGEBELMHPDIENQYCDGQMSFKISKRNLL 3616

RESULT 7

MMMSA
 laminin alpha-1 chain precursor - mouse
 N/Alternate names: laminin chain A1
 C/Species: Mus musculus (house mouse)
 C/Date: 30-Jun-1991 #sequence_revision 30-Jun-1991 #text_change 09-Jul-2004
 C/Accession: A31771; A30449; S00624; A30450; S08895; S02678; S01790; A30451; S14670
 J/Sasaki, M.; Kleinman, H.K.; Huber, H.; Deutzmann, R.; Yamada, Y.
 J. Biol. Chem. 263, 16536-16544, 1988
 A/Title: Laminin, a multidomain protein. The A chain has a unique globular domain and h
 A/Reference number: A31771; M0ID:89034134; EMD:3182802
 A/Accession: A31771
 A/Molecule type: mRNA
 A/Residues: 1-3084 <SAS>
 A/Cross-references: UNIPROT:P91917; EMBL:J04064; NID:G309419; PIRN:AAA9410.1; PIR:G309
 A/Accession: A30449
 A/Molecule type: protein
 A/Residues: 183-195;570-571, 'A', 573-586;596-612, 'X', 614-617, 'EMK', 630-646;1217-1222, 'YF
 2486;2624-2639;2818-2843;3009-3033, 'V', 3035 <SAS>
 R/Hartl, L.; Oberbaumer, I.; Deutzmann, R.
 Eur. J. Biochem. 173, 629-635, 1988
 A/Title: The N terminus of laminin A chain is homologous to the B chains.

A:Reference number: S00624; MUID:88225080; PMID:3267223
A:Accession: S00624
A:Molecule type: mRNA
A:Residues: 1-208, 'T', 210-334 <HAR>
A:Cross-references: EMBL:X07737; NID:952857; PIDN:CAA30561.1; PID:952858
A:Accession: A30450
A:Molecule type: protein
A:Residues: 311-335, 'N', 337-339, 630-642, 'D', 644, 692-734, 737-748, 'X', 750-760, 'G', 762-763, 765-766, 768-769, 771-772, 774-775, 777-778, 780-781, 783-784, 786-787, 789-790, 792-793, 795-796, 798-799, 801-802, 804-805, 807-808, 810-811, 813-814, 816-817, 819-820, 822-823, 825-826, 828-829, 831-832, 834-835, 837-838, 840-841, 843-844, 846-847, 849-850, 852-853, 855-856, 858-859, 861-862, 864-865, 867-868, 870-871, 873-874, 876-877, 879-880, 882-883, 885-886, 888-889, 891-892, 894-895, 897-898, 900-901, 903-904, 906-907, 909-910, 912-913, 915-916, 918-919, 921-922, 924-925, 927-928, 930-931, 933-934, 936-937, 939-940, 942-943, 945-946, 948-949, 951-952, 954-955, 957-958, 960-961, 963-964, 966-967, 969-970, 972-973, 975-976, 978-979, 981-982, 984-985, 987-988, 990-991, 993-994, 996-997, 999-1000, 1002-1003, 1005-1006, 1008-1009, 1011-1012, 1014-1015, 1017-1018, 1020-1021, 1023-1024, 1026-1027, 1029-1030, 1032-1033, 1035-1036, 1038-1039, 1041-1042, 1044-1045, 1047-1048, 1050-1051, 1053-1054, 1056-1057, 1059-1060, 1062-1063, 1065-1066, 1068-1069, 1071-1072, 1074-1075, 1077-1078, 1080-1081, 1083-1084, 1086-1087, 1089-1090, 1092-1093, 1095-1096, 1098-1099, 1101-1102, 1104-1105, 1107-1108, 1110-1111, 1113-1114, 1116-1117, 1119-1120, 1122-1123, 1125-1126, 1128-1129, 1131-1132, 1134-1135, 1137-1138, 1140-1141, 1143-1144, 1146-1147, 1149-1150, 1152-1153, 1155-1156, 1158-1159, 1161-1162, 1164-1165, 1167-1168, 1170-1171, 1173-1174, 1176-1177, 1179-1180, 1182-1183, 1185-1186, 1188-1189, 1191-1192, 1194-1195, 1197-1198, 1200-1201, 1203-1204, 1206-1207, 1209-1210, 1212-1213, 1215-1216, 1218-1219, 1221-1222, 1224-1225, 1227-1228, 1230-1231, 1233-1234, 1236-1237, 1239-1240, 1242-1243, 1245-1246, 1248-1249, 1251-1252, 1254-1255, 1257-1258, 1260-1261, 1263-1264, 1266-1267, 1269-1270, 1272-1273, 1275-1276, 1278-1279, 1281-1282, 1284-1285, 1287-1288, 1290-1291, 1293-1294, 1296-1297, 1299-1300, 1302-1303, 1305-1306, 1308-1309, 1311-1312, 1314-1315, 1317-1318, 1320-1321, 1323-1324, 1326-1327, 1329-1330, 1332-1333, 1335-1336, 1338-1339, 1341-1342, 1344-1345, 1347-1348, 1350-1351, 1353-1354, 1356-1357, 1359-1360, 1362-1363, 1365-1366, 1368-1369, 1371-1372, 1374-1375, 1377-1378, 1380-1381, 1383-1384, 1386-1387, 1389-1390, 1392-1393, 1395-1396, 1398-1399, 1401-1402, 1404-1405, 1407-1408, 1410-1411, 1413-1414, 1416-1417, 1419-1420, 1422-1423, 1424-1425, 1427-1428, 1430-1431, 1433-1434, 1436-1437, 1439-1440, 1442-1443, 1445-1446, 1448-1449, 1451-1452, 1454-1455, 1457-1458, 1460-1461, 1463-1464, 1466-1467, 1469-1470, 1472-1473, 1475-1476, 1478-1479, 1481-1482, 1484-1485, 1487-1488, 1490-1491, 1493-1494, 1496-1497, 1499-1500, 1502-1503, 1505-1506, 1508-1509, 1511-1512, 1514-1515, 1517-1518, 1520-1521, 1523-1524, 1526-1527, 1529-1530, 1532-1533, 1535-1536, 1538-1539, 1541-1542, 1544-1545, 1547-1548, 1550-1551, 1553-1554, 1556-1557, 1559-1560, 1562-1563, 1565-1566, 1568-1569, 1571-1572, 1574-1575, 1577-1578, 1580-1581, 1583-1584, 1586-1587, 1589-1590, 1592-1593, 1595-1596, 1598-1599, 1601-1602, 1604-1605, 1607-1608, 1610-1611, 1613-1614, 1616-1617, 1619-1620, 1622-1623, 1625-1626, 1628-1629, 1631-1632, 1634-1635, 1637-1638, 1640-1641, 1643-1644, 1646-1647, 1649-1650, 1652-1653, 1655-1656, 1658-1659, 1661-1662, 1664-1665, 1667-1668, 1670-1671, 1673-1674, 1676-1677, 1679-1680, 1682-1683, 1685-1686, 1688-1689, 1691-1692, 1694-1695, 1697-1698, 1700-1701, 1703-1704, 1706-1707, 1709-1710, 1712-1713, 1715-1716, 1718-1719, 1721-1722, 1724-1725, 1727-1728, 1730-1731, 1733-1734, 1736-1737, 1739-1740, 1742-1743, 1745-1746, 1748-1749, 1751-1752, 1754-1755, 1757-1758, 1760-1761, 1763-1764, 1766-1767, 1769-1770, 1772-1773, 1775-1776, 1778-1779, 1781-1782, 1784-1785, 1787-1788, 1790-1791, 1793-1794, 1796-1797, 1799-1800, 1802-1803, 1805-1806, 1808-1809, 1811-1812, 1814-1815, 1817-1818, 1820-1821, 1823-1824, 1826-1827, 1829-1830, 1832-1833, 1835-1836, 1838-1839, 1841-1842, 1844-1845, 1847-1848, 1850-1851, 1852-1853, 185

Db 2887 AVA-QEGTVPDGSGYALVKEGVKQSDVNTLLEFRTSSQNGVLLGISTAKVDALIGELV 2945

QY 823 AGKVTTSVSDAGSAGSVSTIPKOS--LCDQGMHSAVAVSIKORI 863

Db 2946 DGRVLPFVNNAGRIPTAPEKTAIVLCDEKWHLLQANKSKHRI 2989

RESULT 10

553868

laminin alpha-2 chain precursor - mouse

N/Alternate names: laminin M chain; merosin heavy chain

C/Species: Mus musculus (house mouse)

C/Date: 21-Aug-1998 #sequence revision 21-Aug-1998 #text_change 09-Jul-2004

C/Accession: I49077; S50829; I48655; S31576; S53866

R/Bermer, S.M.; Utani, A.; Sugiyama, S.; Doi, T.; Polistina, C.; Yamada, Y.

Matrix Biol. 14, 447-455, 1995

A/Title: Cloning and expression of laminin alpha 2 chain (M-chain) in the mouse.

A/Reference number: I49077; MUID:95316259; PMID:7795883

A/Accession: I49077

A/Status: preliminary; translated from GB/EMBL/DBD

A/Molecule type: mRNA

A/Residues: 1-3106 <RES>

A/Cross-references: UNIPROT:Q60675; EMBL:U12147; NID:9699109; PIDN:AAC52165.1; PID:96991

R/Xu, H.; Wu, X.R.; Wewer, U.M.; Engvall, E.

Nature Genet. 8, 297-302, 1994

A/Title: Murine muscular dystrophy caused by a mutation in the laminin alpha-2 (lama2) g

A/Reference number: S50829; MUID:95179178; PMID:7874173

A/Accession: S50829

A/Status: preliminary

A/Molecule type: mRNA

A/Residues: 64-281 <XUH>

A/Cross-references: GB:S75315; NID:9683929; PIDN:AAB3573.1; PID:9683930

R/Chang, A.C.; Madworth, S.; Colligan, J.E.

J. Immunol. 151, 1789-1801, 1993

A/Title: Expression of merosin in the thymus and its interaction with thymocytes.

A/Reference number: I48655; MUID:93346725; PMID:8345183

A/Accession: I48655

A/Status: preliminary; translated from GB/EMBL/DBD

A/Molecule type: mRNA

A/Residues: 2162-2204, 'D', 2206-2213, 'EY', 2216-2279 <RE2>

A/Cross-references: EMBL:X69869; NID:953055; PIDN:CAA9502.1; PID:953056

C/Function: laminins are trimers of an alpha-type, a beta-type, and a gamma-type laminin

C/Description: interact with cells and with other basement membrane proteins to promote

C/Superfamily: laminin alpha-1 chain; laminin G repeat homology; laminin-type EGF-like h

C/Keywords: basement membrane; calcium binding; coiled coil; extracellular matrix; glyco

F/1-22/Domain: signal sequence #status predicted <SIG>

F/23-3106/Product: laminin alpha-2 chain #status predicted <KAT>

F/283-337/Domain: laminin-type EGF-like homology <LE01>

F/340-407/Domain: laminin-type EGF-like homology <LE02>

F/410-462/Domain: laminin-type EGF-like homology <LE03>

F/465-511/Domain: laminin-type EGF-like homology <LE04>

F/514-523/Domain: laminin-type EGF-like homology #status atypical <LE05>

F/720-750/Domain: laminin-type EGF-like homology <LE06>

F/753-800/Domain: laminin-type EGF-like homology <LE07>

F/803-858/Domain: laminin-type EGF-like homology <LE08>

F/861-911/Domain: laminin-type EGF-like homology <LE09>

F/914-960/Domain: laminin-type EGF-like homology <LE10>

F/963-1007/Domain: laminin-type EGF-like homology <LE11>

F/1010-1053/Domain: laminin-type EGF-like homology <LE12>

F/1056-1099/Domain: laminin-type EGF-like homology <LE13>

F/1102-1121/Domain: laminin-type EGF-like homology #status atypical <LE14>

F/1123-1159/Domain: laminin-type EGF-like homology #status atypical <LE15>

F/1162-1171/Domain: laminin-type EGF-like homology #status atypical <LE16>

F/1376-1413/Domain: laminin-type EGF-like homology #status atypical <LE17>

F/1416-1463/Domain: laminin-type EGF-like homology <LE18>

F/1465-1520/Domain: laminin-type EGF-like homology <LE19>

F/1523-1567/Domain: laminin-type EGF-like homology <LE20>

F/2166-2327/Domain: laminin G repeat homology <LG1>

F/2260-2520/Domain: laminin G repeat homology <LG2>

F/2546-2709/Domain: laminin G repeat homology <LG3>

F/2785-2933/Domain: laminin G repeat homology <LG4>

F/2960-3106/Domain: laminin G repeat homology <LG5>

Query Match 11.5%; Score 516.5; DB 1; Length 3106;

Best Local Similarity 23.2%; Pred. No. 9.1e-27;

Matches 220; Conservative 169; Mismatches 375; Indels 183; Gaps 46;

32 RPDIRENG-----GTEDMFVYLGKDKASK--DYIGMAVVDGQLCYVNLGDREA 79

Db 2155 RPEIKKGSYNNIVVHKVAVADNLFLYLG---SAKPIDLAIEBKGVKSVFLVIGSGVG 2211

QY 80 EVOIDOVLTSESQEAVMDRVKFORIYQPAKNTYTBASNKRA---PAVYDLEGSSN 136

Db 2212 RVGPPDLTID---DSYWRIRIEASRGKMSISV---RALDGKASWVSTYHSVSPGY 2264

QY 137 TLNLNDEDAVFYGVGPPDFELPSRLRPPEYGCIELDINENSLVNFYKTPMLNT 196

Db 2265 TILDVD-ANMLFVVGJTGKIKADAVRYTFTGCMGETYFDKXPIGLMNFRE---KSG 2319

QY 197 EYPCRRRKRKESDKN---YEGTGVARIPTOPAPPNFIQTI---QTVDRGLLFFAE 249

Db 2320 DCKGCTVSPQVBSBGTIQFDGEGYLV-SRPTRWYFN-ISTVMFRTFSSALMYLA 2377

QY 250 MOD-NFISLNIEDGNLWRYKLNSEPPKKGIRDTI---NDGKHSLITIGLQKR 302

Db 2378 TRDLKDFMSVSLSDGHVKSVDLGS-----GMTSVSNQNHNDGKWK---FTLSRIQK 2429

QY 303 MWINV-----NRSVRIRIEIFDP-----STYLIGIP---IAIRRFNISTPAFQ 345

Db 2430 ANISVIDISNQEENAVATSSGNNFGDLKADKXITFGSLPTLNLSMKRPEVNVKYS 2489

QY 346 GCKKNT---KTSGVRLNDVTGVTKKCSSEDMKLVRTASPRGG--QMSFTNLDVSTDR 400

Db 2490 GCLKNDIEIKSTPNILSSPDYGVTKCS--LENNVTSVPPKGFELAAVSDVGI--- 2544

QY 401 FQSPFGQTFQPSGTLI-----NHQRTSSLLVTLSDG---HIELSTRD-S 442

Db 2545 -EINLSFTSNBSGIIILGSGGTLTPRRRKRQTOQYVAIFPKNGLLEVHLSGRTMR 2603

QY 443 NIPFSPGYNGMLAHNSVISDTSGRLILDDOYLRRQRPLPSNMQ-QSLRLAGG- 500

Db 2604 KIVIKKEPNLFHGRHSVNV-BRTGIFVQIDEBRHHQNLTEOPIEVKLLFVGAP 2662

QY 501 -----HREGISNVLQRFSPSEVDLASKSTKQDASJGCSLNPPLMF 548

Db 2663 PERQSPRLRIPAFQGCWMLVINSIP-----NDPAQPLAFKADIGKCTYQF----- 2711

QY 549 KSPKRFNKGIFVNNQMDAPATRSTEAODGRCLP-PLNTKA-----SHRAL- 598

Db 2712 ---REBSAFAVAIVQ--PQSVPT-----PAFPFVPTWVHGPCVASEPALLT 2757

QY 599 ---QFGDSPSHLLKLPQELKPRQOFSLDIOTTSBKGLVFTAG--TKDSFLALYADG 653

Db 2758 GSKQFGISRSNHAIVDDTKVKNRLLTLELVETRESGLLFYMGRLNHADFVGOURLNG 2817

QY 654 RVVFLAGAGGKRLRLSKERYHDKMHTVYFGNLGGKARLVVDGLRAQBSGLGNSTSP 713

Db 2818 PPFSTYDLSGSGTRTMIPTKINDQMKIKIVYVKQBGILYVDASQ-----TISP 2869

QY 714 REGVYL-----GLPSRKPKSL--PQHSFVGLCRDQLNSKP--LDSPARFGVSP 760

Db 2870 KKADILLDVGGILVVGGLPIVYTRRIRIGPVYISLDGCCRNLHMQAPVDLDQPTSSFVGT 2929

QY 761 CLGGSLEKGIYFQGGGAVTIANSVSLGPELKTFTSRPSLSLGVLIHVSQSGQRLSVY 820

Db 2930 CFPANA-BSGTYF-DGTFGFAVAGVFVGLDLVAFEFRTTRPGVLLGISQKDKGIB 2987

QY 821 MEAGKVTTSVSDAGSAGSVSTIPKOS--SLCDQGMHSAVAVSIKORI 863

Db 2988 MIDKMLFAYDNGA-GRFTAIYDAEIPGHKCNQWYVTKAKIKRNL 3033

RESULT 11

T43291

laminin alpha chain - Caenorhabditis elegans

Db 925 IADPVTF-----KTKSSYVALATLQAYTS 949
 Qy 607 -HLLKLKPOLKLRPSQSLDIOTSPKGLVFF-AGTKDSFLALYVADG--RVVPALGAG 662
 Db 950 MHLFFQ-----FKTSLDGLILYNSGGDNFIVELVKGLHYVFDLGGNG 994
 Qy 663 GKRLRLSKERHYDGKMTVFPGLNGKARLVVDGLPAQSGSLPGNSTISPREOVLGLP 722
 Db 995 ANLIKSSNKPLNDQNHVMISRDTSNLTATVKIDTKITQTITAGARNLKLKSDLYIGV 1054
 Qy 723 LSRKPSLP-----QHSFVGCCLDPOLNSKPLDSPARFVSPCL--GGSLEKRG----- 769
 Db 1055 AKETVYSLPFLVNAKEGFQCCLASVDLNGRLPDL-----ISDALFCNGQIERGCEGPEST 1108
 Qy 770 -----TYPSQGGGHVIL----- 781
 Db 1109 TCOEDSGSNQGVCLQOWDGISCDOSMTSPFSGPLCNDPGTTYIFPSKGGQITTYKMPNDRP 1168
 Qy 782 ---ANSVSLGPELKLTPSIRPSRLTGYLHVHVSQS--GQRLSYVMEAGKVTTSVSDAGG 836
 Db 1169 STRADRLAIG-----FSTVQKE--AVLVKVDSSSGLDYLBHLHIHQKI--GVKENVGT 1218
 Qy 837 SVTSITPKOSLC-DGQWHSV 855
 Db 1219 DDIAIESNAIINDGKHVV 1238

RESULT 13

A40228
 neurexin I-alpha precursor - rat
 C/Species: Rattus norvegicus (Norway rat)
 C/Date: 21-Jul-1995 #sequence_revision 21-Jul-1995 #text_change 09-Jul-2004
 C/Accession: A40228; S27884
 R/Unkaryov, Y.A.; Petrenko, A.G.; Geppert, M.; Suedhof, T.C.
 Science 257, 50-56, 1992
 A/Title: Neurexins: synaptic cell surface proteins related to the alpha-latrotoxin recep
 A/Reference number: A40228; MUID:92320296; PMID:1621094
 A/Accession: A40228
 A/Status: preliminary; nucleic acid sequence not shown
 A/Molecule type: mRNA
 A/Residues: 1-1507 <USH>
 A/Cross-references: UNIPROT:Q63372; GB:M96374; NID:G205710; PID:AAA41704.1; PID:G205711
 C/Superfamily: neurexin; EGF homology
 C/Keywords: alternative splicing; transmembrane protein
 F:1-30/Domain: signal sequence #status predicted <SIG>
 F:31-1507/Product: neurexin I-alpha #status predicted <MAP>
 F:680-712/Domain: EGF homology <EGF>
 F:1087-1119/Domain: EGF homology <EGF1>

Query Match 7.1%; Score 320; DB 2; Length 1507;
 Best Local Similarity 19.5%; Pred. No. 1.4e-13;
 Matches 201; Conservative 134; Mismatches 354; Indels 344; Gaps 45;

Qy 35 LRENGGTEDMFVNYLGNKASKOYIGMAVVDGQLTCVYNGDRRAEYQIDQVLTSESSQE 94
 Db 315 LQNRG-----LMATGK---SADVNLALKNGANSLVINGSGAFALVVEPV--NGKFN 364
 Qy 95 AAVDRVFEQR-IYQPAKANTYKTSNKPAPAVYDLEGSSNTLNLADPEDAVFYGY 153
 Db 365 NAMHDVAVTNLNLQSHSIGAMWTIS--VDGILTTGYTQEDYTMLGSDD-FFYVGS 419
 Qy 154 PPDEFLPSRLRPFPYKCCILDLNENVLNFKTTFNLTATEVEPCRRKRESDKNYF 213
 Db 420 PSTADLPESVSNFMGCLK-----EYVYKKNVDVRLLELSRLAKQGDPMK 465
 Qy 214 EGT-----GYARIPTQPNAPFPNFIQTITQTVDRGLTFPAENOD- 252
 Db 466 HGVAFAKCEVAVTADPTTETPESFISLPKMAKKTGISFPDRITTPNGLIFSHKPR 525
 Qy 253 -----NFIISLNEEDGNLWRYKLNSPPEKGIKRTINDGKHSLITIGKL 299
 Db 526 HOKDAKHPQMIKVDFAIEMLDGHLVLLDMGSGTIIKALKQKKNVNDG----- 574

(y 300 OKRMWNV-----NERSVRI-----EGEILDF-STYLLGIGIPIAIRERNIST 341
 Db 575 ----WYHVDFOQDGRGRTISVNTLRTPTYPAPGESEILDDDELHYLGLP---ENKAGIVF 627
 Qy 342 P-----AFQGMKRL-----KTSGVVRNDTVGVTKKSEB----- 373
 Db 628 PTEVMTALNVGVGCIKRLFDIGQSKDIRQMAEIOSTGAVKSCSRETFAPCLSNPCKN 687
 Qy 374 -----WK-----LVRTAS-----PBGQGMFTNLDV---STDFQSLFPG 407
 Db 688 NGKCRDGMWRYVCDSCGTGLGSCREAVTSLYDSM-FMKQLPVWHTTEADVSLRP 746
 Qy 408 QTFQPGSTLLNHOYTS--SLVTLLEDGHIESTRDSNPI-----FKSPQTYA-----D 465
 Db 747 RSQRAVGIIMATTSRSDTLRLHLDAGKVLTVNIDCIRINSSKGPETLPAGYNAD 806
 Qy 456 GLAHVYSIDTSGLRLIDDOVLARNQRLPSPFNAQSLRLGGH---FEECISNVLV 511
 Db 807 NEMHTVAVVRGKSLTVDDQAMTQ-----MAGDTRLFEFNIETGILT 853
 Qy 512 QR-FSQSFE-----VLDLASKSTKQDASLGCSLN-KPPFLMLFKSPKR 553
 Db 854 ERYVLSVSPSNFIGHLQSLTFNGMAYIDLC---KNGDIDYCELNARFGFRNIADPV 908
 Qy 554 FNGKRIFNQNLQMDAPQATRSTEAMQDGRSLPPLNTKASHRALQFDSPTS-HLLKL 612
 Db 909 F-----KTKSSYVALATLQAYTSMHLFFQ- 932
 Qy 613 POLKLRPSQSLDIOTSPKGLVFF-AGTKDSFLALYVADG--RVVPALGAGKRLRL 669
 Db 933 -----FKTSLDGLILYNSGGDNFIVELVKGLHYVFDLGGNANLIKGS 978
 Qy 670 SKERHYDGKMTVFPGLNGKARLVVDGLPAQSGSLPGNSTISPREOVLGLP 729
 Db 979 SNKPLNDQNHVMISRDTSNLTATVKIDTKITQTITAGARNLKLKSDLYIGVAKETVYS 1038
 Qy 730 LP-----QHSFVGCCLDPOLNSKPLDSPARFVSPCL--GGSLEKRG----- 769
 Db 1039 LPELVNAKEGFQCCLASVDLNGRLPDL-----ISDALFCNGQIERGCEGPESTTCQEDSC 1092
 Qy 770 -----TYPSQGGGHV-----ILANSV 785
 Db 1093 SNGGVCLQOWDGRSCDCSMTSPFSGPLCNDPGTTYIFPSKGGQITTYKMPNDRSTADRL 1152
 Qy 786 SLGPELKLTPSIRPSRLTGYLHVHVSQS--GQRLSYVMEAGKVTTSVSDAGGSVTSITP 843
 Db 1153 AIG-----FSTVQKE--AVLVKVDSSSGLDYLBHLHIHQKI--GVKENVGTDDIAIEB 1202
 Qy 844 KOSLC-DGQWHSV 855
 Db 1203 SMAINDGKHVV 1215

RESULT 14

A48216
 neurexin III-alpha secreted type 1 precursor - rat
 C/Species: Rattus norvegicus (Norway rat)
 C/Date: 26-May-1994 #sequence_revision 26-May-1994 #text_change 09-Dec-2002
 C/Accession: A48216; B48216
 R/Unkaryov, Y.A.; Suedhof, T.C.
 Proc. Natl. Acad. Sci. U.S.A. 90, 6410-6414, 1993
 A/Title: Neurexin IIIalpha: extensive alternative splicing generates membrane-bound and
 A/Reference number: A48216; MUID:93342001; PMID:8341647
 A/Accession: A48216
 A/Status: preliminary
 A/Molecule type: mRNA
 A/Residues: 1-1438 <USH>
 A/Cross-references: GB:L14851
 A/Accession: B48216
 A/Status: preliminary
 A/Molecule type: mRNA
 A/Residues: 1-1368, 1372-1438 <US2>
 A/Cross-references: GB:L14851

C/Genetics:
A:introns: 1372/1
C:superfamily: neuexin; EGF homology
C:keyword: alternative splicing; brain; cell surface component; duplication; extracellular
F:1-27/Domain: signal sequence #status predicted <SIG>
F:202-234/Domain: EGF homology <EGF>
F:651-683/Domain: EGF homology <EGF1>

Query Match 6.7%; Score 301.5; DB 2; Length 1438;
Best Local Similarity 19.8%; Pred. No. 2, 6e-12;
Matches 204; Conservative 135; Mismatches 342; Indels 349; Gaps 49;

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36 RENGTEDEMFVNLGNKASDQYIGMAVVDGQLTCVYNIAD----- 76
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   |||
295 ORNG-----LIIHTGK---SADYVNLALKDGAIVSLVINGSGAFPAIVEPVNGKFNNDAM 346
   |||
   |||
   |||
77 -----REAEVQIDQVLTSESGEAVMDRVKFORIYQFALNTKATSNKPRAPAV 127
   |||
   |||
   |||
347 HDVKVTRNLKQVTVISVDGILTT-----GYQE----- 374
   |||
   |||
   |||
128 YDEGGSSNTLNLDEPDVAVFYGYPPDFELPSRLFPYKGCIE----- 173
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   |||
   |||
375 -----DYTMIG---SDDFYVGGSPSTADLPGSPVSNMFMCKLGEVYKXNDIRLELS 424
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174 -LDDLNEVNLSTYN---FKTFNLNTEVEPCRRRKEESDKYFEGTGARIPQPNAPF 229
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   |||
425 RLARIIDGTMKIKYGEVVFKE---NVATLDPI-----NFETPEAYISLPKNTKEM 472
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   |||
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230 PNFIOGTIQTVDRLGLFFA-----ENOD-----NFISLNTEDGNLMVRYKLSBPP 275
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   |||
473 GSISPDFTTBENGILFTHGKPOEKRDVRSQKNTKVDFAVALLDGNLYLLDWSGTT 532
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   |||
   |||
276 KEGKIRDTINDGKHSILITIGKLOKRMIVNESVRI---EGEIPDF-STYLLGGLP 330
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   |||
   |||
533 KYKATQKANDGEWYH---VDIQRDGRSGTISVNSRRPTFASGESILDEGMVYLGGLP 590
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   |||
   |||
331 IAIRESFNISTP-----AFQGMKNL-----KTSGVVRLNDVTGVTKCS--- 371
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   |||
591 ---ENRAGILFTELTMTAMLNLYGVGICIRDLFIDGRSKNIRQLAEQNAAGVSCSRMS 647
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   |||
   |||
372 -----EDMK-----LVRTAS-FSRGGMSFTNLDPV--- 396
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648 AKCCDSYPCKNNAVCCKGMNRFICDCTGTGYWGRTERESILSYDSGM-YMKVIMPMVM 706
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397 STDRLPSFGFOTFQPSGTLNHTQRTS--SLVLTEDGHIESTDSNPI---FKSP 450
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707 HTEAEVSVFRMSQRAVGLLVATTSRDSADTLALBEDGRVYKMLWDCIRICNSKGP 766
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451 GTYM-----DGLLHVSVISDTSGLRLLIDQV---LRRNQRLPSFSNAQOQLRLG 499
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767 ETLVAGQKLNDEMHTVVRVVRGSKSLKLVDDOVAEGTVMVGDHTRL-EFNNIRGTMTKE 825
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500 -----GHFEGCISNVLYQFSQSPVULDLASKYTKQASLGGCSLKNPPLMLP 548
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826 RYTSVPSSTFGLHQLSMFNGLL-----YIDLC-----KXGDDIDYCEL----- 863
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549 KSEPRFNKGRIFVNVNOLMDAPQATRSTEAMQDSRCLPPLNTKASHRALOFQDSPTS-H 607
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864 -----KAR-FELRNLIADP-----VFRTKSSYLTIATIGQATTSNG 898
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608 LLILKLPOELIKPSSQPSLDIQTTSPYG-LVFVAGTKDSFIALLYADGRV--VFALGAGSK 664
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899 LFPQ-----FKTTSADGFIIFNSGDGNDFAIVELVNGYIHYVDDLNGNPN 943
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   |||
665 KLABRKERYHDKMHTVVPGLNGKARLVVDGLRABOGSLPENSITISPREQYLL-GLP- 722
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   |||
   |||
944 VINGNDRPLNDQGMHVVITRDNSTHSLKVDTKVTVYINGAKMLDLKGDLYMAGLQ 1003
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DB 1063 ---ANQGVQWQWEGFTCCSMTSYSQNCNDPGATYIFKSGGLILTYTPANRPSYRS 1119
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DB 1120 DRLAVGFSFTYWD--GILVIRIDSAPGLDFQLHTBOGK--GVFNIGTVDISTKERT 1175
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   |||
QY 847 -LCDQGMHSV 855
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DB 1176 PNDGKHVV 1185
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RESULT 15

B48218
neuexin III-alpha membrane-bound type 3 precursor - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 26-May-1994 #sequence_revision 26-May-1994 #text_change 09-Dec-2002
C:Accession: B48218; C48218
R:Ushkaryov, Y.A.; Suedhof, T.C.
Proc. Natl. Acad. Sci. U.S.A. 90, 6410-6414, 1993
A:Title: Neuexin IIIalpha: extensive alternative splicing generates membrane-bound and
A:Reference number: A48216; PMID:93342001; PMID:8341647
A:Accession: B48218
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-1471 <US>
A:Cross-references: GB:L14851
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-1368, 1372-1471 <US2>
A:Cross-references: GB:L14851
C/Genetics:
A:introns: 1372/1
C:superfamily: neuexin; EGF homology
C:keyword: alternative splicing; brain; cell surface component; duplication; receptor;
F:1-27/Domain: signal sequence #status predicted <SIG>
F:202-234/Domain: EGF homology <EGF>
F:651-683/Domain: EGF homology <EGF1>

Query Match 6.7%; Score 301.5; DB 2; Length 1471;
Best Local Similarity 19.8%; Pred. No. 2, 7e-12;
Matches 204; Conservative 135; Mismatches 342; Indels 349; Gaps 49;

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36 RENGTEDEMFVNLGNKASDQYIGMAVVDGQLTCVYNIAD----- 76
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295 ORNG-----LIIHTGK---SADYVNLALKDGAIVSLVINGSGAFPAIVEPVNGKFNNDAM 346
   |||
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   |||
77 -----REAEVQIDQVLTSESGEAVMDRVKFORIYQFALNTKATSNKPRAPAV 127
   |||
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   |||
347 HDVKVTRNLKQVTVISVDGILTT-----GYQE----- 374
   |||
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128 YDEGGSSNTLNLDEPDVAVFYGYPPDFELPSRLFPYKGCIE----- 173
   |||
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375 -----DYTMIG---SDDFYVGGSPSTADLPGSPVSNMFMCKLGEVYKXNDIRLELS 424
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174 -LDDLNEVNLSTYN---FKTFNLNTEVEPCRRRKEESDKYFEGTGARIPQPNAPF 229
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425 RLARIIDGTMKIKYGEVVFKE---NVATLDPI-----NFETPEAYISLPKNTKEM 472
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276 KEGKIRDTINDGKHSILITIGKLOKRMIVNESVRI---EGEIPDF-STYLLGGLP 330
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533 KYKATQKANDGEWYH---VDIQRDGRSGTISVNSRRPTFASGESILDEGMVYLGGLP 590
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331 IAIRESFNISTP-----AFQGMKNL-----KTSGVVRLNDVTGVTKCS--- 371
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591 ---ENRAGILFTELTMTAMLNLYGVGICIRDLFIDGRSKNIRQLAEQNAAGVSCSRMS 647
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372 -----EDMK-----LVRTAS-FSRGGMSFTNLDPV--- 396
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Db 648 ARQCDSPCKNNNAVCXDGMRFICDCTGTYWGRTCEREASISYDSM-YMKVIMPMW 706
QY 397 STDRLPSFGQTFQPSGTLNHTQRTS--SLVLTEDGHIELSTRDSNIPi---FKSP 450
Db 707 HTAEADVSEFRMGQRAYGLVATTSRDSADTLRLRLDGRVKLMVNDICIRINCSKGP 766
QY 451 GTM-----DGLHVSYSIDTSGRLIDDOY-----LRNRQLPSFSNAOQSLRIGG 499
Db 767 ETLVYAGOKLNDNEMHTVVRVRKSKSLKLVDDVABGTMGDHTRL-EFNHIEGTINTEK 825
QY 500 -----GHFEGCISNVLVORFQSPPEVLDLASKSTKQASLQCSLNKPPFLMLF 548
Db 826 RYISVVPSSFTGHLQSLMFGLL-----YIDL-----KNGDIDYCEL----- 863
QY 549 KSPKRFNKGRIENVNOLMODAPQATRSTEAMQDGRSCLPLPLNTKASHRALQFGDSPTS-H 607
Db 864 -----KAR-FGLRNIADP-----VFKTSSYLTLATLQAYTSMH 898
QY 608 LLLKLQELIKPRSQPSLDIQTSPIKG-LVFYAGTKDSFLALYVADGRV--VPALGAGK 664
Db 899 LFPQ-----FKTTSADGFILFNSGDGNDFLAVELVKGYIHVFDLGNGPN 943
QY 665 KLRLSKERYHDKGKHTVVFGLNGGKARLVVDGLRAQEGSLPGNSTISPREOYVL-GLP- 722
Db 944 VIKGNSDRPLANDQMHNVITRDNSTHSLKVDTKVTVYVINGAKNLDLKGDIYMAGLAQ 1003
QY 723 --LSRRPKSL-PQHSFVGCRLRDPQLNSKPLD-----SPSARFQVSPCL 762
Db 1004 GMYSNLPLVASRDGFGCLASVDLNGRLPDLINDALHRSQIDRCCEGSPSTCQEDSC- 1062
QY 763 GGSLEKGI-----YFSQGGHVLANSVSLGP----- 789
Db 1063 ---ANQGVCMQWEGFTCDCSMTSYSNGQCNDPRATYIFKSGGLIITYWPANDRPSTRS 1119
QY 790 -ELKLTFSIRPSLSTVLIHVSGSOS--GQRLSVYMEAGKYTTSVSDAGSVTSITPKOS 846
Db 1120 DRLAVGFSTTVKD--GILVRIDAPGLGDFLQHLIEQKI--GVFNIGTVDISIKEERT 1175
QY 847 -LCDGQMHSHV 855
Db 1176 PVNDGKYHV 1185
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Search completed: February 22, 2005, 08:19:35
Job time : 29.1073 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: February 22, 2005, 08:07:29 ; Search time 146.522 Seconds
(without alignments)
3026.590 Million cell updates/sec

Title: US-10-817-423-2

Perfect score: 4491

Sequence: 1 MEFNGKSGVVRLLPNLEDLKGYTSLFLQRPDLRNGGTFDMFVYLGAKQASKDYIG 60

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : uniprot_03:*

1: uniprot_sprot:*

2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Query length	DB ID	Description
1	4491	100.0	1725	2 P70570	P70570 ratu
2	4043	90.0	3333	1 LMA3_MOUSE	Q61789 mus musculu
3	3562.5	79.3	1668	2 Q6VU69	Q6VU69 homo sapien
4	3562.5	79.3	3327	2 Q6VU67	Q6VU67 homo sapien
5	3562.5	79.3	3333	2 Q6VU68	Q6VU68 homo sapien
6	3560.5	79.3	1713	1 LMA3_HUMAN	Q16787 homo sapien
7	3560.5	79.3	1806	2 Q96TGO	Q96TGO homo sapien
8	3560.5	79.3	3333	2 Q76E14	Q76E14 homo sapien
9	3331	74.2	1725	2 Q867A1	Q867A1 canis fami
10	1190	26.5	1816	1 LMA4_HUMAN	Q16363 homo sapien
11	1185	26.4	1816	2 Q91V70	Q91V70 mus musculu
12	1185	26.4	1816	1 LMA4_MOUSE	P97927 mus musculu
13	1042.5	23.2	3695	1 LMA5_HUMAN	Q15230 homo sapien
14	1042.5	23.2	3695	2 Q8TDF8	Q8TDF8 homo sapien
15	950	21.1	1524	2 Q6ZQA1	Q6ZQA1 mus musculu
16	948	21.1	3718	1 LMA5_MOUSE	Q61001 mus musculu
17	636.5	14.2	3712	1 LMA5_MOUSE	Q61001 mus musculu
18	636.5	14.2	3712	2 Q9VFM0	Q9VFM0 drosophila
19	629	14.0	3616	2 Q7PFP9	Q7PFP9 anopheles g
20	625	13.9	670	2 Q9BTF3	Q9BTF3 homo sapien
21	600.5	13.4	3672	1 LML2_CAEEL	Q81313 caenorhabdi
22	594	13.4	794	2 Q8R3Y7	Q8R3Y7 mus musculu
23	579.5	12.9	1518	2 Q21442	Q21442 caenorhabdi
24	579.5	12.9	3704	2 P91904	P91904 caenorhabdi
25	545	12.1	3084	1 LMA1_MOUSE	P25317 mus musculu
26	529.5	11.8	3075	1 LMA1_HUMAN	P25317 mus musculu
27	526.5	11.7	3110	1 LMA2_HUMAN	P24043 homo sapien
28	523.5	11.5	414	2 Q14731	Q14731 homo sapien
29	516.5	11.5	3106	1 LMA2_MOUSE	Q60675 mus musculu
30	514	11.4	354	2 Q91YGB	Q91YGB mus musculu
31	510	11.4	858	2 Q8R145	Q8R145 mus musculu

32	442	9.8	3375	2 Q8IP51	Q8IP51 drosophila
33	425	9.5	3367	2 Q9XZC9	Q9XZC9 drosophila
34	422.5	9.4	747	2 Q7Z5W6	Q7Z5W6 homo sapien
35	398	8.9	659	2 Q7Q019	Q7Q019 mus musculu
36	374	8.3	3170	2 Q7E880	Q7E880 anopheles g
37	358.5	8.0	3102	2 Q45614	Q45614 caenorhabdi
38	335	7.5	559	2 Q6P6D3	Q6P6D3 homo sapien
39	332.5	7.4	1363	1 NX1A_CHICK	Q96dd0 gallus gall
40	325.5	7.2	1514	1 NX1A_RAT	Q63372 rattus norv
41	322	7.2	1553	2 Q8CH66	Q8CH66 mus musculu
42	321.5	7.2	1530	1 NX1A_BOVIN	Q28146 bos taurus
43	320	7.1	1176	2 Q80Y87	Q80Y87 mus musculu
44	318	7.1	1477	1 NX1A_HUMAN	Q9ulb1 homo sapien
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ALIGNMENTS

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AC P70570		
DT 01-FEB-1997 (TREMBLrel. 02, Created)		
DT 01-FEB-1997 (TREMBLrel. 02, Last sequence update)		
DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)		
DE Laminin-5 alpha 3 chain.		
OS Rattus norvegicus (Rat).		
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.		
OX NCBI_Taxid=10116;		
RN [1]		
RP SEQUENCE FROM N.A.		
RA MEDLINE=97081969; PubMed=8923212;		
RA Baker S.B., Hopkinson S.B., Fitchman M., Andreason G.L., Frasier F.,		
RA Plopper G., Quaranta V., Jones J.C.R.,		
RT "Laminin-5 and hemidesmosomes: role of the alpha 3 chain subunit in		
RT hemidesmosome stability and assembly.",		
RL J. Cell Sci. 109:2509-2520 (1996).		
DR EMBL, U61261; AAB17053.1; -.		
DR HSSP, P35070; 11P0.		
DR GO, GO:0005606; C:laminin-1; IEA.		
DR GO, GO:0005102; P:receptor binding; IEA.		
DR GO, GO:0005198; P:structural molecule activity; IEA.		
DR GO, GO:0030155; P:regulation of cell adhesion; IEA.		
DR GO, GO:0030334; P:regulation of cell migration; IEA.		
DR GO, GO:0045995; P:regulation of embryonic development; IEA.		
DR InterPro, IPR006985; ConA like_1ec_g1.		
DR InterPro, IPR006209; EGF like.		
DR InterPro, IPR002049; Laminin_EGF.		
DR InterPro, IPR001791; Laminin_G.		
DR InterPro, IPR009254; Laminin_I.		
DR InterPro, IPR010307; Laminin_II.		
DR InterPro, IPR003129; TSP N.		
DR Pfam, PR00053; Laminin_G_2.		
DR Pfam, PF02210; Laminin_G_2; 4.		
DR Pfam, PF06008; Laminin_I; 1.		
DR Pfam, PF06009; Laminin_II; 1.		
DR SMART, SM00180; EGF Lam; 2.		
DR SMART, SM00282; LamG; 5.		
DR PROSITE, PS00022; EGF_1; 1.		
DR PROSITE, PS01186; EGF_2; 1.		
DR PROSITE, PS01248; LAMININ_TYPE_EGF; 2.		
DR PROSITE, PS50025; LAM_G_DOMAIN; 5.		
KW Laminin EGF-like domain.		
SQ		
SEQUENCE 1725 AA; 190392 MW; 02EB43B3E72B0FB CRC64;		
Query Match	100.0%;	Score 4491; DB 2; Length 1725;
Best Local Similarity	100.0%;	Pred. No. 56-253;
Matches	866; Conservative	0; Mismatches 0; Indels 0; Gaps 0;
1 MEFNGKSGVVRLLPNLEDLKGYTSLFLQRPDLRNGGTFDMFVYLGAKQASKDYIG 60		

Db 782 MFENKSGVEVRLPNDLEDLKGYSLSLFLQREPDLENGETEDMFVYLGNKDAKDYIG 841
 Qy 61 MAVVDGQLTCVYNIAGREAEVQIDQVLTSESESOEAVMDRYKFORIYQPAKNTYKKAETSN 120
 Db 842 MAVVDGQLTCVYNIAGREAEVQIDQVLTSESESOEAVMDRYKFORIYQPAKNTYKKAETSN 901
 Qy 121 KKAAPAVYDLBEGSSNTLLNLPEDAVFYVGYPPDFELPSRLRPFPYKCIELDLNEN 180
 Db 902 KKAAPAVYDLBEGSSNTLLNLPEDAVFYVGYPPDFELPSRLRPFPYKCIELDLNEN 961
 Qy 181 VLSLVNFKTTPMNTTEVEPCRRRKEESDNRYEGGYARIPIQPAAPFPNFIQTITV 240
 Db 962 VLSLVNFKTTPMNTTEVEPCRRRKEESDNRYEGGYARIPIQPAAPFPNFIQTITV 1021
 Qy 241 DGLLFFAENQDNFISLNIENEDGNMRYKLSPEPKGIRPDTINGKSHIITIGKQ 300
 Db 1022 DGLLFFAENQDNFISLNIENEDGNMRYKLSPEPKGIRPDTINGKSHIITIGKQ 1081
 Qy 301 KKMWINNERSVRIEGRIFDPSTYYIGIPIAIRERFNI STPAFOGCMKRLKKTSGVRL 360
 Db 1082 KKMWINNERSVRIEGRIFDPSTYYIGIPIAIRERFNI STPAFOGCMKRLKKTSGVRL 1141
 Qy 361 NDTVGTCKCSBDMKLVRTASBFRGQMSPTMLDVSTDRFQLSRFGOTPOBGTILNMQ 420
 Db 1142 NDTVGTCKCSBDMKLVRTASBFRGQMSPTMLDVSTDRFQLSRFGOTPOBGTILNMQ 1201
 Qy 421 TETSLVLTLEDGHIESTRDSNIPIFKSPGYMDGLMHSVSIPTSGRLIIDQVLR 480
 Db 1202 TETSLVLTLEDGHIESTRDSNIPIFKSPGYMDGLMHSVSIPTSGRLIIDQVLR 1261
 Qy 481 RNQRLPSFSAQOISLRLGGHFEBCISNVLVQRFQSPVAVDLASHTKSDSLAGCSLN 540
 Db 1262 RNQRLPSFSAQOISLRLGGHFEBCISNVLVQRFQSPVAVDLASHTKSDSLAGCSLN 1321
 Qy 541 KKPRLMFLSPKPRFNGRIENNVQIMODAPQARTSTREANODGSCIPPLNTAKSHALOP 600
 Db 1322 KKPRLMFLSPKPRFNGRIENNVQIMODAPQARTSTREANODGSCIPPLNTAKSHALOP 1381
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 Qy 661 AGGKRLRLSKERYHDGKMTVVFGINGAKRLVVDGLRAQEGSLFGNSTISREQVYIG 720
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 Qy 721 LPLSRKPSLPOHSFVGCARDPOLNKNPLDPSPARFGVSPCLGSLFKGIYFQGGGHYI 780
 Db 1502 LPLSRKPSLPOHSFVGCARDPOLNKNPLDPSPARFGVSPCLGSLFKGIYFQGGGHYI 1561
 Qy 781 LANSVSLGPELKLTFGIRPRLTGVLIHVGSGQSLSYMEAGKVTTSVSDAGGSVTS 840
 Db 1562 LANSVSLGPELKLTFGIRPRLTGVLIHVGSGQSLSYMEAGKVTTSVSDAGGSVTS 1621
 Qy 841 ITPKQSLCDGQWHSVAVSIXORILHL 866
 Db 1622 ITPKQSLCDGQWHSVAVSIXORILHL 1647
 RESULT 2
 LMA3 MOUSE STANDARD, PRT; 3333 AA.
 ID LMA3 MOUSE 061789; 061788; 061966; 090H07;
 AC 061789; 061788; 061966; 090H07;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Laminin alpha-3 chain precursor (Micein alpha subunit).
 GN Name=Lama3;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 ON NCBI_TaxId=10090;
 RN [1]

RP SEQUENCE OF 1-58 FROM N.A., AND SEQUENCE OF 32-38.
 RX MEDLINE=21818471; PubMed=11829758; DOI=10.1042/0264-6021.3620213;
 RA Garbe J.H., Gehring W., Mann K., Timpl R., Saesaki T.;
 RT "Complete sequence, recombinant analysis and binding to laminins and
 RT sulphated ligands of the N-terminal domains of laminin alpha3B and
 RT alpha5 chains.";
 RL Biochem. J. 362:213-221(2002).
 RN [2]
 RP SEQUENCE OF 1-726 FROM N.A.
 RC STRAIN=ICR;
 RX MEDLINE=97296337; PubMed=9151674; DOI=10.1083/jcb.137.3.685;
 RA Miner J.H., Patton B.L., Lentz S.T., Gilbert D.J., Snider W.D.,
 RA Jenkins N.A., Copeland N.G., Sane J.R.;
 RT "The laminin alpha chains: expression, developmental transitions, and
 RT chromosomal locations of alpha1-5, identification of heterotrimeric
 RT laminins 8-11, and cloning of a novel alpha3 isoform.";
 RL J. Cell Biol. 137:685-701(1997).
 RN [3]
 RP SEQUENCE FROM N.A. (ISOFORM A), AND SEQUENCE OF 716-3284 FROM N.A.
 RP (ISOFORM B).
 RC STRAIN=BALB/c; TISSUE=Lung;
 RX MEDLINE=95394948; PubMed=7655604; DOI=10.1074/jbc.270.37.21820;
 RA Galliano M.-F., Aberdam D., Aguzzi A., Ortonne J.-P., Meneguzzi G.;
 RT "Cloning and complete primary structure of the mouse laminin alpha 3
 RT chain. Distinct expression pattern of the laminin alpha 3A and alpha
 RT 3B chain isoforms.";
 RL J. Biol. Chem. 270:21820-21826(1995).
 RN [4]
 RP REVISIONS.
 RA Aberdam D.;
 RL Submitted (Apr-1997) to the EMBL/GenBank/DBJ databases.
 RN [5]
 RP SEQUENCE OF 1767-2485 FROM N.A.
 RC TISSUE=Lung;
 RX MEDLINE=94281750; PubMed=8012114;
 RA Aberdam D., Galliano M.-F., Mattei M.-G., Pisaní-Spadafora A.,
 RA Ortonne J.-P., Meneguzzi G.;
 RT "Assignment of mouse nlc1n genes to chromosomes 1 and 18.";
 RL Mamm. Genome 5:229-233(1994).
 RN [6]
 RP SEQUENCE OF 1767-2485 FROM N.A.
 RC TISSUE=Lung;
 RX MEDLINE=94363405; PubMed=8081888;
 RA Aberdam D., Aguzzi A., Baudoin C., Galliano M.-F., Ortonne J.-P.,
 RA Meneguzzi G.;
 RT "Developmental expression of nlc1n adhesion protein (laminin-5)
 RT subunits suggests multiple morphogenic roles.";
 RL Cell Adhes. Commun. 2:115-129(1994).
 CC -1- FUNCTION: Binding to cells via a high affinity receptor, laminin
 CC is thought to mediate the attachment, migration and organization
 CC of cells into tissues during embryonic development by interacting
 CC with other extracellular matrix components.
 CC -1- FUNCTION: Laminin-5 is thought to be involved in (1) cell adhesion
 CC via integrin alpha-3/beta-1 in focal adhesion and integrin alpha-
 CC 6/beta-4 in hemidesmosomes, (2) signal transduction via tyrosine
 CC phosphorylation of p125-FAK and p80, (3) differentiation of
 CC keratinocytes (by similarity).
 CC -1- SUBUNIT: Laminin is a complex glycoprotein, consisting of three
 CC different polypeptide chains (alpha, beta, gamma), which are bound
 CC to each other by disulfide bonds into a cross-shaped molecule
 CC comprising one long and three short arms with globules at each
 CC end. The alpha-3 chain is a subunit of laminin-5
 CC (epiligrin/kalinin/nlc1n), and possibly also a component of
 CC laminin-6 (K-laminin) and laminin-7 (KS-laminin).
 CC -1- SUBCELLULAR LOCATION: Extracellular; found in the basement
 CC membranes (major component).
 CC -1- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=2;
 CC Name=A;
 CC Name=B;
 CC IsoId=Q61789-1; Sequence=Displayed;
 CC Name=A;
 CC IsoId=Q61789-2; Sequence=VSP_003038, VSP_003039;
 CC -1- TISSUE SPECIFICITY: Basal membrane of the upper alimentary tract

CC and urinary and nasal epithelia, salivary glands and teeth (both
CC variants). Isoform A is predominantly expressed in skin, hair
CC follicles and developing neurons of the trigeminal ganglion.
CC Isoform B was found in bronchi, alveoli, stomach, intestinal
CC crypts, whisker pads, CNS, telencephalic neuroectoderm, thalamus,
CC Rathke's pouch and periventricular subependymal germinal layer.
CC -1- DOMAIN: The alpha-helical domains I and II are thought to interact
CC with other laminin chains to form a coiled coil structure.
CC -1- DOMAIN: Domains IV and G are globular.
CC -1- SIMILARITY: Contains 15 laminin EGF-like domains.
CC -1- SIMILARITY: Contains 5 laminin G-like domains.
CC -1- SIMILARITY: Contains 1 laminin IV domain.
CC -1- SIMILARITY: Contains 1 laminin N-terminal domain.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC or send an email to license@ebi.ac.uk).

CC -----
CC EMBL; AJ293592; CAB99254.2; -;
CC EMBL; U88353; AAC5179.1; -;
CC EMBL; X84014; CA58837.1; -;
CC EMBL; X84013; CA58836.1; ALT_FRAME.
CC EMBL; L20478; AAA68091.1; -;
CC HSSP; P02468; INPE.
CC MGD; MGI:99909; Lama3.
CC GO; GO:0005604; C:basement membrane; IDA.
CC InterPro; IPR008985; Coa1_like_recpt.
CC InterPro; IPR006209; EGF_Like.
CC InterPro; IPR008979; Gal_bind_Like.
CC InterPro; IPR009030; Grow_fac_recpt.
CC InterPro; IPR008212; Lam_N2.
CC InterPro; IPR000034; Laminin_B.
CC InterPro; IPR002049; Laminin_EGF.
CC InterPro; IPR001791; Laminin_G.
CC InterPro; IPR009254; Laminin_I.
CC InterPro; IPR010307; Laminin_II.
CC InterPro; IPR008211; Laminin_N.
CC InterPro; IPR003129; TSP_N.
CC Pfam; PF00052; Laminin_B_1.
CC Pfam; PF00053; Laminin_EGF_10.
CC Pfam; PF00054; Laminin_G_3.
CC Pfam; PF06008; Laminin_I_1.
CC Pfam; PF06009; Laminin_II_1.
CC Pfam; PF00055; Laminin_N_1.
CC PRINTS; PR00011; EGF_LAMININ.
CC PRODOM; PD003031; Laminin_B_1.
CC PROSITE; PS00022; EGF_1; 10.
CC PROSITE; PS01186; EGF_2; 1.
CC PROSITE; PS50025; LAM_G_DOMAIN; 5.
CC PROSITE; PS01248; LAMININ_TYPE_EGF; 10.
CC Alternative splicing; Basement membrane; Cell adhesion; Coiled coil;
CC direct protein sequencing; Extracellular matrix; Glycoprotein;
CC Laminin EGF-like domain; Repeat; Signal.
CC -----
CC FT CHAIN 1 31 Laminin alpha-3 chain.
CC FT DOMAIN 32 333 Laminin N-terminal (domain VI).
CC FT 294 725 Domain V.
CC FT 296 725 Laminin EGF-like 1.
CC FT 350 725 Laminin EGF-like 2.
CC FT 353 420 Laminin EGF-like 3.
CC FT 423 464 Laminin EGF-like 4.
CC FT 488 530 Laminin EGF-like 5.
CC FT 533 576 Laminin EGF-like 6.
CC FT 582 625 Laminin EGF-like 7.
CC FT 628 678 Laminin EGF-like 8.
CC FT 681 725 Laminin EGF-like 9.
CC FT 725 1262 Laminin domain IV 1 (domain IV B).
CC FT 793 1262 Laminin domain III B.
CC FT 1263 1353 Laminin EGF-like 9.
CC FT 1354 1403 Laminin EGF-like 10.

FT DOMAIN 1404 1454 Laminin EGF-like 11.
FT DOMAIN 1455 1464 Laminin EGF-like 12 (N-terminal).
FT DOMAIN 1465 1653 Laminin domain IV (domain IV A).
FT DOMAIN 1654 1821 Domain III A.
FT DOMAIN 1654 1821 Laminin EGF-like 12 (C-terminal).
FT DOMAIN 1654 1686 Laminin EGF-like 13.
FT DOMAIN 1687 1733 Laminin EGF-like 14.
FT DOMAIN 1734 1786 Laminin EGF-like 15 (incomplete).
FT DOMAIN 1787 1821 Domain II and I.
FT DOMAIN 1822 2388 Laminin G-like 1.
FT DOMAIN 2389 2590 Laminin G-like 2.
FT DOMAIN 2597 2759 Laminin G-like 3.
FT DOMAIN 2766 2926 Laminin G-like 4.
FT DOMAIN 2986 3150 Laminin G-like 5.
FT DOMAIN 3157 3330 Laminin G-like 6.
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FT DOMAIN 11685 11720 Laminin G-like 251.
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FT DOMAIN 13341 13376 Laminin G-like 297.
FT DOMAIN 13377 13412 Laminin G-like 298.
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FT DOMAIN 16361 16400 Laminin G-like 377.
FT DOMAIN 16401 16440 Laminin G-like 378.
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FT DOMAIN 16641 16680 Laminin G-like 384.
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FT DOMAIN 16841 16880 Laminin G-like 389.
FT DOMAIN 16881 16920 Laminin G-like 390.
FT DOMAIN 16921 16960 Laminin G-like 391.
FT DOMAIN 16961 17000 Laminin G-like 392.
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FT DOMAIN 17721 17760 Laminin G-like 411.
FT DOMAIN 17761 17800 Laminin G-like 412.
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FT DOMAIN 17881 17920 Laminin G-like 415.
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FT DOMAIN 18121 18160 Laminin G-like 421.
FT DOMAIN 18161 18200 Laminin G-like 422.
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FT DOMAIN 18241 1

Db 2750 NDTVGVTKKCSBDMKLVRTASFSRGQMSFTNLDPVSLDRFQLSFGPQTPOPSGTLNLHQ 2809
Qy 421 TTTSSLVLTLEBDGIELSTRDSNIP1FKSPGYMDGLHHVSYISPTSGRLIIDQVLR 480
Db 2810 TTTSSLVLTLEBDGIELSTRDSNIP1FKSPGYMDGLHHVSYISPTSGRLIIDQVLR 2869
Qy 481 RNQRLPFSNNAOQSLRGGGHEGCIISNVLVORFSGSPVAVDLASIKTKDASLGCCSIN 540
Db 2870 RNQRLPFSNNAOQSLRGGGHEGCIISNVLVORFSGSPVAVDLASIKTKDASLGCCSIN 2929
Qy 541 KPPFLMLFKSPKRFNFKRIFFNVQMLMODAPQATRSREANODGSCLPPLNTKASHRALQ 600
Db 2930 KPPFLMLFKSPKRFNFKRIFFNVQMLMODAPQATRSREANODGSCLPPLNTKASHRALQ 2989
Qy 601 GDSPTSHLLKLPQELLKPKRSQPSLDIQTSSPKGLFYATGKOSPLALVYADGRVVFALQ 660
Db 2990 GDSPTSHLLKLPQELLKPKRSQPSLDIQTSSPKGLFYATGKOSPLALVYADGRVVFALQ 3049
Qy 661 AGGKTLRLSKERYHDKMHTVFGNLNGKARLVVDGLRAQEGSLPKNSTISPREQVYLQ 720
Db 3050 AGGKTLRLSKERYHDKMHTVFGNLNGKARLVVDGLRAQEGSLPKNSTISPREQVYLQ 3109
Qy 721 LPLSRKPKSLPQHSFPGCLADPOLNKPDLSPSARPGVSPCLGSLKGIYFGGGGHYI 780
Db 3110 LPLSRKPKSLPQHSFPGCLADPOLNKPDLSPSARPGVSPCLGSLKGIYFGGGGHYI 3169
Qy 781 LANSVSLGPELKLTFEIRPSLTGVLHVHVSQSGRLSYVMEAGKVTTSVSADGASVTS 840
Db 3170 LANSVSLGPELKLTFEIRPSLTGVLHVHVSQSGRLSYVMEAGKVTTSVSADGASVTS 3229
Qy 841 ITPKQSLCDGQMSHVAVSIRKRIHL 866
Db 3230 ITPKQSLCDGQMSHVAVSIRKRIHL 3255

RESULT 3
Q6VU69
ID Q6VU69 PRELIMINARY; PRT; 1668 AA.
AC Q6VU69;
DT 05-JUL-2004 (TEMBLrel. 27, Created)
DT 05-JUL-2004 (TEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TEMBLrel. 27, Last annotation update)
DE Laminin alpha 3 splice variant a.
GN Name=LAM3;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
OC NCBI_taxid=9606;
RN
RX MEDLINE=2893568; Pubmed=12915477; DOI=10.1093/hmg/ddg234;
RA McLean W.H., Irvine A.D., Hamill K.J., Whitcock N.V.,
RA Coleman-Campbell C.M., Mellerio J.E., Ashton G.S.,
RA Dopping-Hepenstiel P.J., Bady R.A., Jamil T., Phillips R.J.,
RA Shabli S.G., Haroon T.S., Khurshid K., Moore J.E., Page B.,
RA Darling J., Atherton D.J., Van Steensel M.A., Munro C.S., Smith F.J.,
RA McGrath J.A.;
RT "An unusual N-terminal deletion of the laminin (alpha)3 isoform leads
RT to the chronic granulation tissue disorder laryngo-onycho-cutaneous
RT syndrome";
RT Hum. Mol. Genet. 12:2395-2409(2003).
RN
RP SEQUENCE FROM N.A.
RA McLean W.H.I.;
RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL, AY327114; A072569.1; -.
DR GO; GO:000506; C:laminin-1; IEA.
DR GO; GO:0005102; F:receptor binding; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR GO; GO:0030155; P:regulation of cell adhesion; IEA.
DR GO; GO:0030334; P:regulation of cell migration; IEA.
DR GO; GO:0045395; P:regulation of embryonic development; IEA.
DR InterPro; IPR001844; Chaprinin_Cpn60.

DR InterPro; IPR008985; Cona_1like_1ec_g1.
DR InterPro; IPR006209; EGF_1like.
DR InterPro; IPR002049; Laminin_EGF.
DR InterPro; IPR001791; Laminin_G.
DR InterPro; IPR009254; Laminin_I.
DR InterPro; IPR010307; Laminin_II.
DR InterPro; IPR003129; TSP_N.
DR Pfam; PF00053; Laminin_EGF_1.
DR Pfam; PF02210; Laminin_G_2; 4.
DR Pfam; PF06008; Laminin_I_1.
DR Pfam; PF06009; Laminin_II_1.
DR SMART; SM00180; EGF_Lam; 2.
DR SMART; SM00282; LamG; 5.
DR PROSITE; PS00296; CHAPERONINS_CPN60; UNKNOWN_1.
DR PROSITE; PS00022; EGF_1; 1.
DR PROSITE; PS01186; EGF_2; 1.
DR PROSITE; PS01248; LAMININ_TYPE_EGF; 2.
DR PROSITE; PS50025; LAM_G_DOMAIN; 5.
KW Laminin_EGF-like domain.
SQ SEQUENCE 1668 AA; 184053 MW; 9EBF5FC45637645C CRC64;

Query Match 79.3%; Score 3562.5; DB 2; Length 1668;
Best Local Similarity 78.4%; Pred. No. 1.6e-230; Indels 3; Gaps 2;
Matches 680; Conservative 86; Mismatches 98;

Qy 1 MRFNGSGVEVRLPNLELDLKGYSLSLFLQRPDLRENGTEDEMFVMTLGNKDAKDYIG 60
Db 726 MRFNGSGVEVRLPNLELDLKGYSLSLFLQRPDLRENGTEDEMFVMTLGNKDAKDYIG 785
Qy 61 MAVVDGQLTCVNLCDREAVQIDQVLTRESQEAQVMDRVYQFORYQAKLNTYKEATSN 120
Db 786 MAVVDGQLTCVNLCDREAVQIDQVLTRESQEAQVMDRVYQFORYQAKLNTYKEATSN 845
Qy 121 KKPAAVVDLEGGSSNTLNDPEDAVYVGGPPDFELPSRLRPPPKGCTIEDLLEN 180
Db 846 KKPAAVVDLEGGSSNTLNDPEDAVYVGGPPDFELPSRLRPPPKGCTIEDLLEN 905
Qy 181 VLSLYNFKTTFNTTEVEPCRRKEESDKYFBSGTGYARLPTQPNAPFPNFIQTITTV 240
Db 906 VLSLYNFKTTFNTTEVEPCRRKEESDKYFBSGTGYARLPTQPNAPFPNFIQTITTV 965
Qy 241 DRGLLPFAENQDPISLNIEDGNLWRYKLNSEPKKGIKRTINDGKHSLITYGKQ 300
Db 966 DRGLLPFAENQDPISLNIEDGNLWRYKLNSEPKKGIKRTINDGKHSLITYGKQ 1025
Qy 301 KKMWNVNRSVRIGELPDESTYVLGGPIAIRERFNISTPAFQGCCKNKKSGVRL 360
Db 1026 KKMWNVNRSVRIGELPDESTYVLGGPIAIRERFNISTPAFQGCCKNKKSGVRL 1085
Qy 361 NDTVGVTKKCSBDMKLVRTASFSRGQMSFTNLDPVSLDRFQLSFGPQTPOPSGTLNLHQ 420
Db 1086 NDTVGVTKKCSBDMKLVRTASFSRGQMSFTNLDPVSLDRFQLSFGPQTPOPSGTLNLHQ 1145
Qy 421 TTTSSLVLTLEBDGIELSTRDSNIP1FKSPGYMDGLHHVSYISPTSGRLIIDQVLR 480
Db 1146 TTTSSLVLTLEBDGIELSTRDSNIP1FKSPGYMDGLHHVSYISPTSGRLIIDQVLR 1205
Qy 481 RNQRLPFSNNAOQSLRGGGHEGCIISNVLVORFSGSPVAVDLASIKTKDASLGCCSIN 540
Db 1206 RNQRLPFSNNAOQSLRGGGHEGCIISNVLVORFSGSPVAVDLASIKTKDASLGCCSIN 1265
Qy 541 KPPFLMLFKSPKRFNFKRIFFNVQMLMODAPQATRSREANODGSCLPPLNTKASHRALQ 600
Db 1266 KPPFLMLFKSPKRFNFKRIFFNVQMLMODAPQATRSREANODGSCLPPLNTKASHRALQ 1323
Qy 600 GDSPTSHLLKLPQELLKPKRSQPSLDIQTSSPKGLFYATGKOSPLALVYADGRVVFALQ 659
Db 1324 GDSPTSHLLKLPQELLKPKRSQPSLDIQTSSPKGLFYATGKOSPLALVYADGRVVFALQ 1383
Qy 660 AGGKTLRLSKERYHDKMHTVFGNLNGKARLVVDGLRAQEGSLPKNSTISPREQVYLQ 719
Db 1384 AGGKTLRLSKERYHDKMHTVFGNLNGKARLVVDGLRAQEGSLPKNSTISPREQVYLQ 1443

QY 720 GLPLSRKPKSLPOHSFVGCIRDPLQNSKPLDPSAPRGVSPCLGSLKGIYFSQGGGHV 779
 DB 1444 GSPSPGPKPRLPNTNSFVGCILNFKQDLSKPLYTSSSSGVSSCLGPLEKGIYFSBEGHV 1503
 QY 780 ILANSVSLGPELKLTPSIRPRSLTGVLIVHGSQSGQRLSYMEAGKVTTSVSDAGGSVT 839
 DB 1504 VLAHSVLAGPEFLVFSIRPRSLTGVLIVHGSQSGQRLCYLLEAGKVTASMDSGAGGTST 1563
 QY 840 SITPKOSLCDGQWHSVAVSIKORILHL 866
 DB 1564 SITPKOSLCDGQWHSVAVSIKORILHL 1590

RESULT 4
 ID 06VU67 PRELIMINARY; PRT; 3277 AA.
 AC 06VU67;
 DT 05-JUL-2004 (TEMBLrel. 27, Created)
 DT 05-JUL-2004 (TEMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TEMBLrel. 27, Last annotation update)
 DE Laminin alpha 3 splice variant B2.
 GN Name=LAMA3;
 OS Homo sapiens (human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA MEDLINE=22835568; PubMed=12915477; DOI=10.1093/hmg/ddg224;
 RA McLean W.H., Irvine A.D., Hamill K.J., Whitlock N.V.,
 RA Coleman-Cabeall C.M., Mellerio J.B., Ashton G.S.,
 RA Dopping-Hepenstal P.J., Bady R.A., Jamil T., Phillips R.J.,
 RA Shabir S.G., Haroon T.S., Knutshild K., Moore J.E., Page B.,
 RA Darling J., Atherton D.J., Van Steensel M.A., Munro C.S., Smith F.J.,
 RA McGee J.A.;
 RT "An unusual N-terminal deletion of the laminin (alpha)3a isoform leads
 RT to the chronic granulation tissue disorder laryngo-oncho-cutaneous
 RT syndrome".
 RT Hum. Mol. Genet. 12:2395-2409 (2003).
 RL [2]
 RN SEQUENCE FROM N.A.
 RA McLean W.H.I.;
 RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL_A1327116; AA072571.1; -
 DR GO; GO:0005578; C:extracellular matrix (sensu Metazoa); IEA.
 DR GO; GO:0005506; C:laminin-1; IEA.
 DR GO; GO:0005102; P:receptor binding; IEA.
 DR GO; GO:0005198; P:regulation of cell adhesion; IEA.
 DR GO; GO:0030344; P:regulation of cell migration; IEA.
 DR GO; GO:0045395; P:regulation of embryonic development; IEA.
 DR InterPro; IPR001844; Chapman Cpn60.
 DR InterPro; IPR008985; Cona like lec_g1.
 DR InterPro; IPR006209; BGF like.
 DR InterPro; IPR008978; Gal_bind like.
 DR InterPro; IPR006210; IEGF.
 DR InterPro; IPR000034; Laminin B.
 DR InterPro; IPR002049; Laminin EGF.
 DR InterPro; IPR001791; Laminin G.
 DR InterPro; IPR009255; Laminin I.
 DR InterPro; IPR010307; Laminin II.
 DR InterPro; IPR008211; Laminin N.
 DR InterPro; IPR003129; TSP_N.
 DR Pfam; PF00052; Laminin B; 1.
 DR Pfam; PF00210; Laminin EGF; 8.
 DR Pfam; PF02210; Laminin G 2; 4.
 DR Pfam; PF06008; Laminin II; 1.
 DR Pfam; PF06009; Laminin II; 1.
 DR Pfam; PF00055; Laminin N; 1.
 DR PRINTS; PR00011; EGF_LAMININ.
 DR ProDom; PD003031; Laminin_B; 1.
 DR SMART; SM00181; EGF; 8.
 DR SMART; SM00180; EGF_Lam; 14.

DR SMART; SM00281; Lamb; 1.
 DR SMART; SM00282; Lamb; 5.
 DR SMART; SM00136; Lamb; 1.
 DR PROSITE; PS00296; CHAPERONINS_CPN60; UNKNOWN_1.
 DR PROSITE; PS00022; EGF_1; 12.
 DR PROSITE; PS01186; EGF_2; 1.
 DR PROSITE; PS01248; LAMININ TYPE EGF; 13.
 DR PROSITE; PS00025; LAM G DOMAIN; 5.
 DR Laminin EGF-like domain.
 KW Laminin EGF-like domain.
 SQ SEQUENCE 3277 AA; 360209 MW; 3ACFE9983571222 CRC64;

Query Match 79.3%; Score 3562.5; DB 2; Length 3277;
 Best local Similarity 78.4%; Pred. No. 4.6e-230;
 Matches 680; Conservative 86; Mismatches 98; Indels 3; Gaps 2;

QY 1 MRNFGSGVEVRLPNDLBDLKGYSLSLFLQRPDLRENGSDMFVYLGAKNDASDYIG 60
 DB 2335 MRNFGSGVEVRLPNDLBDLKGYSLSLFLQRPDLRENGSDMFVYLGAKNDASDYIG 2394
 QY 61 MAVVDQQLTCVNLGPREAEVQIDVLTESRQEAVMDRKFORIYQFALNTTKATSN 120
 DB 2395 MAVVDQQLTCVNLGPREAEVQIDVLTESRQEAVMDRKFORIYQFALNTTKATSN 2454
 QY 121 KPRAPAVYDLEGSSNTLNTLDPEDAVFYVGYPPDFELPSRLFPFYKGCIELDLNEN 180
 DB 2455 KPRTPGVYDMGDSNTLNTLDPENVFYVGYPPDFELPSRLFPFYKGCIELDLNEN 2514
 QY 181 VLSLYNPKTTFNLTTEVEBCRRRKEESDNVEGEGYARIPTQNPAPFPNTQITTV 240
 DB 2515 VLSLYNPKTTFNLTTEVEBCRRRKEESDNVEGEGYARIPQNPAPFPNTQITTV 2574
 QY 241 DRGLTFPAENQDFISLINTEDGNTLMRYKLNSEPPKEKGRDITNKGHSILITTKQ 300
 DB 2575 DRGLTFPAENQDFISLINTEDGNTLMRYKLNSEPPKEKGRDITNKGHSILITTKQ 2634
 QY 301 KRMVIVNERSVYIEGIFDFSTYYVGGPIALIREPNISPAFOGCMKYLKTSGVVRL 360
 DB 2635 KRMVIVNERSVYIEGIFDFSTYYVGGPIALIREPNISPAFOGCMKYLKTSGVVRL 2694
 QY 361 NDTVGYTKKCEDMDKLVRTASFSRGGQMSFTNLDVPSDTRFQSPGFQPSGTLNMQ 420
 DB 2695 NDTVGYTKKCEDMDKLVRTASFSRGGQMSFTNLDVPSDTRFQSPGFQPSGTLNMQ 2754
 QY 421 TRTSLSLVTEDEHIELSTRDSNIPIPKSGTITMDGILHVASIYSDTSGLRLIDQVLR 480
 DB 2755 TRTSLSLVTEDEHIELSTRDSNIPIPKSGTITMDGILHVASIYSDTSGLRLIDQVLR 2814
 QY 481 RNORLPSFSAQOSLFLGGHPEGICISNLYVORFSQSPHYLDLASSTKQDASLGCSLN 540
 DB 2815 RNORLPSFSAQOSLFLGGHPEGICISNLYVORFSQSPHYLDLASSTKQDASLGCSLN 2874
 QY 541 KPEPLMLFSPKPFNKGRIETVNVQMLQMDAPQAT-RSTEAWQDRSCLPPLNTRASHRALQ 599
 DB 2875 KPEPLMLFSPKPFNKGRIETVNVQMLQMDAPQAT-RSTEAWQDRSCLPPLNTRASHRALQ 2932
 QY 600 FGDSPFTSHLLKLPQELIKRSPQSLDIQTSFKGLVFVAGYOSFLIAYVADGRVFL 659
 DB 2933 FGDIPFTSHLLKLPQELIKRSPQSLDIQTSFKGLVFVAGYOSFLIAYVADGRVFL 2992
 QY 660 GAGGKKLRILRSKERYDKMHTVFPGLNGSKALVVDGARAQSGSLPGNSTISPREQVYL 719
 DB 2993 GAGGKKLRILRSKERYDKMHTVFPGLNGSKALVVDGARAQSGSLPGNSTISPREQVYL 3052
 QY 720 GLPLSRKPKSLPOHSFVGCIRDPLQNSKPLDPSAPRGVSPCLGSLKGIYFSQGGGHV 779
 DB 3053 GSPSPGPKPRLPNTNSFVGCILNFKQDLSKPLYTSSSSGVSSCLGPLEKGIYFSBEGHV 3112
 QY 780 ILANSVSLGPELKLTPSIRPRSLTGVLIVHGSQSGQRLSYMEAGKVTTSVSDAGGSVT 839
 DB 3113 VLAHSVLAGPEFLVFSIRPRSLTGVLIVHGSQSGQRLCYLLEAGKVTASMDSGAGGTST 3172
 QY 840 SITPKOSLCDGQWHSVAVSIKORILHL 866

DB 3173 SVTPKQSLCDGQMHSAVATIKOHILHL 3199

RESULT 5

Q6VU68 PRELIMINARY; PRT; 3333 AA.

ID Q6VU68

AC Q6VU68;

DT 05-JUL-2004 (TrEMBLrel. 27, Created)

DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)

DE Laminin alpha 3 splice variant b1.

GN Name=LAMA3;

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

OX NCBI_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=22833568; PubMed=12915477; DOI=10.1093/hmg/ddg234;

RA McLean W.H., Irvine A.D., Hamill K.J., Whitlock N.V., Coleman-Campbell C.M., Mellerio J.E., Ashton G.S., Doppen-Hepner P.J., Rader R.A., Jamil T., Phillips R.J., Shabbir S.G., Haroon T.S., Khurshid K., Moore J.B., Page B., Darling J., Atcherson D.J., Van Steensel W.A., Munro C.S., Smith F.J., McGrath J.A.;

RA "An unusual N-terminal deletion of the laminin (alpha)3 isoform leads to the chronic granulation tissue disorder laryngo-onycho-cutaneous syndrome.";

RT Hum. Mol. Genet. 12:2395-2409 (2003).

RL [2]

RN SEQUENCE FROM N.A.

RA McLean W.H.1.;

RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.

DR EMBL: AY327115; AAC72570.1; -.

DR GO: GO:0005578; C:extracellular matrix (sensu Metazoa); IEA.

DR GO: GO:0005606; C:laminin-1; IEA.

DR GO: GO:0005102; F:receptor binding; IEA.

DR GO: GO:0005198; F:structural molecule activity; IEA.

DR GO: GO:0030155; P:regulation of cell adhesion; IEA.

DR GO: GO:0030334; P:regulation of cell migration; IEA.

DR GO: GO:0045995; P:regulation of embryonic development; IEA.

DR InterPro: IPR001844; Chaprin_Cp60.

DR InterPro: IPR008985; Cona_Like_Iec_g1.

DR InterPro: IPR006209; EGF_Like.

DR InterPro: IPR006210; Gal_bind_Like.

DR InterPro: IPR006210; IEGF.

DR InterPro: IPR000034; Laminin_B.

DR InterPro: IPR002049; Laminin_EGF.

DR InterPro: IPR001791; Laminin_G.

DR InterPro: IPR009254; Laminin_I.

DR InterPro: IPR010307; Laminin_II.

DR InterPro: IPR008211; Laminin_N.

DR InterPro: IPR003129; TSP_N.

DR Pfam: PF00052; Laminin_B_1.

DR Pfam: PF00053; Laminin_EGF_8.

DR Pfam: PF02210; Laminin_G_2; 4.

DR Pfam: PF06008; Laminin_I_1.

DR Pfam: PF00055; Laminin_II_1.

DR PRINTS: PR00011; EGF_LAMININ.

DR PRODOM: PD003031; Laminin_B_1.

DR SMART: SM00181; EGF_8.

DR SMART: SM00180; EGF_Lam_14.

DR SMART: SM00281; LamE_1.

DR SMART: SM00282; LamE_1.

DR SMART: SM00136; LamNT_1.

DR PROSITE: PS00296; CHAPERONINS_CPN60; UNKNOWN_1.

DR PROSITE: PS00022; EGF_1; 12.

DR PROSITE: PS01186; EGF_2; 1.

DR PROSITE: PS01248; LAMTIN_TYPE_EGF_13.

DR PROSITE: PS50025; LAM_G_DOMAIN; 5.

KW Laminin EGF-like domain.

SQ SEQUENCE 3333 AA; 36646 MW; 9P99AF49B8EF27DD CRC64;

Query Match 79.3%; Score 3562.5; DB 2; Length 3333;
Best Local Similarity 78.4%; Pred. No. 4.7e-230;
Matches 680; Conservative 86; Mismatches 98; Indels 3; Gaps 2;

QY 1 MRFNGSGVEYRLPNDELKGYTSLSLFLOPDLRENGGTEDMFMTLGNKDSKDYIG 60

DB 2391 MRFNGSGVEYRLPNDELKGYTSLSLFLOPDRNGGTEDMFMTLGNKDSRDYIG 2450

QY 61 MAVVDGOLTCVYNGDRABVQIDOVLFSSSQAVMDRVFORVYQAKLNTYEATSN 120

DB 2451 MAVVDGOLTCVYNGDRABVQIDOVLFSSSQAVMDRVFORVYQAKLNTYEATSN 2510

QY 121 KFKAVAVVDLEGGSSNTLLNLDPEDAVFYVGGYPDFELPSLRPPYKGCIEIDLLEN 180

DB 2511 KPEYGVYDMGRNSNTLLNLDPEDAVFYVGGYPDFELPSLRPPYKGCIEIDLLEN 2570

QY 181 VLSLYNFKTENTLNTTEVEPCRRKXESDKNYFEGTGYARIPTOPNAPPNFIQTITV 240

DB 2571 VLSLYNFKTENTLNTTEVEPCRRKXESDKNYFEGTGYARIPTOPNAPPNFIQTITV 2630

QY 241 DRGLFFAENQDNFSLNIEDGNLMVRKYKNSPEPKGIDPTINDGDSILITGLQ 300

DB 2631 DRGLFFAENQDNFSLNIEDGNLMVRKYKNSPEPKGIDPTINDGDSILITGLQ 2690

QY 301 KKMWINVERSVRIEGEIFDESTVYLGCIPIAIRRRFNISTPAFGCKMLKKTSGVRL 360

DB 2691 KKMWINVQNTIIDGVFDFSTVYLGCIPIAIRRRFNISTPAFGCKMLKKTSGVRL 2750

QY 361 NDTVGYTKCSHDMKLVRTASFRGGQMSFTNLDVPSIDRQLSGFTQFQSGTLNMQ 420

DB 2751 NDTVGYTKCSHDMKLVRTASFRGGQMSFTNLDVPSIDRQLSGFTQFQSGTLNMQ 2810

QY 421 TPTSSLVTLIEDGHIELSTRDSNTPIFKSPGYMDGLLHVSVISDTSGLRLIIDOVLR 480

DB 2811 TPTSSLVTLIEDGHIELSTRDSNTPIFKSPGYMDGLLHVSVISDTSGLRLIIDOVLR 2870

QY 481 RNQRLPFSFMAQOQSLRLGGHFECCISNVLYQRFQSSEVVDLASKSTKQASLGCSLN 540

DB 2871 RNQRLPFSFMAQOQSLRLGGHFECCISNVLYQRFQSSEVVDLASKSTKQASLGCSLN 2930

QY 541 KPPFLMLFKSPFRNKGRIFNVNQLMODAPQAT-RSTAMQDGRSLCPPLNTKASHRLQ 599

DB 2931 KPPFLMLFKSPFRNKGRIFNVNQLMODAPQAT-RSTAMQDGRSLCPPLNTKASHRLQ 2988

QY 600 FGDSPSTSHLLKPEELLKPRSQFSLDIQTSPKLVYAGKDSFLALVYADGVVPL 659

DB 2989 FGDSPSTSHLLKPEELLKPRSQFSLDIQTSPKLVYAGKDSFLALVYADGVVPL 3048

QY 660 GAGGKKLRLSKERYHDKMTVVFGLNGKARLVVDGLRAQEGSLPGNSTISPREOYL 719

DB 3049 GAGGKKLRLSKERYHDKMTVVFGLNGKARLVVDGLRAQEGSLPGNSTISPREOYL 3108

QY 720 GLPLSRKPKSLPOHSPVGLRDFOINSKPLDPSPARFVSPCLGSLGKGIYFSGGGHV 779

DB 3109 GLPLSRKPKSLPOHSPVGLRDFOINSKPLDPSPARFVSPCLGSLGKGIYFSGGGHV 3168

QY 780 ILANGSVLGPBLKLTFSIRPSLTGLVLHVGGQSQRSLSYNBAKKTTSVSSDAGSST 839

DB 3169 ILANGSVLGPBLKLTFSIRPSLTGLVLHVGGQSQRSLSYNBAKKTTSVSSDAGSST 3228

QY 840 SITPKQSLCDGQMHSAVATIKOHILHL 866

DB 3229 SITPKQSLCDGQMHSAVATIKOHILHL 3255

RESULT 6

LMA3 HUMAN STANDARD; PRT; 1713 AA.

AC Q16787; Q13679; Q13680;

DT 01-NOV-1997 (Rel. 35, Created)

DT 01-NOV-1997 (Rel. 35, Last sequence update)

DT 25-OCT-2004 (Rel. 45, Last annotation update)

DE Laminin alpha-3 chain precursor (Epiligrin 170 kDa subunit) (E170)
 DE (Nuclein alpha subunit).
 GN Name=LAM3;
 OS Homo sapiens (Human).
 CC Bkaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Keratinocytes;
 RX MEDLINE=94357926; PubMed=8077230;
 RA Ryan M.C., Tizard R., Vandevanter D.R., Carter W.G.;
 RT "Cloning of the lam3 gene encoding the alpha 3 chain of the adhesive
 RT ligand epiligrin. Expression in wound repair.";
 RL J Biol. Chem. 269:22779-22787 (1994).
 RN [2]
 RP SEQUENCE OF 1-1331 FROM N.A. (ISOFORMS A AND B).
 RX MEDLINE=96163880; PubMed=8586427;
 RA Vidal F., Baudoin C., Miquel C., Galliano M.-F., Christiano A.M.,
 RA Uitto J., Ortonne J.-P., Meneguzzi G.;
 RT "Cloning of the laminin alpha 3 chain gene (LAMA3) and identification
 RT of a homozygous deletion in a patient with Herlitz junctional
 RT epidermolysis bullosa.";
 RL Genomics 30:273-280 (1995).
 RN [3]
 RP DISEASE.
 RX PubMed=12915477; DOI=10.1093/hmg/ddg234;
 RA Irwin McLean W.H., Irvine A.D., Hamill K.J., Whitlock N.V.,
 RA Coleman-Campbell C.M., Mellerio J.E., Ashton G.S.,
 RA Dopping-Hepenst P.J.H., Bady R.A.J., Jamil T., Phillips R.J.,
 RA Shabir S.G., Haroon T.S., Khurehd K., Moore J.R., Page B.,
 RA Darling J., Atherton D.J., Van Steensel M.A.M., Munro C.S.,
 RA Smith F.J.D., McGrath J.A.;
 RT "An unusual N-terminal deletion of the laminin alpha3 isoform leads
 RT to the chronic granulation tissue disorder laryngo-oncho-cutaneous
 RT syndrome.";
 RL Hum. Mol. Genet. 12:2395-2409 (2003).
 CC -1- FUNCTION: Binding to cells via a high affinity receptor, laminin
 CC is thought to mediate the attachment, migration and organization
 CC of cells into tissues during embryonic development by interacting
 CC with other extracellular matrix components.
 CC -1- FUNCTION: Laminin-5 is thought to be involved in (1) cell adhesion
 CC via integrin alpha-3/beta-1 in focal adhesion and integrin alpha-
 CC 6/beta-4 in hemidesmosomes, (2) signal transduction via tyrosine
 CC phosphorylation of p125-FAK and p60, (3) differentiation of
 CC keratinocytes.
 CC -1- SUBUNIT: Laminin is a complex glycoprotein, consisting of three
 CC different polypeptide chains (alpha, beta, gamma), which are bound
 CC to each other by disulfide bonds into a cross-shaped molecule
 CC comprising one long and three short arms with globules at each
 CC end. The alpha-3 chain is a subunit of laminin-5
 CC (epiligrin/kalin/nicein), and possibly also a component of
 CC laminin-6 (K-laminin) and laminin-7 (KS-laminin).
 CC -1- SUBCELLULAR LOCATION: Extracellular; found in the basement
 CC membranes (major component).
 CC -1- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=2;
 CC Name=A;
 CC IsoId=Q16787-1; Sequence=Displayed;
 CC Name=B;
 CC IsoId=Q16787-2; Sequence=VSP_003037;
 CC Note=incomplete sequence;
 CC -1- TISSUE SPECIFICITY: Skin; respiratory, urinary, and digestive
 CC epithelia and in other specialized tissues with prominent
 CC secretory or protective functions. Epithelial basement membrane,
 CC and epithelial cell tongue that migrates into a wound bed. A
 CC differential and focal expression of the alpha-3 chain is observed
 CC in the CNS.
 CC -1- INDUCTION: Laminin-5 is up-regulated in wound sites of human skin.
 CC -1- DOMAIN: The alpha-helical domains I and II are thought to interact
 CC with other laminin chains to form a coiled coil structure.
 CC -1- DOMAIN: Domain G is globular.
 CC -1- DISEASE: Defects in LAMA3 are a cause of junctional epidermolysis

CC bullosa gravis (JEB) [MIM:226700]; also known as junctional
 CC epidermolysis bullosa Herlitz-Pearson type. JEB is a blistering
 CC disorder in skin that is characterized by a separation of basal
 CC cells from the basement membrane due to a decreased number of
 CC hemidesmosomes. Laminin-5 is missing from the basement membrane of
 CC patients with the gravis form of epidermolysis bullosa.
 CC -1- DISEASE: Defects in LAMA3 are the cause of laryngoonychocutaneous
 CC syndrome (LOCS) [MIM:245601]. LOCS is an autosomal recessive
 CC epithelial disorder confined to the Punjabi Muslim population. The
 CC condition is characterized by cutaneous erosions, nail dystrophy
 CC and exuberant vascular granulation tissue in certain epithelia,
 CC especially conjunctiva and larynx.
 CC -1- SIMILARITY: Contains 3 laminin EGF-like domains.
 CC -1- SIMILARITY: Contains 5 laminin G-like domains.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -
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 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL; L34155; AA59483.1; -;
 CC EMBL; X85107; CA59428.1; -;
 CC EMBL; X85108; CA59429.1; -;
 CC FTR; A55347; A55347.
 CC HSSP; P02468; INPB.
 CC Genew; HGNC:6483; LAMA3.
 CC MIM; 600805; -;
 CC MIM; 226700; -;
 CC MIM; 245601; -;
 CC GO; GO:0005604; C:basement membrane; TAS.
 CC GO; GO:0008544; P:epidermal differentiation; TAS.
 CC InterPro; IPR008985; Conn_1ike_1ec_g1.
 CC InterPro; IPR009030; Grov_fac_recept.
 CC InterPro; IPR002049; Laminin_Egf.
 CC InterPro; IPR001791; Laminin_G.
 CC InterPro; IPR009254; Laminin_I.
 CC InterPro; IPR010307; Laminin_II.
 CC InterPro; IPR003129; TSP_N.
 CC Pfam; PF00053; Laminin_EGF; 2.
 CC Pfam; PF00054; Laminin_G; 2.
 CC Pfam; PF06008; Laminin_I; 1.
 CC Pfam; PF06009; Laminin_II; 1.
 CC PROSITE; PS00022; EGF_1; 1.
 CC PROSITE; PS01186; EGF_2; 1.
 CC PROSITE; PS01248; LAMININ_TYPE_EGF; 2.
 CC PROSITE; PS50025; LAM_G_DOMAIN; 5.
 CC Alternative splicing; Basement membrane, Cell adhesion; Coiled coil;
 CC Epidermolysis bullosa; Extracellular matrix; Glycoprotein;
 CC Laminin EGF-like domain; Repeat; Signal.
 CC FT SIGNAL 1 20 Potential.
 CC FT CHAIN 21 1713 Laminin alpha-3 chain.
 CC FT DOMAIN 46 201 Domain III A.
 CC FT DOMAIN 67 113 Laminin EGF-like 1.
 CC FT DOMAIN 114 166 Laminin EGF-like 2.
 CC FT DOMAIN 167 185 Laminin EGF-like 3 (incomplete).
 CC FT DOMAIN 186 769 Domain II and I.
 CC FT DOMAIN 971 971 Laminin G-like 1.
 CC FT DOMAIN 978 1140 Laminin G-like 2.
 CC FT DOMAIN 1147 1307 Laminin G-like 3.
 CC FT DOMAIN 1366 1530 Laminin G-like 4.
 CC FT DOMAIN 1537 1710 Laminin G-like 5.
 CC FT DOMAIN 231 327 Coiled coil (Potential).
 CC FT DOMAIN 396 548 Coiled coil (Potential).
 CC FT DOMAIN 594 621 Coiled coil (Potential).
 CC FT DOMAIN 702 765 Coiled coil (Potential).
 CC FT DOMAIN 1686 1713 Coiled coil (Potential).
 CC FT DISULFID 67 76 By similarity.
 CC FT DISULFID 69 83 By similarity.
 CC FT DISULFID 86 95 By similarity.

FT DISULFID 98 111 By similarity.
FT DISULFID 114 126 By similarity.
FT DISULFID 116 135 By similarity.
FT DISULFID 137 146 By similarity.
FT DISULFID 149 164 By similarity.
FT DISULFID 202 202 Interchain (probable).
FT DISULFID 205 205 Interchain (probable).
FT SITP 658 660 Cell attachment site (potential).
FT CARBOHYD 542 542 N-linked (GlcNAc...) (potential).
FT CARBOHYD 645 645 N-linked (GlcNAc...) (potential).
FT CARBOHYD 745 745 N-linked (GlcNAc...) (potential).
FT CARBOHYD 882 882 N-linked (GlcNAc...) (potential).
FT CARBOHYD 964 964 N-linked (GlcNAc...) (potential).
FT CARBOHYD 1108 1108 N-linked (GlcNAc...) (potential).
FT CARBOHYD 1131 1131 N-linked (GlcNAc...) (potential).
FT CARBOHYD 1325 1325 N-linked (GlcNAc...) (potential).
FT CARBOHYD 1477 1477 N-linked (GlcNAc...) (potential).
FT CARBOHYD 1667 1667 N-linked (GlcNAc...) (potential).
FT VARSPLIC 1 45 MCHMTFGALGCGLCGYSQQQVPPFLQPPGSGQLQASVYE
FRPS -> KYSSYGYLYTOAKSFALGDMVLEKKPVDL
TQGMKSIYEETWTPPPDLHGRVAVBGNFHLASRAV
SRELMTVLSRLADVRIQGLYFTETQRLTSEVLEADT
GSGRIALAVRICACPPAVAGDSC (in isoform B).
/FTid=VSP_003037.
W -> R (in Ref. 2).
ATG -> GNC (in Ref. 2).
M -> K (in Ref. 2).
R -> L (in Ref. 2).
E -> Q (in Ref. 2).
D -> A (in Ref. 2).
G -> A (in Ref. 2).
Query Match 79.3%; Score 3560.5; DB 1; length 1713;
Best local Similarity 78.4%; Pred. No. 2,3e-230;
Matches 680; Conservative 86; Mismatches 98; Indels 3; Gaps 2;
QY 1 MRFNGSGVYRLPNLEDKGTTSLFLQRPDLBNGTEPMFYTLGNKQASQDYIG 60
DB 771 MRFNGSGVYRLPNLEDKGTTSLFLQRPDLBNGTEPMFYTLGNKQASQDYIG 830
QY 61 MAVVDQQLCVNYLGRREAVOIDLTVSESEGEAVMDRKPORITQPAKNTTKRATSN 120
DB 831 MAVVDQQLCVNYLGRREAVOIDLTVSESEGEAVMDRKPORITQPAKNTTKRATSN 890
QY 121 KPRKAPVYDLEGGSSNTLNTLDEDDVFFVGGYPPPELPSRLRPPYKCIELDLNEN 180
DB 891 KPRKAPVYDLEGGSSNTLNTLDEDDVFFVGGYPPPELPSRLRPPYKCIELDLNEN 950
QY 181 VLSLNPFTTNLNTTVEBPCRRRKEESDKNYEGGYARIPTQPNAPPPNFIQTITTV 240
DB 951 VLSLNPFTTNLNTTVEBPCRRRKEESDKNYEGGYARIPTQPNAPPPNFIQTITTV 1010
QY 241 DRGLLFFAENQDFISLNTEDGLMRYKLNSEPKKGRDITNGKXHSILITIGKQ 300
DB 1011 DRGLLFFAENQDFISLNTEDGLMRYKLNSEPKKGRDITNGKXHSILITIGKQ 1070
QY 301 KRWMINVRSVRIEIEIPDFSTYYLGGIPAIAREFNISTPAFQCGMKLAKTSGVNL 360
DB 1071 KRWMINVRSVRIEIEIPDFSTYYLGGIPAIAREFNISTPAFQCGMKLAKTSGVNL 1130
QY 361 NDTVGVTKKCSBDMKLVRTASFRGGQMSFTNLDPVSTDRFQUSFGQTFQPSGILLNQ 420
DB 1131 NDTVGVTKKCSBDMKLVRTASFRGGQMSFTNLDPVSTDRFQUSFGQTFQPSGILLNQ 1190
QY 421 TRTSLLVLTEDGHIELSTRDSNIPFKSGTYMDGLHHVSYIPTSGLRIILIDQVLR 480
DB 1191 TRTSLLVLTEDGHIELSTRDSNIPFKSGTYMDGLHHVSYIPTSGLRIILIDQVLR 1250
QY 481 RNQRLPFSNAQOQLRIGGHPFGCISNVLVQRFSSPEVLDASSTYKQDASIGGCSLN 540
DB 1251 RNQRLPFSNAQOQLRIGGHPFGCISNVLVQRFSSPEVLDASSTYKQDASIGGCSLN 1310

QY 541 KPPFLMLKSPKPKFKKRIENVNQLMODAPQAT-RSTANQDGRSCPLPLNTKASHRALQ 599
DB 1311 KPPFLMLKSGTRFKKTIFFRLNQLDTPVAPSPRSVWOD--ACSLPPTQANHGAQLQ 1368
QY 600 FQDSPTSHLLKLPBELKPPRSQFSLDIQTSFKLVVYAGKQSFLLALVYADGRVFLAL 659
DB 1369 FQDITSHLLKLPBELKPPRSQFSLDIQTSFKLVVYAGKQSFLLALVYADGRVFLAL 1428
QY 660 GAGGKKRLRSKERYHDKMHTVVGELNGKRAVLVVDGLRAQEGSLPQNSTISPREQVYL 719
DB 1429 GAGGKKRLRSKERYHDKMHTVVGELNGKRAVLVVDGLRAQEGSLPQNSTISPREQVYL 1488
QY 720 GLPLRKPKSLPQHSFVGLDPLQNSKPLDPSAPRFGVSPCLGSLKGIYFSQGGHV 779
DB 1489 GLPLRKPKSLPQHSFVGLDPLQNSKPLDPSAPRFGVSPCLGSLKGIYFSQGGHV 1548
QY 780 IIANVSGLPELKLFPSTRPSLTGVLJHVSQSGQRLSYVMEAGKYTTSVSDGGSVT 839
DB 1549 IIANVSGLPELKLFPSTRPSLTGVLJHVSQSGQRLSYVMEAGKYTTSVSDGGSVT 1608
QY 840 SITPKQSLDQGMHSVAVSIRQRIHL 866
DB 1609 SITPKQSLDQGMHSVAVSIRQRIHL 1635

RESULT 7
Q96TGO PRELIMINARY; PRT; 1806 AA.
AC Q96TGO
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Alpha 3B chain of laminin-5 (fragment).
GN Name=LAMA3;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Aberdam D., Vidal, Baudoin, Miquel, Ortonne, Meneguzzi;
RL Submitted (FEB-1995) to the EMBL/Genbank/DBJ databases.
DR EMBL; X84960; CAA59325.1; -.
DR HSSP; P02468; INPE.
DR GO; GO:0005606; C:laminin-1; IEA.
DR GO; GO:0005102; F:receptor binding; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR GO; GO:0030155; P:regulation of cell adhesion; IEA.
DR GO; GO:0030334; P:regulation of cell migration; IEA.
DR GO; GO:0045995; P:regulation of embryonic development; IEA.
DR InterPro; IPR001844; Chaprinin_Cpno6.
DR InterPro; IPR008985; Cona like_1ec_g1.
DR InterPro; IPR006209; EGF like
DR InterPro; IPR000034; laminin_B
DR InterPro; IPR002049; laminin_BGF.
DR InterPro; IPR001791; laminin_G.
DR InterPro; IPR009254; laminin_I.
DR InterPro; IPR010307; laminin_II.
DR InterPro; IPR003129; TSP_N
DR Pfam; PF00052; laminin_B_1.
DR Pfam; PF00053; laminin_EGF_2.
DR Pfam; PF02210; laminin_G_2; 4.
DR Pfam; PF06008; laminin_I_1.
DR Pfam; PF06009; laminin_II_1.
DR Pfam; PF06009; laminin_II_1.
DR Pfam; PF06009; laminin_II_1.
DR SMART; SM00180; EGF_lam; 2.
DR SMART; SM00281; lamB; 1.
DR SMART; SM00282; lamB; 1.
DR PROSITE; PS00296; CHAPERONINS_CPN60; UNKOWN_1.
DR PROSITE; PS00022; EGF_1; 2.
DR PROSITE; PS01186; EGF_2; 1.
DR PROSITE; PS01248; LAMININ_TYPE_EGF; 3.
DR PROSITE; PS00025; LAM_G_DOMAIN; 5.

KM Laminin EGF-like domain.
 FT NON TER 1 1
 SQ SEQUENCE 1806 AA; 199411 MW; EF94CBE2A8A52B93 CRC64;
 Query Match 79.3%; Score 3560.5; DB 2; Length 1806;
 Best Local Similarity 78.4%; Pred. No. 2.5e-230;
 Matches 680; Conservative 86; Mismatches 98; Indels 3; Gaps 2;

QY 1 MRNNGSGVEVRIPNDLEDIKGTTSLFLQRPDLRENGGTEDMFWYLGAKDASXDYIG 60
 DB 864 MRNNGSGVEVRIPNDLEDIKGTTSLFLQRPDLRENGGTEDMFWYLGAKDASXDYIG 923
 QY 61 MAVVDGQLTCVYMLGDBEAEOVDQVLTSESGOAVMDRYKFORIYOPAKLNTTKATSN 120
 DB 924 MAVVDGQLTCVYMLGDBEAEOVDQVLTSESGOAVMDRYKFORIYOPAKLNTTKATSN 963
 QY 121 KPRAPAVYDLEGGSSNTLNLDPEDAVFYVGYPPDFELPSRLRPPPYKCIELDNLN 180
 DB 984 KPRAPAVYDLEGGSSNTLNLDPEDAVFYVGYPPDFELPSRLRPPPYKCIELDNLN 1043
 QY 181 VLSLNFKTTNNTTEVEPCRRKESDKNYREGTYANIPPOPNAPFPNFIQTIQTV 240
 DB 1044 VLSLNFKTTNNTTEVEPCRRKESDKNYREGTYANIPPOPNAPFPNFIQTIQTV 1103
 QY 241 DRGLFPAENQDPISLNTEDNLMRYKLNSEBPKEKGRDPTINDGKHSILITGKIQ 300
 DB 1104 DRGLFPAENQDPISLNTEDNLMRYKLNSEBPKEKGRDPTINDGKHSILITGKIQ 1163
 QY 301 KRWMINNERSVRIEGEIPDFSTYLLGDIPIAIRERFNISTPAFOGCMKMLKTTSGVRL 360
 DB 1164 KRWMINNERSVRIEGEIPDFSTYLLGDIPIAIRERFNISTPAFOGCMKMLKTTSGVRL 1223
 QY 361 NDTVGVTKKCESEDMKLVRIASFSRGGQMSFTNLDVPESTRFQUSFGFTQFSGTLINQ 420
 DB 1224 NDTVGVTKKCESEDMKLVRIASFSRGGQMSFTNLDVPESTRFQUSFGFTQFSGTLINQ 1283
 QY 421 TRTSLLVLTEDGHIELSTDSNIPFKSGTYMDGLHIVSVISDPSGRLIIDQVLR 480
 DB 1284 TRTSLLVLTEDGHIELSTDSNIPFKSGTYMDGLHIVSVISDPSGRLIIDQVLR 1343
 QY 481 RNORLPSFNAOQSLRLGAGHFEAGCISNVVLPFSQSEPVLDLASKTKDASLGCSLN 540
 DB 1344 RNORLPSFNAOQSLRLGAGHFEAGCISNVVLPFSQSEPVLDLASKTKDASLGCSLN 1403
 QY 541 KPPFLMLFKSPKPKNGRIINNVQMODAPQAT-RSTEANODGSCCLPINTKASHRALQ 599
 DB 1404 KPPFLMLFKSPKPKNGRIINNVQMODAPQAT-RSTEANODGSCCLPINTKASHRALQ 1461
 QY 600 RGDSPFTHLLKLPQELIKRSPQSLDIQTTSPKGVAFVAGTDSPLALVVAAGRVRL 659
 DB 1462 RGDSPFTHLLKLPQELIKRSPQSLDIQTTSPKGVAFVAGTDSPLALVVAAGRVRL 1521
 QY 660 GAGGKQLRLSKERVDGKMTVVFGLNGGKARLVVDGLRAOQSLPGNSTISPREOVL 719
 DB 1522 GAGGKQLRLSKERVDGKMTVVFGLNGGKARLVVDGLRAOQSLPGNSTISPREOVL 1581
 QY 720 GLPLSRPKSLPHQSPVGLRDLFQNLNPKPLDSPAPFVSPCLGGSLKGIYRSGGAV 779
 DB 1582 GLPLSRPKSLPHQSPVGLRDLFQNLNPKPLDSPAPFVSPCLGGSLKGIYRSGGAV 1641
 QY 780 ILANSVSLGDELKLTGIRPSRLTGVLINHGSGOGLSYVMRAKGTTSVSDAGASVT 839
 DB 1642 ILANSVSLGDELKLTGIRPSRLTGVLINHGSGOGLSYVMRAKGTTSVSDAGASVT 1701
 QY 840 SITPKOSLCDGQWHSVAVSIKORILHL 866
 DB 1702 SITPKOSLCDGQWHSVAVSIKORILHL 1728

RESULT 8
 Q76E14 PRELIMINARY; PRT; 3333 AA.
 AC Q76E14;

OT 05-JUL-2004 (Tremblrel. 27, Created)
 DT 05-JUL-2004 (Tremblrel. 27, Last sequence update)
 DT 05-JUL-2004 (Tremblrel. 27, Last annotation update)
 DE Laminin alpha 3b chain.
 GN Name=LAM3;
 OS Homo sapiens (human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OX NCBI_TaxID=9606;
 RN (1)
 RP SEQUENCE FROM N.A.
 RA Kariya Y., Yasuda C., Nakashima Y., Ishida K., Teubota Y.,
 RA Miyazaki K.;
 RT "Characterization of laminin 5B and NH2-terminal proteolytic fragment
 of its alpha3b chain: promotion of cellular adhesion, migration, and
 proliferation.";
 RL J. Biol. Chem. 279:24774-24784 (2004).
 DR EMBL; AB107369; BAD13428.1; -;
 DR GO; GO:0005578; Extracellular matrix (sensu Metazoa); IEA.
 DR GO; GO:0005606; C.laminin-1; IEA.
 DR GO; GO:0005102; F:receptor binding; IEA.
 DR GO; GO:0005198; F:structural molecule activity; IEA.
 DR GO; GO:0030155; P:regulation of cell adhesion; IEA.
 DR GO; GO:0030334; P:regulation of cell migration; IEA.
 DR GO; GO:0045995; P:regulation of embryonic development; IEA.
 DR InterPro; IPR001844; Chaprin_Cpn60.
 DR InterPro; IPR008965; Cona_like_1ec_g1.
 DR InterPro; IPR006209; EGF_like.
 DR InterPro; IPR008979; Gal_bind_like.
 DR InterPro; IPR006210; IEGF.
 DR InterPro; IPR000034; Laminin_B.
 DR InterPro; IPR002049; Laminin_EGF.
 DR InterPro; IPR001791; Laminin_G.
 DR InterPro; IPR009254; Laminin_I.
 DR InterPro; IPR010307; Laminin_II.
 DR InterPro; IPR008211; Laminin_N.
 DR InterPro; IPR003129; TSP_N.
 DR Pfam; PF00052; Laminin_B_1.
 DR Pfam; PF00053; Laminin_EGF_8.
 DR Pfam; PF02210; Laminin_G_2_4.
 DR Pfam; PF06008; Laminin_I_1.
 DR Pfam; PF06009; Laminin_II_1.
 DR Pfam; PF00055; Laminin_N_1.
 DR PRINTS; PRO0011; EGF_LAMININ.
 DR ProDom; PD003031; Laminin_B_1.
 DR SMART; SM00181; EGF; 8.
 DR SMART; SM00180; EGF_Lam; 14.
 DR SMART; SM00281; LamB; 1.
 DR SMART; SM00282; LamG; 5.
 DR SMART; SM00136; LamNT; 1.
 DR PROSITE; PS00296; CHAPERONINS_CPN60; UNKNOWN_1.
 DR PROSITE; PS00022; EGF_1; 12.
 DR PROSITE; PS01186; EGF_2; 1.
 DR PROSITE; PS01248; LAMININ_TYPE_EGF; 13.
 DR PROSITE; PS00025; LAM_G_DOMAIN; 5.
 KW Laminin EGF-like domain.
 SQ SEQUENCE 3333 AA; 36616 MW; 6F99AF4D4B99FCB0 CRC64;
 Query Match. 79.3%; Score 3560.5; DB 2; Length 3333;
 Best Local Similarity 78.4%; Pred. No. 6.4e-230;
 Matches 680; Conservative 86; Mismatches 98; Indels 3; Gaps 2;

QY 1 MRNNGSGVEVRIPNDLEDIKGTTSLFLQRPDLRENGGTEDMFWYLGAKDASXDYIG 60
 DB 864 MRNNGSGVEVRIPNDLEDIKGTTSLFLQRPDLRENGGTEDMFWYLGAKDASXDYIG 923
 QY 61 MAVVDGQLTCVYMLGDBEAEOVDQVLTSESGOAVMDRYKFORIYOPAKLNTTKATSN 120
 DB 2451 MAVVDGQLTCVYMLGDBEAEOVDQVLTSESGOAVMDRYKFORIYOPAKLNTTKATSN 2510
 QY 121 KPRAPAVYDLEGGSSNTLNLDPEDAVFYVGYPPDFELPSRLRPPPYKCIELDNLN 180
 DB 2511 KPRAPAVYDLEGGSSNTLNLDPEDAVFYVGYPPDFELPSRLRPPPYKCIELDNLN 2570


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QY 720 GLEPLSRKSLPGHSPFGCLRDPLNKSPLDSPARGVSPCLGSLKGIYFGGGHY 779
DB 1501 GSSPAKPKYASLPQNSPFGCLRNPLDLPDPSPASVSPCLGSLKGIYFSGGHV 1560
QY 780 ILANSVSLGPELKLTPESIRPSRLTGVLIVHSGSGQRLSYMEAGKVTYSSDAGGSVT 839
DB 1561 ILANSVSLGPELKLTPESIRPSRLTGILMHVSGQPGRLCYMEAGKVTASVDSAGSILT 1620
QY 840 SITPKOSLCDGQWHSVAVSIKORILHL 866
DB 1621 SITPKOSLCDGQWHSVAVTIKQIHVHL 1647

RESULT 10
LMA4 HUMAN STANDARD; PRT; 1816 AA.
ID LMA4 HUMAN STANDARD; PRT; 1816 AA.
AC Q16363; Q14735; Q15335; Q9UB18; Q9UUN9;
DT 01-NOV-1997 (Rel. 35, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 03-JUL-2004 (Rel. 44, Last annotation update)
DE Laminin alpha-4 chain precursor.
GN Name=LMA4;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
OC NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Fetal lung;
RX MEDLINE=95300971; PubMed=7781776; DOI=10.1016/0014-5793(95)00462-1;
RA Iivanainen A., Sainio K., Sariola H., Tryggvason K.;
RT "Primary structure and expression of a novel human laminin alpha 4
chain.";
RL FEBS Lett. 365:183-188(1995).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Heart;
RX MEDLINE=97454279; PubMed=9310354;
RA Richards A.J., Luccarini C., Pope F.M.;
RT "The structural organisation of LMA4, the gene encoding laminin
alpha4.";
RL Eur. J. Biochem. 248:15-23(1997).
RN [3]
RP SEQUENCE OF 236-1816 FROM N.A.
RC TISSUE=Heart;
RX MEDLINE=95048381; PubMed=7959779;
RA Richards A.J., Al-Imara L., Carter N.P., Lloyd J.C., Leverah M.A.,
POPE F.M.;
RT "Localization of the gene (LMA4) to chromosome 6q21 and isolation of
a partial cDNA encoding a variant laminin A chain.";
RL Genomics 22:237-239(1994).
RN [4]
RP SEQUENCE OF 66-1816 FROM N.A.
RA Tubbby B.;
RT Submitted (MAR-1999) to the EMBL/GenBank/DBJ databases.
RC -1- FUNCTION: Binding to cells via a high affinity receptor, laminin
is thought to mediate the attachment, migration and organization
of cells into tissues during embryonic development by interacting
with other extracellular matrix components.
CC -1- SUBUNIT: Laminin is a complex glycoprotein, consisting of three
different polypeptide chains (alpha, beta, gamma), which are bound
to each other by disulfide bonds into a cross-shaped molecule
comprising one long and three short arms with globules at each
end.
CC -1- SUBCELLULAR LOCATION: Extracellular; found in the basement
membrane (major component).
CC -1- TISSUE SPECIFICITY: In adult, strong expression in heart, lung,
ovary small and large intestines, placenta, liver; weak or no
expression in skeletal muscle, kidney, pancreas, testis, prostate,
brain. High expression in fetal lung and kidney. Expression in
fetal and newborn tissues is observed in certain mesenchymal cells
in tissues such as smooth muscle and dermis.

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CC -1- DOMAIN: The alpha-helical domains I and II are thought to interact
with other laminin chains to form a coiled coil structure.
CC -1- DOMAIN: Domain G is globular.
CC -1- SIMILARITY: Contains 4 laminin EGF-like domains.
CC -1- SIMILARITY: Contains 5 laminin G-like domains.
CC -1- CAUTION: Gene LMA4 was formerly called LMA3.
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CC EMBL; S78569; AAB34635.1; -.
CC EMBL; X91171; CAA62596.1; -.
CC EMBL; Y14240; CAA74636.1; -.
CC EMBL; X76939; CAA54258.1; -.
CC EMBL; Z99289; -. NOT_ANNOTATED_CDS.
CC PIR; S68960; S68960.
CC HSSP; P02468; INPE.
CC Genew; HGNC:6484; LMA4.
CC MIM; 600133; -.
CC GO; GO:0005605; C:basal lamina; TAS.
CC GO; GO:0005201; F:extracellular matrix structural constituent; TAS.
CC InterPro; IPR008985; Comp_1like_1ec_g1.
CC InterPro; IPR006209; EGF_like.
CC InterPro; IPR002049; Laminin_EGF.
CC InterPro; IPR001791; Laminin_G.
CC InterPro; IPR009254; Laminin_I.
CC InterPro; IPR010307; Laminin_II.
CC InterPro; IPR003129; TSP_N.
CC Pfam; PF00053; Laminin_EGF; 3.
CC Pfam; PF00054; Laminin_G; 3.
CC Pfam; PF06008; Laminin_I; 1.
CC Pfam; PF06009; Laminin_II; 1.
CC PROSITE; PS00022; EGF_1; UNKNOWN 1.
CC PROSITE; PS00025; LAM_G_DOMAIN; 5.
CC PROSITE; PS01248; LAMININ_TYPE_EGF; 3.
CC KEGG; KEGG00025; Cell adhesion; Coiled coil; Extracellular matrix;
Glycoprotein; Laminin EGF-like domain; Repeat; Signal.
CC SIGMUL 1 24
CC CHAIN 25 1816
CC DOMAIN 82 131 Laminin EGF-like 1.
CC DOMAIN 132 186 Laminin EGF-like 2.
CC DOMAIN 187 240 Laminin EGF-like 3.
CC DOMAIN 241 255 Laminin EGF-like 4 (incomplete).
CC DOMAIN 256 825 Domain II and I.
CC DOMAIN 826 1028 Laminin G-like 1.
CC DOMAIN 1040 1220 Laminin G-like 2.
CC DOMAIN 1227 1395 Laminin G-like 3.
CC DOMAIN 1462 1633 Laminin G-like 4.
CC DOMAIN 1640 1813 Laminin G-like 5.
CC DOMAIN 313 396 Coiled coil (Potential).
CC DOMAIN 466 521 Coiled coil (Potential).
CC DOMAIN 574 607 Coiled coil (Potential).
CC DOMAIN 655 717 Coiled coil (Potential).
CC DOMAIN 770 799 Coiled coil (Potential).
CC SITE 717 719 Cell attachment site (Potential).
CC DISULFID 82 91 By similarity.
CC DISULFID 84 98 By similarity.
CC DISULFID 101 110 By similarity.
CC DISULFID 113 129 By similarity.
CC DISULFID 132 146 By similarity.
CC DISULFID 134 155 By similarity.
CC DISULFID 157 166 By similarity.
CC DISULFID 169 184 By similarity.
CC DISULFID 187 202 By similarity.
CC DISULFID 189 209 By similarity.
CC DISULFID 212 221 By similarity.
CC DISULFID 224 238 By similarity.
CC DISULFID 266 266 Interchain (Probable).

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FT DISULFID 269 269 Interchain (Probable).
FT CARBOHYD 104 104 N-linked (GlcNAc...) (Potential)
FT CARBOHYD 215 215 N-linked (GlcNAc...) (Potential)
FT CARBOHYD 308 308 N-linked (GlcNAc...) (Potential)
FT CARBOHYD 458 458 N-linked (GlcNAc...) (Potential)
FT CARBOHYD 524 524 N-linked (GlcNAc...) (Potential)
FT CARBOHYD 550 550 N-linked (GlcNAc...) (Potential)
FT CARBOHYD 571 571 N-linked (GlcNAc...) (Potential)
FT CARBOHYD 574 574 N-linked (GlcNAc...) (Potential)
FT CARBOHYD 631 631 N-linked (GlcNAc...) (Potential)
FT CARBOHYD 639 639 N-linked (GlcNAc...) (Potential)
FT CARBOHYD 735 735 N-linked (GlcNAc...) (Potential)
FT CARBOHYD 751 751 N-linked (GlcNAc...) (Potential)
FT CARBOHYD 754 754 N-linked (GlcNAc...) (Potential)
FT CARBOHYD 780 780 N-linked (GlcNAc...) (Potential)
FT CARBOHYD 803 803 N-linked (GlcNAc...) (Potential)
FT CARBOHYD 1086 1086 N-linked (GlcNAc...) (Potential)
FT CARBOHYD 1281 1281 N-linked (GlcNAc...) (Potential)
FT CARBOHYD 1359 1359 N-linked (GlcNAc...) (Potential)
FT CARBOHYD 1411 1411 N-linked (GlcNAc...) (Potential)
FT CONFLICT 143 143 A -> P (in Ref. 1).
FT CONFLICT 178 178 L -> F (in Ref. 1).
FT CONFLICT 265 265 G -> GMDCTPIS (in Ref. 4).
FT CONFLICT 276 276 D -> A (in Ref. 4).
FT CONFLICT 491 491 Y -> H (in Ref. 2 and 3).
FT CONFLICT 1057 1057 T -> P (in Ref. 1).
FT CONFLICT 1110 1110 SGR -> GGP (in Ref. 4).
SQ SEQUENCE 1816 AA; 201908 MW; 04E9AF379A0FAAD CAC64;

Query Match 26.5%; Score 1190; DB 1; Length 1816;
Best Local Similarity 33.2%; Pred. No. 1.le-70;
Matches 310; Conservative 161; Mismatches 372; Indels 90; Gaps 27;

QY 1 MRFNKSGVVRLEPNLEDDIKGYTSLFL----QRDLKENGSTEDMFMYVNGNDASK 56
DB 829 MMRFDGSAVSHSRSTSDMLKAFSLSLYMKPKRRLTE---TLDQFLLYLGSNAKK 885
QY 57 DYIGMAVVDGQLTCVYNLGDREAEVQIDQVLTSESQEAVMDRKFORIYQAFKALNYTKE 116
DB 886 EYWGMLAKNDNLVYVNLGDKVDIPLDS--KPVSSMPAFSLVTKLKEVGHKQKVLTPV 943
QY 117 ATSNKPKAPAVYDLEGGSSNTLLNLPEDAVFYGVGPPPELPSRLRPYKICIEILD 176
DB 944 SLSTSEKEFKIKKGEFSGDSDLDPEDPDTVFYGVGPPSNFKLPTSLNLPFGVLELAT 1003
QY 177 LNSNVSLVNFKTTENTTEVEPCRRK-----EESDKYFPGTGA--RIYQNR--A 227
DB 1004 LNDVSLVNFKAHYNDPSTVPCADKLAFTQSRASLYFPDGSGLVAVRDITRRGKFG 1063
QY 228 PFPNFLOTQTVDRCGLLFFAENQDNFISINIEDGNLMVY-----KLNSEPKKGI 280
DB 1064 QVTRFDEIVRTPADNGILLMNVGSMFRLKMGNGYLAHYVDGFGSSGRHLEDYTKKA- 1122
QY 281 RDTINDGKDSILITGKLOKRMWINVESVRI--EGEIPFSTYIAGIP-----I 331
DB 1123 --OINAKYHIBISI-IYHNDKMKILVYDRHVKSMDEKKKIFPTDIYIGAPPEILOSR 1179
QY 332 AIRERFNISIRPAFOGCKMKNL---KTISSGVRLNDYGVTKKSGEDMVLVTASFSRGGM 388
DB 1180 ALPAHPLDI-NRGGCKMGFOFOQDKDNLEQETTLGVGVCPEDSLISRRAFN--GQS 1236
QY 389 SFTNLD-VPSITDRFOLSFQTFQPSGTLNHRQRTSLAVTLEDGHIIEISTDNSNPIR 447
DB 1237 FMSIQKISFPDFEGGFNFRITQPNGLLFFYASGSVPSISLDNGVIMDKV--GIKVV 1294
QY 448 KSPFTYMDGLLHVSVISDTSGLR--LLID-DQVLRNRQLPFSFNAQSLR--LGG-- 499
DB 1295 SVDKQYVDGISHF--VISSVSPRYELIYDKSRVSKNPKKGLBQQAEEKKFFYFGGSP 1352
QY 500 -----GHFECCISNVLVQRFSGSEPVLDLASKYKQDASIGCGSLNKPPLMFKSKRF 554
DB 1353 ISAQYANFTGCSISNAYFTRVDRDVEVDFORVTEKVTSLSYECPIESSPLFLHKKGKKNL 1412

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QY 555 NKGRIFNVNQ--LMQDAPQATSTRTEAMODGRSCLEPLNT-----KASHRALQF 600
DB 1413 SKPKASQNKKGKSKSDAP-----SWDPVALKLPBRTVPRNSHGLNSPRAIETHAYQ 1465
QY 601 GDSPTSHLLKLPQELLRPSQFSLDIOTTSPEKGLVFPAFTKD--SFLALYADRRVPA 658
DB 1466 GGTANSRQEFHLLKDPGAKSQFSIRLTRSSHGMI FVYSQDEENDFTMLFLAHRRLVYM 1525
QY 659 LDAGGKCLRBSKERHYHDKHTTVFGLNGCARLVNDQAEQSL--PGNSTISPRQV 717
DB 1526 FVNGHKKIKTRNGEKTNDGLMDVIFIRBSRSGRLVIGLRYLESLEPTETATMKIKGPI 1585
QY 718 YLGLPSRKPXSLPQ-----HSFVGLRDFOINSKRELDSPARFVSPCLGSLKGIYFS 773
DB 1586 YLGGAVAPGAVANVQINSIYSPSGLSNQLNGLASITSQTFYSVTPCEBGMETGYFS 1645
QY 774 QCGGHVILANSVSLPELKLTRSIIPRSLITGLVHVGSQSGQRLSVYNEAGKVTYSSD 833
DB 1646 TEGGYVVDSESNFNGIKKEIAPFVVRPRSSGTLVHGHSVNGEYLVNHNKQGVIVKVNNG 1705
QY 834 AGGSVTSITPKQLCDGQMSVAVSIKQRIHL 866
DB 1706 IRDFTSVTPKQSLCDGRNHRITVIRDSNVQL 1738

RESULT 11
Q91V00 PRELIMINARY; PRT; 1254 AA.
AC Q91V00, 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Lama4 protein (Fragment).
GN Name=Lama4;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
ON NCBI_TaxID=10090;
RX SEQUENCE FROM N.A.
RC STRAIN=mx FVB/N; TISSUE=Mammary tumor;
RX MEDLINE=2238257; PubMed=12477932; DOI=10.1073/pnae.242603899;
RA Strausberg R.L., Feingold B.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shemen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Cabavant T.L., Scheetz T.E.,
RA Baha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Vailley D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywicki M.I., Skalska U., Smailus D.E., Scherch A., Schein J.B.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=mx FVB/N; TISSUE=Mammary tumor;
RA Strausberg R.;
RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC008533; AA008533.1; -.
DR HSSP; 060675; 1Q0D.
DR MGD; MGI:109321; Lama4.
DR GO; GO:0005605; C:basal lamina; IDA.
DR GO; GO:0005615; C:extracellular space; TAS.
DR GO; GO:0001568; P:blood vessel development; IMP.

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QY 392 NLD-VPSTDRFOLSPFQFOTFQPSGTLNHTQRTSLVLEEDGHEILSTDSNIPKSP 450
 DB 1242 SIOKISFDFEGEGFNRTIQPNLFLYTSGSVBSISLDNGVWVVK--GIKWSTSD 1299
 QY 451 GTYMDGLLHH-VSVISPTSGRLRLIDQVLRNORLPSFSNAQGS-----LRLGK---- 499
 DB 1300 KOYHDDGLPHFVTVMSISDTR-YELVVDKSRLRGKN--PTKGABEQTOTTEKKFYGGSPIS 1356
 QY 500 ---GHEPGCISNVLVQFQSPPEVLDAKSTYKDAKSLGCGSLANKPFLMLFSPKPKFK 556
 DB 1357 POYANFGCISNMYFTLDRDVEVEDQRYSEKHTSLYSCPIESSPLFLHKKGNKSK 1416
 QY 557 GRIFNVQALQADAP-----OATRSTEAMQGRSGCLPPLNFKASHRALOPGSDP 604
 DB 1417 PKTKNGQSKSKDAPSPMDPTGLKFLQKAPDSDH-----CHUSSPRALEHAYQYGTIA 1469
 QY 605 TSHLLKLPOELLKPRSPSLDIQTSPKGLVPAAGTKD--SFPLVYADGRVVFALGAG 662
 DB 1470 NSROEPHEHGQDGEKSGQFAIRLKTBSHGMIFVVSQGEENDFWTLFLAGRLVFMNVG 1529
 QY 663 GKTLRLSKRRYHDKKHTVVFGLNGKALVVDGLFAQSGSL-PGNSSTISPREQVTL-G 720
 DB 1530 HKTLKTRSQEKYNDGLMHDVIFIREKSGRLVIDGLVLEBRLPFGSAWKIKGPIYLGG 1589
 QY 721 LPLSRKPKSL---PQHSFVGCGLDPOLNSKPLDPSAPFGVSPCLGSLKGIYFSGCGG 777
 DB 1590 VADGRVAVKNQVITSVVSFSGCLGTLNGLASITSAOSTFVTPTCPESPMETGYFSTEEG 1649
 QY 778 HVLIANSVSLPELKLTPSIRPSRLNGLVHVSQSGQRLSVVMEAGKVTTSVSDAGGS 837
 DB 1650 YVVLDBSFNIGLKEFLAEFRPRSSGTLVHGHSVNGEYLVNHRNQVYVKNNGVGRDF 1709
 QY 838 VTSITPKQSLCDGQWHSVAVSIKORILH 866
 DB 1710 STSVTPKQNLCDGWRHRTYTRDSNVQL 1738

RESULT 13
 LMA5_HUMAN STANDARD; PRT; 3695 AA.
 AC 015230; Q8WZ47; Q9H1P1;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE laminin alpha-5 chain precursor.
 GN Name=LMA5; Synonyms=K1AA0533, K1AA1907;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OC NCBI_TaxId=9606;
 RN
 RP SEQUENCE FROM N.A.
 RX MEDLINE=21638749; Pubmed=11780052; DOI=10.1038/414865a;
 RA DeLoraine P., Matthews L.H., Ashurst J.L., Burton J., Gilbert J.G.R.,
 RA Jones M., Stavrides G., Almeida J.P., Babbage A.K., Bagunley C.L.,
 RA Bailey J., Barlow K.F., Bates K.N., Beard L.M., Beate D.M.,
 RA Beasley O.P., Bird C.P., Blakey S.E., Bridgeman A.M., Brown A.J.,
 RA Buck D., Burrill W.D., Butler A.P., Carder C., Carter N.P.,
 RA Chapman J.C., Clamp M., Clark G., Clark L.N., Clark S.Y., Clee C.M.,
 RA Clegg S., Cobley V.E., Collier R.E., Connor R.E., Corby N.R.,
 RA Coulson A., Coville G.J., Deadman R., Dhami P.D., Dunn M.P.,
 RA Ellington A.G., Frankland J.A., Frazer A., French L., Garner P.,
 RA Graffam D.V., Griffiths C., Griffiths M.N.D., Gwilliam R., Hall R.E.,
 RA Hammond S., Harley J.L., Heath P.D., Ho S., Holden J.L., Howden P.J.,
 RA Huckle E., Hunt A.R., Hunt S.E., Jekosch K., Johnson C.M., Johnson D.,
 RA Kay M.P., Kimberley A.M., King A., Knights A., Laird G.K., Lawlor S.,
 RA Leveson-Hall M.H., Leverish M.A., Lloyd C., Lloyd D.M., Lovell J.D.,
 RA Marsh V.L., Martin S.L., McComachie L.J., McJury K., McMurtry A.A.,
 RA Milne S.A., Mistry D., Moore M.V.F., Mullikin J.C., Nickerson T.,
 RA Olliver K., Parker A., Patel R., Pearce T.A.V., Peck A.I.,
 RA Phillips B.J.C.T., Prathalingam S.R., Plumb R.W., Ramay H.,
 RA Rice C.M., Ross M.T., Scott C.E., Sehra H.K., Shownkeen R., Sims S.,
 RA Stuce C.D., Smith M.L., Soderlund C., Steward C.A., Sulten J.E.,

RA Swann R.M., Sycamore N., Taylor R., Tee L., Thomas D.W., Thorpe A.,
 RA Tracey A., Tromans A.C., Vaudin M., Wall M., Wallis J.M.,
 RA Whitehead S.L., Whiteaker P., Willey D.L., Williams L., Williams S.A.,
 RA Wilming L., Wray P.W., Hubbard T., Durbin R.M., Bentley D.R., Beck S.,
 RA Rogers J.;
 RT "The DNA sequence and comparative analysis of human chromosome 20.";
 RL Nature 414:865-871(2001).
 RP SEQUENCE OF 197-1934 FROM N.A.
 RC TISSUE=Brain;
 RX MEDLINE=21456161; Pubmed=11572484;
 RA Nagase T., Kikuno R., Ohara O.;
 RT "Prediction of the coding sequences of unidentified human genes. XXI.
 RT The complete sequences of 60 new cDNA clones from brain which code for
 RT large proteins.";
 RL DNA Res. 8:179-187(2001).
 RP SEQUENCE OF 2051-3695 FROM N.A.
 RC TISSUE=Brain;
 RX MEDLINE=98290545; Pubmed=9628581;
 RA Nagase T., Ishikawa K.-I., Miyajima N., Tanaka A., Kotani H.,
 RA Nomura N., Ohara O.;
 RT "Prediction of the coding sequences of unidentified human genes. IX.
 RT The complete sequences of 100 new cDNA clones from brain which can
 RT code for large proteins in vitro.";
 RL DNA Res. 5:31-35(1998).
 RP SEQUENCE OF 2743-3695 FROM N.A.
 RC TISSUE=Placenta;
 RX MEDLINE=97415425; Pubmed=9271224; DOI=10.1016/S0014-5793(97)00686-8;
 RA Durkin M.E., Leochel F., Mattei M.-G., Gilpin B.J., Albrechtsen R.,
 RA Newer U.M.;
 RT "Tissue-specific expression of the human laminin alpha5-chain, and
 RT mapping of the gene to human chromosome 20q13.2-13.3 and to distal
 RT mouse chromosome 2 near the locus for the ragged (Ra) mutation.";
 RL FEBS Lett. 411:296-300(1997).
 RP EXPRESSION IN RETINA.
 RX MEDLINE=20422761; Pubmed=10964957;
 RA Libby R.T., Champilaud M.-F., Claudepierre T., Xu Y., Gibbons E.P.,
 RA Koch M., Burgess R.E., Hunter D.D., Brunken W.J.;
 RT "Laminin expression in adult and developing retinae: evidence of two
 RT novel CNS laminins.";
 RL J. Neurosci. 20:6517-6528(2000).
 CC -1- FUNCTION: Binding to cells via a high affinity receptor, laminin
 CC is thought to mediate the attachment, migration and organization
 CC of cells into tissues during embryonic development by interacting
 CC with other extracellular matrix components.
 CC -1- SUBUNIT: Laminin-15 complex is an heterotrimer composed of three
 CC chains (alpha-5/beta-2/gamma-3) which are bound to each other by
 CC disulfide bonds into a cross-shaped molecule comprising one long
 CC and three short arms with globules at each end.
 CC -1- SUBCELLULAR LOCATION: Extracellular; found in the basement
 CC membranes (major component).
 CC -1- TISSUE SPECIFICITY: Expressed in heart, lung, kidney, skeletal
 CC muscle, pancreas, retina and placenta. Little or no expression in
 CC brain and liver.
 CC -1- DOMAIN: Domain G is globular and is part of the major cell-binding
 CC site located in the long arm of the laminin heterotrimer.
 CC -1- SIMILARITY: Contains 22 laminin EGF-like domains.
 CC -1- SIMILARITY: Contains 5 laminin G-like domains.
 CC -1- SIMILARITY: Contains 1 laminin N-terminal domain.
 CC -1- SIMILARITY: Contains 1 laminin N-terminal domain.
 CC THIS SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC EMBL, AL354836; CAC22309.1; ALT_SEQ.

DR EMBL: AL354836; CAC22310.1; -.
DR EMBL: AB067494; BAB67800.1; -.
DR EMBL: AB011105; BAA25459.1; -.
DR EMBL: Z95636; CAB09137.1; -.
DR HSSP: P02468; INPE.
DR Genew: HGNC:6485; LAMA5.
DR MIM: 601033; -.
DR InterPro: IPR008985; Cona1_like_1ec_g1.
DR InterPro: IPR006209; EGF_like.
DR InterPro: IPR008979; Gal_bind_like.
DR InterPro: IPR009030; Grow_fac_recept.
DR InterPro: IPR000034; Laminin_B.
DR InterPro: IPR002049; Laminin_EGF.
DR InterPro: IPR001791; Laminin_G.
DR InterPro: IPR009254; Laminin_H.
DR InterPro: IPR010307; Laminin_II.
DR InterPro: IPR008211; Laminin_N.
DR InterPro: IPR008212; Lam_N2.
DR InterPro: IPR003129; TSP_N.
DR Pfam: PF000052; Laminin_B; 1.
DR Pfam: PF000053; Laminin_EGF; 18.
DR Pfam: PF00054; Laminin_G; 2.
DR Pfam: PF06008; Laminin_I; 1.
DR Pfam: PF06009; Laminin_II; 1.
DR Pfam: PF00055; Laminin_N; 1.
DR PRINTS: PR00011; EGFLAMININ.
DR ProDom: PD003031; Laminin_B; 1.
DR PROSITE: PS00022; EGF_1; 19.
DR PROSITE: PS01186; EGF_2; 3.
DR PROSITE: PS01248; LAMTININ_TYPE_EGF; 19.
DR PROSITE: PS50025; LAM_G_DOMAIN; 5.
DR Basement membrane; Cell adhesion; Coiled coil; Extracellular matrix;
KW Glycoprotein; Laminin EGF-like domain; Repeat; signal.
FT SIGNAL 1 35 Potential.
FT CHAIN 36 3695 Laminin alpha-5 chain.
FT DOMAIN 36 299 Laminin N-terminal (domain VI).
FT DOMAIN 300 358 Laminin EGF-like 1.
FT DOMAIN 359 428 Laminin EGF-like 2.
FT DOMAIN 429 474 Laminin EGF-like 3.
FT DOMAIN 494 540 Laminin EGF-like 4.
FT DOMAIN 541 586 Laminin EGF-like 5.
FT DOMAIN 587 631 Laminin EGF-like 6.
FT DOMAIN 632 676 Laminin EGF-like 7.
FT DOMAIN 677 722 Laminin EGF-like 8.
FT DOMAIN 723 775 Laminin EGF-like 9.
FT DOMAIN 776 828 Laminin EGF-like 10.
FT DOMAIN 829 850 Laminin EGF-like 11 (incomplete).
FT DOMAIN 851 1437 Laminin domain IV 1 (domain IV B).
FT DOMAIN 1438 1483 Laminin EGF-like 12.
FT DOMAIN 1484 1527 Laminin EGF-like 13.
FT DOMAIN 1528 1576 Laminin EGF-like 14.
FT DOMAIN 1577 1627 Laminin EGF-like 15.
FT DOMAIN 1628 1637 Laminin EGF-like 16 (N-terminal).
FT DOMAIN 1638 1830 Laminin domain IV 2 (domain IV A).
FT DOMAIN 1831 1863 Laminin EGF-like 17 (C-terminal).
FT DOMAIN 1864 1912 Laminin EGF-like 18.
FT DOMAIN 1913 1968 Laminin EGF-like 19.
FT DOMAIN 1969 2022 Laminin EGF-like 20.
FT DOMAIN 2023 2069 Laminin EGF-like 21.
FT DOMAIN 2070 2116 Laminin EGF-like 22.
FT DOMAIN 2117 2166 Laminin G-1-like 1.
FT DOMAIN 2167 2735 Laminin G-1-like 2.
FT DOMAIN 2736 2929 Laminin G-1-like 3.
FT DOMAIN 2941 3115 Laminin G-1-like 4.
FT DOMAIN 3124 3292 Laminin G-1-like 5.
FT DOMAIN 3340 3513 Laminin G-1-like 6.
FT DOMAIN 3520 3692 Laminin G-1-like 7.
FT DOMAIN 3693 4221 Laminin G-1-like 8.
FT DOMAIN 4222 4235 Coiled coil (Potential).
FT DOMAIN 4236 4266 Coiled coil (Potential).
FT DOMAIN 4267 4270 Coiled coil (Potential).
FT SITE 1722 1724 Cell attachment site (potential).
FT SITE 1838 1840 Cell attachment site (potential).
FT DISULFID 300 309 By similarity.

FT DISULFID 302 322 By similarity.
FT DISULFID 324 333 By similarity.
FT DISULFID 336 356 By similarity.
FT DISULFID 359 368 By similarity.
FT DISULFID 361 393 By similarity.
FT DISULFID 396 405 By similarity.
FT DISULFID 408 426 By similarity.
FT DISULFID 429 440 By similarity.
FT DISULFID 441 447 By similarity.
FT DISULFID 449 458 By similarity.
FT DISULFID 461 471 By similarity.
FT DISULFID 494 506 By similarity.
FT DISULFID 496 515 By similarity.
FT DISULFID 517 526 By similarity.
FT DISULFID 529 538 By similarity.
FT DISULFID 541 553 By similarity.
FT DISULFID 543 560 By similarity.
FT DISULFID 562 571 By similarity.
FT DISULFID 574 584 By similarity.
FT DISULFID 587 599 By similarity.

Query Match 23.2% Score 1042.5; DB 1; Length 3695;

Best Local Similarity 31.6%; Pred. No. 2.9e-60; Matches 294; Conservative 159; Mismatches 367; Indels 109; Gaps 32;

QY 1 MEFNKSGVEVRLPNDELDKGYTSLDFQRPDLRKNGGTEDEMFVYLGKNDASKDYIG 60
DB 2737 MFENRSGVQARTPRDLADLAAYTALKFYQLQBPBPQGTEDRFRVMTNGSRQATGYMG 2796
QY 61 MAVVDGQLTCVNLGDR-BAEVQIDQVLTBSBSQAVNDKRYKQRIYPAKILNTYKE--- 116
DB 2797 VSLRKKTKVMYVQLGABAPVALSIDEDIGEQ-----PAVSLDITLQFGHMSVVERQM 2850
QY 117 --ATSNKKAPAVVDLGGSSNTLNLDPBAVFYGVGYPDPFELPSRLRPPYKCIEL 174
DB 2851 IGETGDTVAPEA---EG-----LNLKRPDDVFYVGISTFTTPPLRPFPGYCIEM 2902
QY 175 DDLNENVLALYNFKTTFMNLTEVEPCRRRKE-----SDKNYFEGTYARIPTOPN-AP 228
DB 2903 DLTNEBVSLVNFERTFQDLDAVDRPCARSKSTGDPWLTDSYLDGTGPARISPSQST 2962
QY 229 PNFPIQTITQTYDRGLTPFAENQDNFISLNEGNTMRYKLS-----EPP----- 275
DB 2963 TKRFQCELRALVSYSGLVFLKXQSOFLCLAVGEGSLVLYPFGAGLKKAVPLQPPPLTS 3022
QY 276 KKGGRDITNDCKDLSLITGKLGKRMWVNER---SVREGEIPDFTYLLGI--- 329
DB 3023 ASKAIQ-----VFLGSGRKRVLVVERATVYSVEQNDLELADAYLLGAVPPD 3071
QY 330 --PIAIRERFNISTPAFOGCMKLNK---KTSGVVLANDTVGVTKKCSBDMKLVRTASFSR 384
DB 3072 QLPPLRLWLF-P-TGGSVAGCVVGIKALGVYDKLN--TTGVSACTADLVIGRAMTFHG 3129
QY 385 GG-QMSFNLNDVPESTDTPOLSPFGQTPQPSGTLNHOCTRSSLLVTEDEGHIELSTDS 442
DB 3130 HGFPLRLSNV-APLTGVVSGFGFHSADSLALTYRASPGCLCOVSLQOGGVSLQLART 3188
QY 443 NPIRKSPGTWMDGLHHVSVISDTSGLRLIDDOV--LRRNQRLPSRNNQGS-----LR 496
DB 3189 EV---KTOAGFADGAPHYVAFTSNATGVWLVDLDLOQKKRPGRPPBLQPPBGPPLRL 3245
QY 497 LGG-----GHFEGCISNVLVQFSPQSEVVDLALASKSTKQDASIGCSLKKPPLMLFK 549
DB 3246 LGGLESQGTINVFSGCISNVFQRLRGORVFDLOQNGSVNVST--GCA---PALQA-Q 3299
QY 550 SPKRKNKGRIFNVNOLMODAPQATSTEAQWQDGRSCLPPLNTKASHRALQFDSPTSHLL 609
DB 3300 TGLGPRG-----LQATARKASRRSROPAPAHAPKALPPIHRTTRDSYQFGSLSH-- 3350
QY 610 LKLPELKKPR--QPSLDIOTSPKGLVFTAG---TDSFLALVVAQGRVVFALGAGXK 664
DB 3351 LRFVGLIARHNRWPSLSMHWLPRSSRGILLFTARLRPSPSLALFLSNGHVPAQMEGLGT 3410


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Db      3471 GIPASSHSKLPVTYVFGSCVKKRLRHGRPLGAPTYMAGVTPCIIIGPLRAGLFFPGSGGV 3530
QY      779 VILANSVSLGPELKTFFSIRPSRLTGVLIVHG-SOSGQRLSYVMEAGKTTYSVSDAGGS 837
Db      3531 ITLDLPGALPLPVGLELRYPLAVALTGLITHLGQARKPPYLOLVTEKQVLLRADGAGF 3590
QY      838 VTSITPKQSLCDQGMHSAVAISIKORILHL 866
Db      3591 STSVTRPSVLCDOGMHRLAVALMKSQNVRL 3619

RESULT 15
Q6ZQAI
ID      06ZQAI PRELIMINARY; PRT; 1524 AA.
AC      06ZQAI
DT      05-JUL-2004 (TEMBLrel. 27, Created)
DT      05-JUL-2004 (TEMBLrel. 27, Last sequence update)
DT      05-JUL-2004 (TEMBLrel. 27, Last annotation update)
DE      MKIA0533 protein (Fragment).
GN      Name=MKIA0533;
OS      Mus musculus (Mouse).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OX      Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
RN      [1]
RP      SEQUENCE FROM N.A.
RC      TISSUE=Embryonic tail;
RX      PubMed=14621295;
RA      Okazaki N., Kikuno R., Ohara R., Imanoto S., Koeeki H., Hiraoka S.,
RA      Saga Y., Nagase T., Ohara O., Koga H.;
RT      Prediction of the coding sequences of mouse homologues of KIAA gene:
RT      I1. the complete nucleotide sequences of 500 mouse KIAA-homologous
RT      cDNAs identified by screening of terminal sequences of cDNA clones
RT      randomly sampled from size-fractionated libraries."
RL      DNA Res. 10:167-180(2003).
DR      EMBL; AK129157; BAC97967.2; -.
DR      GO; GO:0005604; C:basement membrane; IDA.
DR      GO; GO:0005615; C:extracellular space; TAS.
DR      GO; GO:0005178; P:integrin binding; IDA.
DR      GO; GO:0005515; P:protein binding; IPT.
DR      GO; GO:0001763; P:branching morphogenesis; IDA.
DR      GO; GO:0030324; P:tumorigenesis; IMP.
DR      GO; GO:0007517; P:muscle development; IMP.
DR      InterPro; IPR008985; Cona like_1ec_g1.
DR      InterPro; IPR006209; EGF like.
DR      InterPro; IPR009030; Grow fac. recept.
DR      InterPro; IPR002049; Laminin_EGF.
DR      InterPro; IPR001791; Laminin_G.
DR      InterPro; IPR009254; Laminin_I.
DR      InterPro; IPR010307; Laminin_II.
DR      InterPro; IPR001368; TNFR_c6.
DR      InterPro; IPR003129; TSP_N.
DR      Pfam; PF000653; Laminin_EGF; 2.
DR      Pfam; PF02210; Laminin_G_2; 4.
DR      Pfam; PF06008; Laminin_I; 1.
DR      Pfam; PF06009; Laminin_II; 1.
DR      PRINTS; PR00011; EGF_LAMININ.
DR      SMART; SM00282; EGF_Lam; 2.
DR      PROSITE; PS00022; EGF_1; UNKNOWN_3.
DR      PROSITE; PS01248; LAMININ_TYPE_EGF; UNKNOWN_1.
DR      PROSITE; PS50025; LAM_G_DOMAIN; 5.
DR      PROSITE; PS00652; TNFR_NGFR_1; UNKNOWN_1.
KW      Laminin EGF-like domain.
FT      NON_TER 1
FT      NON_TER 1524
SQ      SEQUENCE 1524 AA; 166516 MW; F43411828F8B691 CRC64;
Query Match 21.2%; Score 950; DB 2; Length 1524;
Best local Similarity 30.6%; Pred. No. 1.3e-54;
Matches 285; Conservative 167; Mismatches 360; Indels 120; Gaps 37;

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QY      1 MRFNGSGVEVRLPNDLEDLKGYSLSLFLQRPDLRENGS--TEBDMFVYMLGNKADSDQY 58
Db      572 MKEFNGSGVRLPTPLDLADLAAYTALKFHIQSPVAPAPRPKNGTGDHFLYMGSRQATDY 631
QY      59 IGMVAVDQQLTCVNYLGR-EAEVQIDQVLTESESGEAVMDRYKQRTYQAKNTYTEA 117
Db      632 MGVSLRNKQVHWVNYLGAAGPTTSLIDENIBQ-----FAVSLDRTLQGFHMSVYE- 684
QY      118 TSNKPKAVVYDLBGS-----SNTLLNDDPEDAVFYGGYPPDFELPRLRPPPKGIC 173
Db      685 -----KQWHEIKQDTPAGSSEGLNHPDDPVYVGYSNTPPRLRPPGLGIC 738
QY      174 LDDLNEVLSLYNFKTFTNLTTEVEPCRRKER-----SDKNYFEGTVARIPQPNAP 228
Db      739 METLNEBVSLYNFQTPMLDTAVDKPCARSKATGDPMLTDGSYLDGSGFARISPEXQ-- 796
QY      229 PPN--PIQTIQTVYDRGLPFAENQDNFISLNTEDGLMRYKLNS-----EPK- 276
Db      797 FSNTRRFOEHLVSYNGIIFFLKQESQFLCVAQEGTLVFPYBGSGLKADPLQAPQA 856
QY      277 -----EKGIQRTINDGKHSILITIGKLQKRMWINNERSVRIEGRIFPSTYLAGI--- 329
Db      857 LTAASKAIQVPLLAGNKRKVLV--RVRATVPSVDQDML--EMAD--AYLGAVPE 908
QY      330 --PIAIRERFNISTPAFGQCMKNLK--KTSGVRLNDTVGVYKXCSQEDMKLVPTASFSR 384
Db      909 QLPLSLRLQLP-SGGSVRCIGIKIKALKGVYDLKRLN-TTGISFCCTADLLVGRMTFHG 966
QY      365 GQGMFTMLDV-PSIDRFQLSFGPOTFQPSGTLNHQRTSSLVLTLEDGHIELSTRSN 443
Db      967 HGFLLALPDAVLTVEVYSGGFGFGYDNNMLLYRTSPDGPYQVLSLEGHVTLEFMQ 1026
QY      444 IPIFSPGYMDGLHHYVSIIDTSGRLRLIDD--QVLRBNQRLPSFSAQA----QSRL 497
Db      1027 V---ETQVVPADGAHHYVAFSNVTGWLVYDDQQLYKSHRTYPMQLQPEBSRLL 1083
QY      498 GG-----GHEEGISNVLVQFESQSPEDVLDAKSKTKKQDASLGCSLNRPFLMLFKS 550
Db      1084 GGLPVSGTFHNSGCGISNVFQRLRGQRFVDLHQMGSVNVSV-GCT----PAQLIETS 1138
QY      551 PRRFRKGIIFNNQMODAPQATRSTEAM-----QDGRSCLPRLNTKASHALQF-GSP 604
Db      1139 RATAQK----VSRSRQPSQDLACTTPTMLPQTIDAVQFGGRLPS-----YLQVGLSP 1188
QY      605 TSHLLKLKPOELKPRSQFSLDIOTSPKGLVYAGTQDSFATLVADGRVVFALGAGAK 664
Db      1189 SHRNKLHLSM-LVRPHASQGLLSTAP-----MGGRSPS-LVFLNIGHFVAQTEGCP 1241
QY      665 KILRSKERYHDGKWHYVFGINGKARLVVDGLRA-QEGSLPGNSTISPREQVYL---- 719
Db      1242 RLQVSRQHSRAGQWHRYSVRWGMQQLQLVVDGSGTWSQKALHHRVPAERPPQYTLVG 1301
QY      720 GIPLRKPKSLP-QHSFPGCLDPQLNPKRPLDSPARKGVSPCLGSLSEKGIYFSGGGH 778
Db      1302 GIPASSYSKLPVSVGFGCLKQLQDKQPLRTPPQMGVVPYPCGSPLEDGIFFGSGGV 1361
QY      779 VILANSVSLGPELKTFFSIRPSRLTGVLIVHGSQSGQRLSYVMEAGKTTYSV-SSDA 834
Db      1362 VTLLEPKAKMPYVSLLEKRPPLAAGLPHL-----GQALATPYMQLKVLTEBVLLQANDG 1417
QY      835 GGSVTSITPKQSLCDQGMHSAVAISIKORILHL 866
Db      1418 AGSFSTWYTPKLCDOGMHRAVAVINGRDTLRL 1449

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Search completed: February 22, 2005, 08:24:20
 Job time : 151.522 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: February 22, 2005, 08:04:10 ; Search time 159.651 Seconds
(without alignments)
2097.921 Million cell updates/sec

Title: US-10-817-423-2

Perfect score: 4491

Sequence: 1 MRFNGKSGYVRLPNDL.....LDCGMHSAVAIKRIHL 866

Scoring table:

BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

A_Geneseq.16Dec04:*
1: geneseq1980s:*
2: geneseq1990s:*
3: geneseq2000s:*
4: geneseq2001s:*
5: geneseq2002s:*
6: geneseq2003as:*
7: geneseq2003bs:*
8: geneseq2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	4491	100.0	1694	3 AAB48461	Aab48461 Rat lamin
2	4491	100.0	1725	3 AAB48460	Aab48460 Rat lamin
3	3560.5	79.3	1693	3 AAB48459	Aab48459 Human lam
4	3560.5	79.3	1693	3 AAB48457	Aab48457 Human lam
5	3560.5	79.3	1713	3 AAB48458	Aab48458 Human cer
6	3560.5	79.3	1713	6 ABR92102	Abi92102 Human cer
7	3560.5	79.3	1713	7 ADD29904	Add29904 Human lam
8	3560.5	79.3	1713	7 ADG37225	Adg37225 Human lam
9	3560.5	79.3	1713	8 ABM81957	Abm81957 Tumour-as
10	3560.5	79.3	1713	8 ADR87606	Adr87606 Human lam
11	3560.5	79.3	1724	3 AAB48456	Aab48456 Human lam
12	3560.5	79.3	3332	7 ADB08094	Adb08094 Novel pro
13	3552.5	79.1	1713	2 AAR70148	Aar70148 Deduced s
14	1599	35.6	469	4 AAG75103	Agg75103 Human col
15	1310	29.2	770	2 AAW26584	Aaw26584 Rat hemid
16	1198	26.7	1792	3 AAB48443	Aab48443 Human lam
17	1198	26.7	1800	3 AAB48445	Aab48445 Human lam
18	1198	26.7	1816	3 AAB48442	Aab48442 Human lam
19	1198	26.7	1816	8 ADR87600	Adr87600 Human lam
20	1198	26.7	1824	3 AAB48444	Aab48444 Human lam
21	1192	26.5	1823	5 ABP63020	Abp63020 Human pol
22	1190	26.5	1581	7 ADU68348	Adu68348 Human hea
23	1190	26.4	1816	8 ADP08401	Adp08401 Human lam
24	1187	26.4	984	5 ABB80819	Abb80819 Heparin b
25	1187	26.4	1816	7 ADC01877	Adc01877 Human lam

ALIGNMENTS

26	1185	26.4	1816	7 ADC01879	Adc01879 Human lam
27	1183	26.3	1792	3 AAB48447	Aab48447 Mouse lam
28	1183	26.3	1816	3 AAB48446	Aab48446 Mouse lam
29	1181.5	26.3	1815	5 ABB80853	Abb80853 Heparin b
30	1170.5	26.1	983	5 ABB80818	Abb80818 Heparin b
31	1045.5	23.3	1677	8 ADM87708	Adm87708 Human EST
32	1045.5	23.3	3695	8 ADI28030	Adi28030 ECMCAD pr
33	1045.5	23.3	3695	8 ADN04478	Adn04478 Antipeori
34	1045.5	23.3	3695	8 ABR17310	Abr17310 Human lam
35	1045.5	23.3	3705	5 AAB17309	Aab17309 Human lam
36	1042.5	23.2	1601	4 AAM39009	Aam39009 Human pol
37	1042.5	23.2	1645	7 ADI15098	Adi15098 Human mal
38	1042.5	23.2	1645	7 ADN95658	Adn95658 Human BRC
39	1042.5	23.2	3695	5 ABR81588	Abi81588 Human lam
40	1042	23.2	1640	5 ABR09504	Abi09504 Human lam
41	1042	23.2	1640	8 ADO10049	Ado10049 Novel hum
42	1041	23.2	3690	8 ADM87254	Adm87254 Human pro
43	1015.5	22.6	953	5 AAM50358	Aam50358 Human lam
44	948	21.1	3635	5 ABB81589	Abb81589 Mouse lam
45	948	21.1	3635	5 AAM50357	Aam50357 Mouse lam

RESULT 1
AAB48461
ID AAB48461 standard; protein; 1694 AA.
AC AAB48461;
XX
XX
DT 02-MAR-2001 (first entry)
DE Rat laminin 5 polypeptide, SEQ ID NO: 12.
XX
XX Rat; laminin 5; vulnery; antilucer; antiinflammatory; antidiabetic;
KM cell adhesion promoter; wound healing; ulcers; burn; skin graft;
KW periodontitis; gingivitis; Type I diabetes; angiogenesis regulation.
XX
XX Rattus norvegicus.
OS
PN W0200066731-A2.
XX
PD 09-NOV-2000.
XX
PF 28-APR-2000; 2000MO-US011459.
XX
PR 30-APR-1999; 99US-0131720P.
PR 21-AUG-1999; 99US-0149738P.
PR 24-SEP-1999; 99US-0155945P.
XX
PA (BIOS-) BIOSTATUM INC.
PI Boutaud A;
DR WPI, 2000-687538/67.
DR N-PSDB; AAC83722.
PT Laminin 5-expressing cells, used to accelerate wound healing associated
PT with diabetic foot ulcers, venous ulcers, pressure sores, skin surgery,
PT burn, acute wounds and skin grafts.
XX
XX Claim 3; Page 117-122; 232pp; English.
XX
XX The present sequence is a laminin 5 chain polypeptide. Recombinant
XX laminin 5-expressing cells are used to accelerate wound healing,
XX especially diabetic foot ulcers, venous ulcers, pressure sores, skin
XX surgery, burns, acute wounds, skin grafts, corneal ulcerations, gastro-
XX intestinal ulcers, periodontitis, and gingivitis. They are also used to
XX improve the biocompatibility of medical devices, and to promote cell
XX adhesion to a surface. They can be used for the ex vivo treatment of Type
XX I diabetes. Laminin can also be used to regulate angiogenesis. The cell
XX line produces and secretes recombinant heterotrimeric laminin, whereas

CC prior art cell lines have been created that produce but do not secrete
CC only one or two chain laminins
XX
XX
SQ Sequence 1694 AA;

Query Match 100.0%; Score 4491; DB 3; Length 1694;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 866; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRFNGSGVEVRLPNDLEDKGYTSLFLQRPDLRENGTEDMFVMTLGNDAKXDYIG 60
DB 751 MRFNGSGVEVRLPNDLEDKGYTSLFLQRPDLRENGTEDMFVMTLGNDAKXDYIG 810
QY 61 MAVVDQQLTCVYNLGDREAEVQIDQVLTSESGQEAVMDRVKFQRIYQPAKNTYKEATSN 120
DB 811 MAVVDQQLTCVYNLGDREAEVQIDQVLTSESGQEAVMDRVKFQRIYQPAKNTYKEATSN 870
QY 121 KKPAPAVYDLEGGSSNTLNLDPEDAVFYGGYPPDFELPSRLRPPYKGCIELDLNEN 180
DB 871 KKPAPAVYDLEGGSSNTLNLDPEDAVFYGGYPPDFELPSRLRPPYKGCIELDLNEN 930
QY 181 VLSVNFKTTFNLTTEVEPCRRKESDKNYFEQGYARIPTQNPAPFPNFQTIQTTV 240
DB 931 VLSVNFKTTFNLTTEVEPCRRKESDKNYFEQGYARIPTQNPAPFPNFQTIQTTV 990
QY 241 DRGLLPPAENQDNFISLINEDGNLMVRYKLNSEPPKEGIRDTINDGKHSILITIGKQ 300
DB 991 DRGLLPPAENQDNFISLINEDGNLMVRYKLNSEPPKEGIRDTINDGKHSILITIGKQ 1050
QY 301 KRWIVNERSVAREGIRPFSTYYIGLPIARERNISTPAPQCGMKLKTSGVNL 360
DB 1051 KRWIVNERSVAREGIRPFSTYYIGLPIARERNISTPAPQCGMKLKTSGVNL 1110
QY 361 NDVVGATKCKSEPMKLVRTASFSRGQMSFTNLDPVSTDFOLSPFGQTPQPSGTLNMQ 420
DB 1111 NDVVGATKCKSEPMKLVRTASFSRGQMSFTNLDPVSTDFOLSPFGQTPQPSGTLNMQ 1170
QY 421 TRTSSLVLTLEDGHIELSTDSNIPIFKSPGYMDGLHHVYSISPTSGRLIIDQVLR 480
DB 1171 TRTSSLVLTLEDGHIELSTDSNIPIFKSPGYMDGLHHVYSISPTSGRLIIDQVLR 1230
QY 481 RNORLRSFSNAQOSLRLGGGHFPGCISNVLYVQPSQPEVLDLASKSTKDAKSLGCSLN 540
DB 1231 RNORLRSFSNAQOSLRLGGGHFPGCISNVLYVQPSQPEVLDLASKSTKDAKSLGCSLN 1290
QY 541 KPPFLMLFKSPKPFNGRIFNVNQLMODAPQATRSSTAMODGRSCPLMTKASHRALQ 600
DB 1291 KPPFLMLFKSPKPFNGRIFNVNQLMODAPQATRSSTAMODGRSCPLMTKASHRALQ 1350
QY 601 GDSPTSHLLKLPQELLKPRSQPSLDIQTTSPKGLVFACTKOSPLALVYADGRVVFALQ 660
DB 1351 GDSPTSHLLKLPQELLKPRSQPSLDIQTTSPKGLVFACTKOSPLALVYADGRVVFALQ 1410
QY 661 AGGKCLRLSKERYHNGKMTTVFGLNGKARLYVDGLAQESLPGNSTISPREQVYIG 720
DB 1411 AGGKCLRLSKERYHNGKMTTVFGLNGKARLYVDGLAQESLPGNSTISPREQVYIG 1470
QY 721 LPLSRKPKSLPQHSFVGCLRDPOLNSKPLDPSARFVSPLDGSLEKGYFQGGGHV 780
DB 1471 LPLSRKPKSLPQHSFVGCLRDPOLNSKPLDPSARFVSPLDGSLEKGYFQGGGHV 1530
QY 781 LANSVSLGPELKLTFISIRPSLTGVLIHVSQSGQRLSYVMEAGKVTTSVSDAGSVYS 840
DB 1531 LANSVSLGPELKLTFISIRPSLTGVLIHVSQSGQRLSYVMEAGKVTTSVSDAGSVYS 1590
QY 841 ITPKOSICDQOMHSVAVSIKORILHL 866
DB 1591 ITPKOSICDQOMHSVAVSIKORILHL 1616

RESULT 2
AAB48460 standard; protein; 1725 AA.

XX AAB48460;
AC
XX
XX
DT 02-MAR-2001 (first entry)
XX
XX Rat laminin 5 polypeptide, SEQ ID NO: 10.
DE
XX Rat; laminin 5; vulnery; antilucer; antinflammatory; antidiabetic;
XX cell adhesion promoter; wound healing; ulcers; burn; skin graft;
XX periodontitis; gingivitis; Type I diabetes; angiogenesis regulation.
OS
XX Rattus norvegicus.
XX
XX WO20066731-A2.
XX
XX PD 09-NOV-2000.
XX
XX 28-APR-2000; 2000WO-US011459.
XX
XX 30-APR-1999; 99US-0131720P.
XX 21-AUG-1999; 99US-0149738P.
XX 24-SEP-1999; 99US-0155945P.
XX
XX (BIO-) BIOSTATUM INC.
XX
XX Boutaud A;
XX
XX WPI; 2000-687538/67.
XX N-PSDB; AAC83721.
XX
XX Laminin 5-expressing cells, used to accelerate wound healing associated
XX with diabetic foot ulcers, venous ulcers, pressure sores, skin surgery,
XX burns, acute wounds and skin grafts.
XX
XX Claim 3; Page 104-109; 232pp; English.
XX
XX The present sequence is a laminin 5 chain polypeptide. Recombinant
XX laminin 5-expressing cells are used to accelerate wound healing,
XX especially diabetic foot ulcers, venous ulcers, pressure sores, skin
XX surgery, burns, acute wounds, skin grafts, corneal ulcerations, gastro-
XX intestinal ulcers, periodontitis, and gingivitis. They are also used to
XX improve the biocompatibility of medical devices, and to promote cell
XX adhesion to a surface. They can be used for the ex vivo treatment of Type
XX I diabetes. Laminin can also be used to regulate angiogenesis. The cell
XX line produces and secretes recombinant heterotrimeric laminin, whereas
XX prior art cell lines have been created that produce but do not secrete
XX only one or two chain laminins
XX
XX SQ Sequence 1725 AA;
XX
XX Query Match 100.0%; Score 4491; DB 3; Length 1725;
XX Best Local Similarity 100.0%; Pred. No. 0;
XX Matches 866; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX 1 MRFNGSGVEVRLPNDLEDKGYTSLFLQRPDLRENGTEDMFVMTLGNDAKXDYIG 60
DB 782 MRFNGSGVEVRLPNDLEDKGYTSLFLQRPDLRENGTEDMFVMTLGNDAKXDYIG 841
QY 61 MAVVDQQLTCVYNLGDREAEVQIDQVLTSESGQEAVMDRVKFQRIYQPAKNTYKEATSN 120
DB 842 MAVVDQQLTCVYNLGDREAEVQIDQVLTSESGQEAVMDRVKFQRIYQPAKNTYKEATSN 901
QY 121 KKPAPAVYDLEGGSSNTLNLDPEDAVFYGGYPPDFELPSRLRPPYKGCIELDLNEN 180
DB 902 KKPAPAVYDLEGGSSNTLNLDPEDAVFYGGYPPDFELPSRLRPPYKGCIELDLNEN 961
QY 181 VLSVNFKTTFNLTTEVEPCRRKESDKNYFEQGYARIPTQNPAPFPNFQTIQTTV 240
DB 962 VLSVNFKTTFNLTTEVEPCRRKESDKNYFEQGYARIPTQNPAPFPNFQTIQTTV 1021
QY 241 DRGLLPPAENQDNFISLINEDGNLMVRYKLNSEPPKEGIRDTINDGKHSILITIGKQ 300
DB 1022 DRGLLPPAENQDNFISLINEDGNLMVRYKLNSEPPKEGIRDTINDGKHSILITIGKQ 1081


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QY 301 KRWIVNERSVIREGIPDSTYYLIGIPAIAREPNISTPAFGCKMLKKTSGVRL 360
DB 1082 KRWIVNERSVIREGIPDSTYYLIGIPAIAREPNISTPAFGCKMLKKTSGVRL 1141
QY 361 NDTVGVTKKCESEDMKLVRTASFSRGGOMSTNLDVPESTRFOLSFQGFOTQPSGTLNHQ 420
DB 1142 NDTVGVTKKCESEDMKLVRTASFSRGGOMSTNLDVPESTRFOLSFQGFOTQPSGTLNHQ 1201
QY 421 TRTSLLVTLDEGHIELSTDSNIPFKSPQTYMDGLHHVSVISDTSGRLIIDQVLR 480
DB 1202 TRTSLLVTLDEGHIELSTDSNIPFKSPQTYMDGLHHVSVISDTSGRLIIDQVLR 1261
QY 481 RNORLPSFNAOOSLRIGGHPFGCISNVAVQPSQSPRYLDLASKTKDASLGGCSLN 540
DB 1262 RNORLPSFNAOOSLRIGGHPFGCISNVAVQPSQSPRYLDLASKTKDASLGGCSLN 1321
QY 541 KPPFLMLFKSPKPKRGRIFNVNQLMODAPQATSTAMODGRSCPLPLNTKASHRALQ 600
DB 1322 KPPFLMLFKSPKPKRGRIFNVNQLMODAPQATSTAMODGRSCPLPLNTKASHRALQ 1381
QY 601 GDSPTSHLLKLPQELKPRSQPSLDIQTTSFKGLVFACTKOSFLALVYADGRVPAAG 660
DB 1382 GDSPTSHLLKLPQELKPRSQPSLDIQTTSFKGLVFACTKOSFLALVYADGRVPAAG 1441
QY 661 AGGKCLRLSKERYHDKMTTVYFGLNGKARLYVDGLRAOEGSLPKNSTIISPREQVYL 720
DB 1442 AGGKCLRLSKERYHDKMTTVYFGLNGKARLYVDGLRAOEGSLPKNSTIISPREQVYL 1501
QY 721 LPLSRKPKSLPOHSFVGCALDPOLNSKPLDPSARFVSPCLGGSLKGIYFSQGGSHV 780
DB 1502 LPLSRKPKSLPOHSFVGCALDPOLNSKPLDPSARFVSPCLGGSLKGIYFSQGGSHV 1561
QY 781 IANSVSLGPELKLTFISIRPSRLTGVLIHVSQSQSQRSLVYMEAGKVTTSVSDAGSVTS 840
DB 1562 IANSVSLGPELKLTFISIRPSRLTGVLIHVSQSQSQRSLVYMEAGKVTTSVSDAGSVTS 1621
QY 841 ITPKQSLCDGQMSVAVSIKORILHL 866
DB 1622 ITPKQSLCDGQMSVAVSIKORILHL 1647

RESULT 3
AAB48459 standard; protein; 1693 AA.
AC AAB48459;
DB 02-MAR-2001 (first entry)
XX Human laminin 5 polypeptide, SEQ ID NO: 8.
DE Human laminin 5; vulnerability; antiulcer; antiinflammatory; antidiabetic;
KW cell adhesion promoter; wound healing; ulcers; burn; skin graft;
KW periodontitis; gingivitis; type 1 diabetes; angiogenesis regulation.
XX Homo sapiens.
XX
XX WO200066731-A2.
XX
XX 09-NOV-2000.
XX
XX 28-APR-2000; 2000WO-US011459.
XX
XX 30-APR-1999; 99US-0131720P.
XX 21-AUG-1999; 99US-0149738P.
XX 24-SEP-1999; 99US-0155945P.
XX
XX (BIOS-) BIOSTATUM INC.
XX
XX Boutaud A;
XX
XX WPI; 2000-687538/67.

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DR N-PSDB; AAC83720.
XX Laminin 5-expressing cells, used to accelerate wound healing associated
PT with diabetic foot ulcers, venous ulcers, pressure sores, skin surgery,
PT burns, acute wounds and skin grafts.
XX
XX Claim 3; Page 91-97; 232pp; English.
XX
XX The present sequence is a laminin 5 chain polypeptide. Recombinant
CC laminin 5-expressing cells are used to accelerate wound healing, skin
CC especially diabetic foot ulcers, venous ulcers, pressure sores, skin
CC surgery, burns, acute wounds, skin grafts, corneal ulcerations, gastro-
CC intestinal ulcers, periodontitis, and gingivitis. They are also used to
CC improve the biocompatibility of medical devices, and to promote cell
CC adhesion to a surface. They can be used for the ex vivo treatment of type
CC I diabetes. Laminin can also be used to regulate angiogenesis. The cell
CC line produces and secretes recombinant heterotimeric laminin, whereas
CC prior art cell lines have been created that produce but do not secrete
CC only one or two chain laminins
XX
XX Sequence 1693 AA:
XX
XX Query Match 79.3%; Score 3560.5; DB 3; Length 1693;
XX Best Local Similarity 78.4%; Pred. No. 2.9e-307;
XX Matches 680; Conservative 86; Mismatches 98; Indels 3; Gaps 2;
XX
QY 1 MRFNGSGVHEVRLPNDLEDKGYTSLPLQRPDLAENGTEDMFWYLLGNKASCHYIG 60
DB 751 MRFNGSGVHEVRLPNDLEDKGYTSLPLQRPDLAENGTEDMFWYLLGNKASCHYIG 810
QY 61 MAVVDGLTCVNLGDBREAVOIDVLTSESOEAVMDRYKFORIYOFALNTYKATSN 120
DB 811 MAVVDGLTCVNLGDBREAVOIDVLTSESOEAVMDRYKFORIYOFALNTYKATSN 870
QY 121 KPRAPAVYDLEGSSNTLNLDEDAVFYVGYPPPELPSRLRFPYKGCIBLDLNN 180
DB 871 KPRAPAVYDLEGSSNTLNLDEDAVFYVGYPPPELPSRLRFPYKGCIBLDLNN 930
QY 181 VLSLYNFKTNTNTTEVEPCRRKESDKNYBEGGYARIPIOPNAPFNFOTIOTTV 240
DB 931 VLSLYNFKTNTNTTEVEPCRRKESDKNYBEGGYARIPIOPNAPFNFOTIOTTV 990
QY 241 DRGLPFAENQDNFISLNIEDGULMVRKLNSEPKKGRDITNDCKHSILITIKLO 300
DB 991 DRGLPFAENQDNFISLNIEDGULMVRKLNSEPKKGRDITNDCKHSILITIKLO 1050
QY 991 DRGLPFAENQDNFISLNIEDGULMVRKLNSEPKKGRDITNDCKHSILITIKLO 1050
DB 1051 KRWIVNERSVIREGIPDSTYYLIGIPAIAREPNISTPAFGCKMLKKTSGVRL 1110
QY 301 KRWIVNERSVIREGIPDSTYYLIGIPAIAREPNISTPAFGCKMLKKTSGVRL 360
DB 1051 KRWIVNERSVIREGIPDSTYYLIGIPAIAREPNISTPAFGCKMLKKTSGVRL 1110
QY 361 NDTVGVTKKCESEDMKLVRTASFSRGGOMSTNLDVPESTRFOLSFQGFOTQPSGTLNHQ 420
DB 1111 NDTVGVTKKCESEDMKLVRTASFSRGGOMSTNLDVPESTRFOLSFQGFOTQPSGTLNHQ 1170
QY 421 TRTSLLVTLDEGHIELSTDSNIPFKSPQTYMDGLHHVSVISDTSGRLIIDQVLR 480
DB 1171 TRTSLLVTLDEGHIELSTDSNIPFKSPQTYMDGLHHVSVISDTSGRLIIDQVLR 1230
QY 481 RNORLPSFNAOOSLRIGGHPFGCISNVAVQPSQSPRYLDLASKTKDASLGGCSLN 540
DB 1231 RNORLPSFNAOOSLRIGGHPFGCISNVAVQPSQSPRYLDLASKTKDASLGGCSLN 1290
QY 541 KPPFLMLFKSPKPKRGRIFNVNQLMODAPQAT-RSTEAMODGRSCPLPLNTKASHRALQ 599
DB 1291 KPPFLMLFKSPKPKRGRIFNVNQLMODAPQAT-RSTEAMODGRSCPLPLNTKASHRALQ 1348
QY 600 RGSPTSHLLKLPQELKPRSQPSLDIQTTSFKGLVFACTKOSFLALVYADGRVPAAG 659
DB 1349 RGSPTSHLLKLPQELKPRSQPSLDIQTTSFKGLVFACTKOSFLALVYADGRVPAAG 1408
QY 660 GAGGKCLRLSKERYHDKMTTVYFGLNGKARLYVDGLRAOEGSLPKNSTIISPREQVYL 719
DB 1409 GAGGKCLRLSKERYHDKMTTVYFGLNGKARLYVDGLRAOEGSLPKNSTIISPREQVYL 1468

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QY 720 GPLESRKPSLPOHSPVGCRLDPOLNSKPLDSPSARFVSPCLGSLERKGIYFSSQGGHY 779
DB 1469 GSPSGKPSLPTNSFVGCRLKKNFOLDSPKLYTPSSSFVSSCLGSLERKGIYFSSQGGHY 1528
QY 780 ILANSVSLPELKLTFPSIRPSRLTGVLHVSGSGORLSVYMEAGVTTSSVSDAGGSVT 839
DB 1529 VLAHSTVLDPERFCLVFSIRPSRLTGVLHVSGSGORLSVYMEAGVTTSSVSDAGGSVT 1588
QY 840 SITPKOSLCDGQWHSVAVSIRKRIHL 866
DB 1589 SITPKOSLCDGQWHSVAVTIKQHILHL 1615

RESULT 4
AAB48457
ID AAB48457 standard; protein; 1693 AA.

AC AAB48457;
DT 02-MAR-2001 (first entry)
XX
DB Human laminin 5 polypeptide, SEQ ID NO: 4.
XX Human; laminin 5; vulnery; antilucer; antinflammatory; antidiabetic;
XX cell adhesion promoter; wound healing; ulcers; burn; skin graft;
XX periodontitis; gingivitis; Type I diabetes; angiogenesis regulation.
OS Homo sapiens.
XX MO200066731-A2.
XX 09-NOV-2000.
PD
PF 28-APR-2000; 2000MO-US011459.
XX 30-APR-1999; 99US-0131720P.
XX 21-AUG-1999; 99US-0149738P.
PR 24-SEP-1999; 99US-0155945P.
XX
PA (BIOS-) BIOSTATUM INC.
XX
PI Boudaud A;
XX
DR MPI; 2000-687538/67.
DR N-PSDB; AAC83718.
XX
PT Laminin 5-expressing cells, used to accelerate wound healing associated
PT with diabetic foot ulcers, venous ulcers, pressure sores, skin surgery,
PT burns, acute wounds and skin grafts.
XX
XX
PS Claim 3; Page 66-71; 232pp; English.
XX
XX The present sequence is a laminin 5 chain polypeptide. Recombinant
CC laminin 5-expressing cells are used to accelerate wound healing,
CC especially diabetic foot ulcers, venous ulcers, pressure sores, skin
CC surgery, burns, acute wounds, skin grafts, corneal ulcerations, gastro-
CC intestinal ulcers, periodontitis, and gingivitis. They are also used to
CC improve the biocompatibility of medical devices, and to promote cell
CC adhesion to a surface. They can be used for the ex vivo treatment of type
CC I diabetes. Laminin can also be used to regulate angiogenesis. The cell
CC line produces and secretes recombinant heterotrimeric laminin, whereas
CC prior art cell lines have been created that produce but do not secrete
CC only one or two chain laminins
XX
SQ Sequence 1693 AA;

Query Match 79.3%; Score 3560.5; DB 3; Length 1693;
Best Local Similarity 78.4%; Pred. No. 2.9e-307;
Matches 680; Conservative 86; Mismatches 98; Indels 3; Gaps 2;
QY 1 MRVNGSGVEVRLPNDLEDLKGYSLSLFLQRLDLENGTEPMFYVTLAKNDASRDYIG 60
|||||

DB 751 MRVNGSGVEVRLPNDLEDLKGYSLSLFLQRLDLENGTEPMFYVTLAKNDASRDYIG 810
QY 61 MAVVDGQLTCVYNLADREARVQIDQVLTESSQEAVMQVRFQRYQPAKNTYKATSN 120
DB 811 MAVVDGQLTCVYNLADREARVQIDQVLTESSQEAVMQVRFQRYQPAKNTYKATSN 870
QY 121 KKKABAVYDLRGSSNTLLNTLDPEDAVFYVGGPPDFELPSRLRPPYKGIELDLNEN 180
DB 871 KPEPQVYDMQGRNNTLLNTLDPEDAVFYVGGPPDFELPSRLRPPYKGIELDLNEN 930
QY 181 VLSLNFKTPRLNTTVEPCRRRKESEDKRYFEGTGARLPQGNAPFNPFIQTIQTV 240
DB 931 VLSLNFKTPRLNTTVEPCRRRKESEDKRYFEGTGARLPQGNAPFNPFIQTIQTV 990
QY 241 DRGLLFPANODNFISSLNIEDQNLAVRYKLNSEPPKEGIDTINDGSHLITIGLQ 300
DB 991 DRGLLFPANODNFISSLNIEDQNLAVRYKLNSEPPKEGIDTINDGSHLITIGLQ 1050
QY 301 KKMWINNERSVRLBGEIIFDEFTYLLGGIPIAIRERFNISTPAFGCKMNLKKTSGVVRL 360
DB 1051 KKMWINNERSVRLBGEIIFDEFTYLLGGIPIAIRERFNISTPAFGCKMNLKKTSGVVRL 1110
QY 361 NDTVGVTKKCSBDMCLVYRTASPSRGGQMSFTNLDPVPSIDRQLSTRFQTPQSGTILNHQ 420
DB 1111 NDTVGVTKKCSBDMCLVYRTASPSRGGQMSFTNLDPVPSIDRQLSTRFQTPQSGTILNHQ 1170
QY 421 TPTSILVLEBDEGHIELSTRDSNIPFSPGTYMDGLLHVSVISDTSGRLILDDQYLK 480
DB 1171 TPTSILVLEBDEGHIELSTRDSNIPFSPGTYMDGLLHVSVISDTSGRLILDDQYLK 1230
QY 481 RNQRLPSFSMAQOSLRLGQHEGECISNVLVQRFSSQSPFVLDLASKSTKQDASLGGCSLN 540
DB 1231 NSKRLKHTSSSRQSLRLAGSNBEGCISNVFQRLSLSEVLDLTSNLSKRDVSLGGCSLN 1290
QY 541 KPPFLMLKSPKRFKRGRIENVNQLMODAPQAT-RSTANQDGRCLPLNTKASHRLQ 599
DB 1291 KPPFLMLKSPKRFKRGRIENVNQLMODAPQAT-RSTANQDGRCLPLNTKASHRLQ 1348
QY 600 FGDSPFTHLLKLPOLKLPSPQSLDQITTSFKGLVYAGTKDSFLLAYVADGVFPAL 659
DB 1349 FGDSPFTHLLKLPOLKLPSPQSLDQITTSFKGLVYAGTKDSFLLAYVADGVFPAL 1408
QY 660 GAGGKKLRLSKERYHDKMHTVVFGLNGKARLVVDGLRAQEGSLPNSNTISPREQVYL 719
DB 1409 GTDGKKLRLSKERYHDKMHTVVFGLNGKARLVVDGLRAQEGSLPNSNTISPREQVYL 1468
QY 720 GPLESRKPSLPOHSPVGCRLDPOLNSKPLDSPSARFVSPCLGSLERKGIYFSSQGGHY 779
DB 1469 GSPSGKPSLPTNSFVGCRLKKNFOLDSPKLYTPSSSFVSSCLGSLERKGIYFSSQGGHY 1528
QY 780 ILANSVSLPELKLTFPSIRPSRLTGVLHVSGSGORLSVYMEAGVTTSSVSDAGGSVT 839
DB 1529 VLAHSTVLDPERFCLVFSIRPSRLTGVLHVSGSGORLSVYMEAGVTTSSVSDAGGSVT 1588
QY 840 SITPKOSLCDGQWHSVAVSIRKRIHL 866
DB 1589 SITPKOSLCDGQWHSVAVTIKQHILHL 1615

RESULT 5
AAB48458
ID AAB48458 standard; protein; 1713 AA.

AC AAB48458;
DT 02-MAR-2001 (first entry)
XX
XX Human laminin 5 polypeptide, SEQ ID NO: 6.
DB Human; laminin 5; vulnery; antilucer; antinflammatory; antidiabetic;
XX cell adhesion promoter; wound healing; ulcers; burn; skin graft;
XX periodontitis; gingivitis; Type I diabetes; angiogenesis regulation.
XX

OS Homo sapiens.
 PN WO200066731-A2.
 PD 09-NOV-2000.
 XX 28-APR-2000; 2000WO-US011459.
 PF 30-APR-1999; 99US-0131720P.
 PR 21-ADG-1999; 99US-0149738P.
 PR 24-SEP-1999; 99US-0155945P.
 PA (BIOS-) BIOSTATUM INC.
 XX Boutaud A;
 PI WPI; 2000-687538/67.
 DR N-PSDB; AAC83719.
 XX Laminin 5-expressing cells, used to accelerate wound healing associated
 PT with diabetic foot ulcers, venous ulcers, pressure sores, skin surgery,
 PT burns, acute wounds and skin grafts.
 PS Claim 3; Page 79-84; 232pp; English.
 XX The present sequence is a laminin 5 chain polypeptide. Recombinant
 CC laminin 5-expressing cells are used to accelerate wound healing,
 CC especially diabetic foot ulcers, venous ulcers, pressure sores, skin
 CC surgery, burns, acute wounds, skin grafts, corneal ulcerations, gastro-
 CC intestinal ulcers, periodontitis, and gingivitis. They are also used to
 CC improve the biocompatibility of medical devices, and to promote cell
 CC adhesion to a surface. They can be used for the ex vivo treatment of Type
 CC I diabetes. Laminin can also be used to regulate angiogenesis. The cell
 CC line produces and secretes recombinant heterotrimeric laminin, whereas
 CC prior art cell lines have been created that produce but do not secrete
 CC only one or two chain laminins
 XX
 SQ Sequence 1713 AA;
 Query Match 79.3%; Score 3560.5; DB 3; Length 1713;
 Best Local Similarity 78.4%; Pred. No. 2.9e-307;
 Matches 680; Conservative 86; Mismatches 98; Indels 3; Gaps 2;
 QY 1 MRNNGSGGVYRLPNLEDDIKGTTSLSPQRPDLRENGTDMFWYLGKMSADYTG 60
 DB 771 MRNNGSGGVYRLPNLEDDIKGTTSLSPQRPDLRENGTDMFWYLGKMSADYTG 830
 QY 61 MAYVDDQLTCVYMLGDRERAEVQIDOVLTSESQEAAMDVKYKFORIYQFALNTTKATSN 120
 DB 831 MAYVDDQLTCVYMLGDRERAEVQIDOVLTSESQEAAMDVKYKFORIYQFALNTTKATSN 890
 QY 121 KPRAPAVYDLEGSSNTLNTLDEPDVAVYVGGYPPPELPSRLRFPYKGCIELDLNEN 180
 DB 891 KPRAPAVYDLEGSSNTLNTLDEPDVAVYVGGYPPPELPSRLRFPYKGCIELDLNEN 950
 QY 181 VLSLVNFKTTFNLTTEVEPCRRKESDKNYFEGTGYARIPTQENAPFNPTQITQTV 240
 DB 951 VLSLVNFKTTFNLTTEVEPCRRKESDKNYFEGTGYARIPTQENAPFNPTQITQTV 1010
 QY 241 DRGLTFAENQDPFISINIDGNLMAVRYKLNSEPKKGRDPTINOKSHSIITLGKQ 300
 DB 1011 DRGLTFAENQDPFISINIDGNLMAVRYKLNSEPKKGRDPTINOKSHSIITLGKQ 1070
 QY 301 KRWMINVNSVRIEGERIPDFSTYYLGIPAIAREFNISTPAFQGMKNLKTSGVRL 360
 DB 1071 KRWMINVNSVRIEGERIPDFSTYYLGIPAIAREFNISTPAFQGMKNLKTSGVRL 1130
 QY 361 NDVVGVTKKCSBWKLVRTASFSRGGMSNTNDVETDFQLSFGQTQPSGTILAHQ 420
 DB 1131 NDVVGVTKKCSBWKLVRTASFSRGGMSNTNDVETDFQLSFGQTQPSGTILAHQ 1190
 QY 421 TRTSLLVLTLEDGIELSTSDSNPIPKSGPYWADGILHHVSVSDTSGRLTIDDOVR 480
 DB 421 TRTSLLVLTLEDGIELSTSDSNPIPKSGPYWADGILHHVSVSDTSGRLTIDDOVR 480

1191 TWTBRLQVLTABDGYIELSTSDSGGPIFKSPQTYMDGLAHYVSIIDNSGLRLTIDDOVR 1250
 QY 481 RNQRLPSFENAAQSLRIGGHEGCI SNLYVRFSSPEVLDLASKSTKQASLGCSIN 540
 DB 1251 NSRRLKHSSRSQSLAGSNEGCI SNVFDLSLSPVLDLTSNLRADVSLGCSIN 1310
 QY 541 KPPFLMLFKSPKRFNKGRIENYVQMLQDAPQAT-RSTBAMODGRSCLPPLNTKASHRALQ 599
 DB 1311 KPPFLMLKSGTRFNKTKTFRLNQLLDTPVASPRVTKWQD--ACSPLEKQANHALQ 1368
 QY 600 FSDSPTSHLLKLPQELKPRSQFSLDIQTTSPKGLVFACTGDSFLAYADGRVVAL 659
 DB 1369 FGDIPFTHLLFKLPQELKPRSQFADVMQTSRGLVFHTGTGNSFMALYLSGRLVVAL 1428
 QY 660 GAGGKRLRKSERKRYHDKWHTVVRGLNGKXRLVYVDDGLRABGSLPGNSTISPREQVLT 719
 DB 1429 GTDGKRLRKSKKCKNDGMHTVVFHDEKGLVVDGLRABGSLPGNSTISIRAPVLT 1488
 QY 720 GLPLSRKPSLPOHSPVGCILDPQLNSKPLDPSARFVSPCLGSLKGIYPSQGGHY 779
 DB 1489 GSPSGKPSLPTNSVPGCLKRFQDLKPLTPSPSSFGVSSCLGPLEKGIYPSBEGHY 1548
 QY 780 IIAVSYLGPBELKLTYSIRPSLTVGLIHVGSQSGRLSVYMEAGKVTTSVSSDAGSVT 839
 DB 1549 VLAHVTLAGPBPFLVPSIRPSLTGILIHGSPGKHLCVYLEAGKVTASMDGAGTST 1608
 QY 840 SITPKQSLCDGQWHSVAVSIGKRIHL 866
 DB 1609 SYTPKQSLCDGQWHSVAVITKOHITL 1635
 RESULT 6
 ABR92102
 ID ABR92102 standard; protein; 1713 AA.
 XX ABR92102;
 AC 10-SEP-2003 (first entry)
 DT Human cervical cancer cell marker encoding cDNA SEQ ID NO:113.
 DE Human; cervical cancer; cervical cancer marker; cancer therapy;
 XX Human; cervical cancer; cervical cancer marker; cancer therapy;
 KM detection; gene therapy; vaccine.
 XX Homo sapiens.
 OS WO2002101075-A2.
 PN 19-DEC-2002.
 PD 12-JUN-2002; 2002WO-US018638.
 PF 13-JUN-2001; 2001US-0298155P.
 PR 13-JUN-2001; 2001US-0298155P.
 PR 14-NOV-2001; 2001US-0335936P.
 XX (MILL-) MILLENNium PHARM INC.
 PA Schlegel R, Chen Y, Zhao X, Monahan JB, Kamatkar S;
 PI Gannavarapu M, Glatt K, Hoersch S;
 DR WPI; 2003-156967/15.
 DR N-PSDB; ACF12884.
 XX New isolated nucleic acid molecule useful for detecting, characterizing,
 PT preventing and treating human cervical cancers, in various prognostic and
 PT diagnostic assays, in pharmacogenomics and in monitoring clinical trials.
 PS Claim 4; Page 269-273; 386pp; English.
 XX ACF12828 to ACF12947 encode the human cervical cancer marker proteins (1)
 CC given in ABR92047 to ABR92164. A higher level of expression of (1) than
 CC normal indicates the presence of cervical cancer. Also described: (1) a

CC vector (II) containing (1); (2) a host cell (III) containing (1); and (3)
 CC assessing (M1) whether a patient is afflicted with cervical cancer,
 CC comprising comparing the level of expression of a marker in a patient's
 CC sample, and the normal level of expression of the marker in a control non
 CC -cervical cancer sample, where a significant increase in the level of
 CC expression of the marker in the patient's sample relative to that in the
 CC control sample is an indication that the patient is afflicted with
 CC cervical cancer. (1) has cytostatic activity, and can be used in gene
 CC therapy and in vaccines. (1) is useful in detecting, characterizing,
 CC preventing and treating human cervical cancers. (1) may also be used in
 CC various prognostic and diagnostic assays, pharmacogenomics and in
 CC monitoring clinical trials

XX Sequence 1713 AA;

Query Match 79.3%; Score 3560.5; DB 6; Length 1713;
 Best Local Similarity 78.4%; Pred. No. 2.9e-307;
 Matches 680; Conservative 86; Mismatches 98; Indels 3; Gaps 2;

QY 1 MRFNGSGVEVRLPNDLEDKGYTSLSLFLQRPDLRENGGTEDMFVMTIGNKDSKDYIG 60
 DB MRFNGSGVEVRLPNDLEDKGYTSLSLFLQRPNSRNGGTEDMFVMTIGNKDSKDYIG 830
 QY 61 MAVVDGQLTCVNLGDRBAVQIDVLTBSRSGEAVMDRVRKQRIYQFARLNTTKATSN 120
 DB MAVVDGQLTCVNLGDRBAELQVDQILTKSEKBAVMDRVRKQRIYQFARLNTTKATSS 890
 QY 121 KKPAPAVYDLGGSSNTLNLDPEDAVFYVGGYPPDFELPSRLRPPYKGCIELDLINEN 180
 DB 891 KETPGVYDMGNSNTLNLDPENAVFYVGGYPPDFKLPRLSPFPYKGCIELDLINEN 950
 QY 181 VLSLYNFKTTFNLTTEVEPCRRRKEESDKNFEGETGYARIPTQNPAPFNFITQITTV 240
 DB VLSLYNFKTFFNLNTTEVEPCRRRKEESDKNFEGETGYARVPTQNPAPFNFITQITTV 1010
 QY 241 DRELTFPAENQDNFISLNTEDGNLRYKLNSEPPKEKGRDITNGKHSILITGKQ 300
 DB 1011 DRELTFPAENGDRFISLNTEDGFLMYKLNSELPEREGADLNNGRDHSIDIKIGKQ 1070
 QY 301 KRMWNNRERSVRLEGIFPFTYVGGYPIARERFNISTPAFQGMKMLKKTSGVNL 360
 DB 1071 KRMWINDVQNTIIDGVPFSTYVGGYPIARERFNISTPAFQGMKMLKKTSGVNL 1130
 QY 361 NDTVGYTKCCSEDMKLVRTASFSGQMSPTNLDVSTDRFQSLFSGFQTPQSGTLLNQ 420
 DB 1131 NDTVGYTKCCSEDMKLVRSASFSGQSLFTTDGLPTDGLQSLFSGFQTPQSGTLLNQ 1190
 QY 421 TRSSSLVLTEDHIELSTDSNIPFKSPGTMDGLHNVSYISPTSGRLIIDQVLR 480
 DB 1191 TWRNLQVLTLEDGYIELSTDSGSPFKSPGTMDGLHNVSVISDNGRLIIDQVLR 1250
 QY 481 RNORLPSFNAQSLRLGSGFEGCISNVVQRFSGOSEVLDLASKSTKQDASIGGCSLN 540
 DB 1251 NSGRKLHISRSRSLRGLSGSNFEGCISNVVQRLSLSPVLDLTSNLSKRDVSLGGCSLN 1310
 QY 541 KPPFLMLFKSPKPFNGRIRFNVNQLMDAPQAT-RSTEANQDGRSCLPPLNTKASHRALQ 599
 DB 1311 KPPFLMLFKSSTRFNTKTRINQILQDTPVASPRSVKWNQ--ACSPLEKTOQANGALQ 1368
 QY 600 FGSFSPSHLLKLPQELIKRSPSLDIQTSFKGLVFNAGTQDFALYVADGRVFL 659
 DB 1369 FGSFIPSHLLFKLPQELIKRSPQFAVDMQTSRGLVFHGTGNSFWALYLSGRVFL 1428
 QY 660 GAGGKQLRLSKRERHDKWTVVFGNLGSKARLVVDGLAORGSLPGNSITSPRQVYL 719
 DB 1429 GTGGKQLRLSKRCKNDGKMHVFGHDGKGRVLVDGLPAKRGSLPGNSTITRPAVYL 1488
 QY 720 GLPLSRKPKSLPOHSFVGLRLDPQLNSKPLDSPARGVSPCLGSLKGIYSQGGGHY 779
 DB 1489 GSPSGKPKSLPNSFVGLKFNQDLKPLVYTSSSSFVSSCLGGLPKGIYFSBGGGHY 1548
 QY 780 ILANSVSLGRELKLTBSIRPRSLTGVLIHVGSGQRLSYMEAKYTTSSVSSDAGGSVT 839
 DB ILANSVSLGRELKLTBSIRPRSLTGVLIHVGSGQRLSYMEAKYTTSSVSSDAGGSVT 839

DB 1549 VLAHSVLLGPEPKLVFSIRPSRLTGILIHISQPEKLCVYLEAGKTASMDSGAGTST 1608
 QY 840 SITPKQSLCDGQMSHVAVSIRKQRIHL 866
 DB 1609 SITPKQSLCDGQMSHVAVTIKQHIHL 1635

RESULT 7
 ADD29904
 ID ADD29904 standard; protein; 1713 AA.
 XX
 AC ADD29904;

DT 15-JAN-2004 (first entry)

DE Human laminin alpha 3 seq id 2.

KW ophthalmological; dermatological; laminin alpha 3; G3 domain;
 KW cell adhesion function; cell movement effect; epithelial tissue function;
 KW retinal detachment; cosmetic surgery; skin graft; human.

OS Homo sapiens.

PN JP2003093064-A.

PD 02-APR-2003.

PF 20-SEP-2001; 2001JP-00287519.

PR 20-SEP-2001; 2001JP-00287519.

PA (KAGA-) KAGAKU GIJUTSU SHINKO JIGYODAN.
 PA (KIHA-) ZH KIHARA KINEN YOKOHAMA SEIMEI KAGAKU.

DR WPI: 2003-817304/77.

DR N-PSDB; ADD29903.

PT Novel identified G3 domain of laminin alpha 3 chain useful for controlling
 PT cell adhesion and cell movement.

PS Claim 1; SEQ ID NO 2; 489p; Japanese.

CC The invention describes a modified laminin alpha3 chain comprising one or
 CC more amino acid deletions, substitutions or additions at region
 CC corresponding to a region of G3 domain having amino acids 1214-1324 of
 CC laminin alpha3 chain having a fully defined sequence of 1713 amino acids
 CC as given in the specification. (1) can control cell adhesion function and
 CC cell movement effect. A composition comprising laminin is useful for
 CC maintaining or treating the function of epithelial tissue and for
 CC treatment or prevention of retinal detachment and in cosmetic surgery and
 CC skin graft. The modified region of laminin alpha3 chain can control cell
 CC adhesion function and cell movement effect. This is the amino acid
 CC sequence of human laminin alpha 3.

XX Sequence 1713 AA;

Query Match 79.3%; Score 3560.5; DB 7; Length 1713;
 Best Local Similarity 78.4%; Pred. No. 2.9e-307;
 Matches 680; Conservative 86; Mismatches 99; Indels 3; Gaps 2;

QY 1 MRFNGSGVEVRLPNDLEDKGYTSLSLFLQRPDLRENGGTEDMFVMTIGNKDSKDYIG 60
 DB MRFNGSGVEVRLPNDLEDKGYTSLSLFLQRPNSRNGGTEDMFVMTIGNKDSKDYIG 830
 QY 771 MRFNGSGVEVRLPNDLEDKGYTSLSLFLQRPNSRNGGTEDMFVMTIGNKDSKDYIG 830
 DB 771 MRFNGSGVEVRLPNDLEDKGYTSLSLFLQRPNSRNGGTEDMFVMTIGNKDSKDYIG 830
 QY 61 MAVVDGQLTCVNLGDRBAVQIDVLTBSRSGEAVMDRVRKQRIYQFARLNTTKATSN 120
 DB 831 MAVVDGQLTCVNLGDRBAELQVDQILTKSEKBAVMDRVRKQRIYQFARLNTTKATSS 890
 QY 121 KKPAPAVYDLGGSSNTLNLDPEDAVFYVGGYPPDFELPSRLRPPYKGCIELDLINEN 180
 DB 891 KETPGVYDMGNSNTLNLDPENAVFYVGGYPPDFKLPRLSPFPYKGCIELDLINEN 950
 QY 181 VLSLYNFKTTFNLTTEVEPCRRRKEESDKNFEGETGYARIPTQNPAPFNFITQITTV 240

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Db 951 VLSVYFKTPTNNTTEVEPCRRKESDKNYFEGGYAVPQPHAPITPFGQITQTV 1010
QY 241 DRGLLFAENODNFISLNTEDGNLAVRYKLNSEPPYKGIKRTITNDKHSIIITGKLQ 300
Db 1011 DRLLFFAENGDFRISLNTEDGKLMVRYKLNSELPKRGDGINNGRDHSIQIKIGKLQ 1070
QY 301 KRWIVNERSVRIEGRIPDSTYYIGIPAIERFNISTPAFOGCMKLTXTSGVRL 360
Db 1071 KRWIVNVDQNTIIDGVDFSTYYIGIPAIERFNISTPAFOGCMKLTXTSGVRL 1130
QY 361 NDVGVYKCSSEDMKLVRTASFRGGOMSFNTLVDVSTDRFOLSPFGQTFQPSGTLINHQ 420
Db 1131 NDVGVYKCSSEDMKLVRSASFRCGLSTFDGLPPTDHLQASFQGTQFPGIILDHQ 1190
QY 421 TRTSLLVLTLEDGHIESTRDSNIPFKSPGYMDGLLHVSVISDTSGLRLIIDQVLR 480
Db 1191 TWTRNLQVLTLEDGYIELSTDSGAPIFKSPGYMDGLLHVSVISDTSGLRLIIDQVLR 1250
QY 481 RNRQLPSFNAOQSLRIGGHEPGCTSNLVORFSGSPVLDLASKSTKDAISGGCSLN 540
Db 1251 NSRRLKHISSSRQSLRIGGSENFEGCISNVFQRLISPEVLDLTSNLRKDVSLGGCSLN 1310
QY 541 KPFFLMFKSPKRFNKGRIFNVMQMODAPQAT-RSTFAMODGRSCLPPLNTKASHRALQ 599
Db 1311 KPFFLMFKSTFNTKTRINQLODTVPASPRSVKQWD--ACSPLEKTOANGALQ 1368
QY 600 FGDSPTSHLLKLPOELIKERSQPSLDIQTSPKGLVFAGYTOSPLATLVADGRVVAL 659
Db 1369 FGDIPTSHLLFKLPOLILKERSQFAVDMQTTSSRGVLFHTGTGNSFWALYLSKRLVFL 1428
QY 660 GAGGKTLRLSKRYDGRKHTVYFGLANGKALVYDGLRAOGSLPNSGTISPREVYL 719
Db 1429 GTDGKTLRLSKRYDGRKHTVYFGLANGKALVYDGLRAOGSLPNSGTISIRAVYL 1488
QY 720 GLPLSRPKSLPQHSFVGLRDQLNSKPLDPSARFVSPCLGSLKGIYFSGGSHV 779
Db 1489 GSPSPGKPSLPNTNSFVGLKNTFQDSKPLYPSSSGVSSCLGSLKGIYFSEEGSHV 1548
QY 780 ILANSVSLGPELKLRTSIRPSRLTGLVLIHVSGSGQRLSYMEAGKVTTSVSSDAGGSVT 839
Db 1549 VLHNSVSLGPEFLVPSIRPSRLTGLIHLHGSQPGKLCVYLEAGKVTATAMDSGAGTST 1608
QY 840 SITPKOSLCTGQWHSVAVSIKORILH 866
Db 1609 SVTPKOSLCTGQWHSVAVSIKORILH 1635

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RESULT 8
ADG37225
ID ADG37225 standard; protein; 1713 AA.
XX
AC ADG37225;
XX
DT 26-FEB-2004 (first entry)
XX
DE Human laminin-6 alpha 3 subunit.
XX
KW human; laminin-6; alpha 3; B1 subunit; B2 subunit; cell-movement;
KW cell-adhesion; dermatological; neuroprotective; muscular;
KW epithelial tissue; nervous tissue; varicella disease.
XX
OS Homo sapiens.
XX
PN JP2003212791-A.
XX
PD 30-JUL-2003.
XX
PF 17-JAN-2002; 2002JP-00009227.
XX
PR 17-JAN-2002; 2002JP-00009227.
XX
PA (KAGA-) KAGAKU GIJUTSU SHINKO JIGYODAN.

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XX WPI: 2003-819667/77.
JR N-PSDB; ADG37224.
JR Composition comprising laminin-6 for regulation of cell-movement activity
PT and/or cell-adhesion activity, useful for treating or maintaining
PT function of epithelial tissue, nervous tissue and muscles.
XX
PS Claim 2; SEQ ID NO 2; 55pp; Japanese.
XX
CC This invention describes a novel composition comprising the human laminin
CC -6 alpha 3, B1 or B2 subunits for regulation of cell-movement activity
CC and/or cell-adhesion activity. The products of the invention have
CC dermatological, neuroprotective and muscular activity. The composition of
CC the invention is useful for treating or maintaining the function of the
CC epithelial tissue, the nervous tissue and muscles and is also useful for
CC treatment or prevention of varicella disease.
XX
SQ Sequence 1713 AA;

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Query Match 79.3%; Score 3560.5; DB 7; Length 1713;
Best Local Similarity 78.4%; Pred. No. 2.9e-307;
Matches 680; Conservative 86; Mismatches 98; Indels 3; Gaps 2;

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QY 1 MRFNGSGVEVRLPNDLBDLKGYSLSLFLQREDLRENGGTEDEPMVYLGAKDASRDYIG 60
Db 771 MRFNGSGVEVRLPNDLBDLKGYSLSLFLQRENSHENGSTETMFMVYLGAKDASRDYIG 830
QY 61 MAVVDQGLTCVYNLGDREAEVQIDQVLTSESGEAVMDRYKFORIYQPAKANTYKATSN 120
Db 831 MAVVDQGLTCVYNLGDREAEVQIDQVLTSESGEAVMDRYKFORIYQPAKANTYKATSN 890
QY 121 KKPAPAVYDLEGSSNTLNLDPEDAVFYGYGPPPELPSRLRPPYKCIILDLNEN 180
Db 891 KPETPGYMDGNSNTLNLDPENVFYGYGPPPELPSRLRPPYKCIILDLNEN 950
QY 181 VLSVYFKTPTNNTTEVEPCRRKESDKNYFEGGYAVRIPQPHAPITPFGQITQTV 240
Db 951 VLSVYFKTPTNNTTEVEPCRRKESDKNYFEGGYAVPQPHAPITPFGQITQTV 1010
QY 241 DRGLLFAENODNFISLNTEDGNLAVRYKLNSEPPYKGIKRTITNDKHSIIITGKLQ 300
Db 1011 DRLLFFAENGDFRISLNTEDGKLMVRYKLNSELPKRGDGINNGRDHSIQIKIGKLQ 1070
QY 301 KRWIVNERSVRIEGRIPDSTYYIGIPAIERFNISTPAFOGCMKLTXTSGVRL 360
Db 1071 KRWIVNVDQNTIIDGVDFSTYYIGIPAIERFNISTPAFOGCMKLTXTSGVRL 1130
QY 361 NDVGVYKCSSEDMKLVRTASFRGGOMSFNTLVDVSTDRFOLSPFGQTFQPSGTLINHQ 420
Db 1131 NDVGVYKCSSEDMKLVRSASFRCGLSTFDGLPPTDHLQASFQGTQFPGIILDHQ 1190
QY 421 TRTSLLVLTLEDGHIESTRDSNIPFKSPGYMDGLLHVSVISDTSGLRLIIDQVLR 480
Db 1191 TWTRNLQVLTLEDGYIELSTDSGAPIFKSPGYMDGLLHVSVISDTSGLRLIIDQVLR 1250
QY 481 RNRQLPSFNAOQSLRIGGHEPGCTSNLVORFSGSPVLDLASKSTKDAISGGCSLN 540
Db 1251 NSRRLKHISSSRQSLRIGGSENFEGCISNVFQRLISPEVLDLTSNLRKDVSLGGCSLN 1310
QY 541 KPFFLMFKSPKRFNKGRIFNVMQMODAPQAT-RSTFAMODGRSCLPPLNTKASHRALQ 599
Db 1311 KPFFLMFKSTFNTKTRINQLODTVPASPRSVKQWD--ACSPLEKTOANGALQ 1368
QY 600 FGDSPTSHLLKLPOELIKERSQPSLDIQTSPKGLVFAGYTOSPLATLVADGRVVAL 659
Db 1369 FGDIPTSHLLFKLPOLILKERSQFAVDMQTTSSRGVLFHTGTGNSFWALYLSKRLVFL 1428
QY 660 GAGGKTLRLSKRYDGRKHTVYFGLANGKALVYDGLRAOGSLPNSGTISPREVYL 719
Db 1429 GTDGKTLRLSKRYDGRKHTVYFGLANGKALVYDGLRAOGSLPNSGTISIRAVYL 1488
QY 720 GLPLSRPKSLPQHSFVGLRDQLNSKPLDPSARFVSPCLGSLKGIYFSGGSHV 779

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Db 1489 GSPSPGKPSLPTNSFVGLCKNFQDLSKPLTYPSSSFVSSCLGGGLEKGIYFSEEGHY 1548
QY 780 ILANSVSLGPELTLTFSIRPSRLTGVLIHVGSQSGORLSVYMEAGKVTTSVSDAGGSVT 839
Db 1549 VLAHSLVLRPEFLVFSIRPSRLTGLIHIGSQPKHLCVYLEAGKVTASMSDAGGIST 1608
QY 840 SITPKQSLCDGQWHSVAVSIKORILHL 866
Db 1609 SVTPKQSLCDGQWHSVAVTIKOHILHL 1635

RESULT 9
ABM81957 standard; protein; 1713 AA.
XX
XX ABM81957;
AC
XX 18-NOV-2004 (first entry)
DT
XX
XX Tumour-associated antigenic target (TAT) polypeptide PRO2799, SEQ:5041.
DE
XX Tumour-associated antigenic target; TAT: human; overexpression; cancer;
KM tumour; diagnosis; cell proliferative disorder; breast cancer;
KM colorectal cancer; lung cancer; ovarian cancer; liver cancer;
KM central nervous system cancer; bladder cancer; pancreatic cancer;
KM cervical cancer; melanoma; leukaemia; hybridisation probe;
KM chromosome identification; chromosome mapping; gene mapping;
KM gene therapy; cytostatic.
XX
XX Homo sapiens.
OS
XX MO2004030615-A2.
PN
XX 15-APR-2004.
PD
XX 29-SEP-2003; 2003MO-US028547.
PF
XX 02-OCT-2002; 2002US-0414971P.
PR
XX (GETH) GENENTECH INC.
PA Wu TD, Zhang Z, Zhou Y,
PI
XX WPI; 2004-347921/32.
DR N-PSDB; ACN40327.
XX
XX New tumor-associated antigenic target polypeptides and nucleic acids,
PT useful in preparing a medicament for treating or detecting a
XX proliferative disorder, e.g. breast, lung, colorectal, ovarian or
PT prostate cancer or tumor.
XX
XX Claim 12; SEQ ID NO 5041; 7273pp; English.

The invention relates to human tumour-associated antigenic target (TAT) polypeptides, and their related nucleic acids. The TAT polypeptides are overexpressed in cancer tissues compared to normal tissues, and may thus serve as effective targets for the diagnosis and treatment of cancer in mammals. The invention also relates to nucleic acid and polypeptide sequences at least 80% identical to the TAT nucleic acids and polypeptides; expression vectors and host cells comprising a TAT nucleic acid; an antibody specific for a TAT polypeptide; a peptide or organic molecule which binds to a TAT polypeptide; fusion proteins comprising a TAT polypeptide; and methods and compositions for the treatment or diagnosis of cancer in mammals. TAT polypeptides, nucleic acids, antibodies, antagonists, binding molecules and compositions are useful for diagnosing or treating a cell proliferative disorder associated with increased TAT expression, particularly cancers such as breast cancer, colorectal cancer, lung cancer, ovarian cancer, liver cancer, bladder cancer, pancreatic cancer, cervical cancer, cancers of the central nervous system, melanoma and leukaemia. TAT nucleic acids may further be used as hybridisation probes, in chromosome and gene mapping, in chromosome identification and in gene therapy. The present sequence

CC represents a TAT polypeptide of the invention
XX
SQ Sequence 1713 AA;
Query Match 79.3%; Score 3560.5; DB 8; Length 1713;
Best Local Similarity 78.4%; Pred. No. 2.9e-307;
Matches 680; Conservative 86; Mismatches 98; Indels 3; Gaps 2;

1 MFNFGSGVEVRLPNDLEDLKGYSLSLFLORPDLRKNGTEDEMEVMTAKNDASKDYIG 60
Db 771 MFNFGSGVEVRLPNDLEDLKGYSLSLFLORPDLRKNGTEDEMEVMTAKNDASRDYIG 830
QY 61 MAVVDGQLTCVYNIADREAEVQIDQVLTSSBSQEAVMRVKFORIYQPAKNTYKATSN 120
Db 831 MAVVDGQLTCVYNIADREAEVQIDQVLTSSBSQEAVMRVKFORIYQPAKNTYKATSN 890
QY 121 KKPAPAVYDLBEGSSNTLINDPEBAVYVYGPPDPPLBRLRPPKGCIEIDDLNEN 180
Db 891 KKPAPAVYDLBEGSSNTLINDPEBAVYVYGPPDPPLBRLRPPKGCIEIDDLNEN 950
QY 181 VLSLNFPTTFLNTTEVEPCRRRKEESDKNYFEGTGARLPTOPNAPFPNFIQTITTV 240
Db 951 VLSLNFPTTFLNTTEVEPCRRRKEESDKNYFEGTGARLPTOPNAPFPNFIQTITTV 1010
QY 241 DGLLPFAENODNFISLIEDGNLMVRYKLNSEPPKEKGINDTINDGHSILITIGKLQ 300
Db 1011 DGLLPFAENODNFISLIEDGNLMVRYKLNSEPPKEKGINDTINDGHSILITIGKLQ 1070
QY 301 KKMWINNERSVRIIGELFPDSTYLLGGIPLAIRERNISTPAPGCMKNLKTSGVYRL 360
Db 1071 KKMWINNERSVRIIGELFPDSTYLLGGIPLAIRERNISTPAPGCMKNLKTSGVYRL 1130
QY 361 NDTVGATKCSBDMFLVNTASFSRGGOMSFNLDVPSFDRFOLSGFOTFOPSGTILNHQ 420
Db 1131 NDTVGATKCSBDMFLVNTASFSRGGOMSFNLDVPSFDRFOLSGFOTFOPSGTILNHQ 1190
QY 421 TRTSSILVLTBEDGHELTSTROSNIPFSPGTYMDGLLHHVSVISDTSGRLILDDQVLR 480
Db 1191 TRTSSILVLTBEDGHELTSTROSNIPFSPGTYMDGLLHHVSVISDTSGRLILDDQVLR 1250
QY 481 RNRQRPSPSNMOQSIRLGGHREGCISNVLYVORFQSPRYVLDLAKSTKCAASLGGCSLN 540
Db 1251 RNRQRPSPSNMOQSIRLGGHREGCISNVLYVORFQSPRYVLDLAKSTKCAASLGGCSLN 1310
QY 541 KPPPLMLFKSPRRFNKGRIFNVNQLOMDAPQAT-RSTFAMODGRSCLPPLNTKASHRALQ 599
Db 1311 KPPPLMLFKSPRRFNKGRIFNVNQLOMDAPQAT-RSTFAMODGRSCLPPLNTKASHRALQ 1368
QY 600 FGDSPFTHLLKLPQELLKPRSQFSLDIQTSPKGLVFYAGTKDSPLALVYADGVEVRL 659
Db 1369 FGDSPFTHLLKLPQELLKPRSQFSLDIQTSPKGLVFYAGTKDSPLALVYADGVEVRL 1428
QY 660 GAGGKKLRKSKERHNDGKMTVVVFGNGKRLVYVDGLRAQEGSLPENGSTISPREQYTL 719
Db 1429 GAGGKKLRKSKERHNDGKMTVVVFGNGKRLVYVDGLRAQEGSLPENGSTISPREQYTL 1488
QY 720 GLPLRKRPKSLRQHSFVGLRDFOLNSKPLDSRFVSGPCLGSLKGIYFSGGGGHV 779
Db 1489 GLPLRKRPKSLRQHSFVGLRDFOLNSKPLDSRFVSGPCLGSLKGIYFSGGGGHV 1548
QY 780 ILANSVSLGPELTLTFSIRPSRLTGVLIHVGSQSGORLSVYMEAGKVTTSVSDAGGSVT 839
Db 1549 VLAHSLVLRPEFLVFSIRPSRLTGLIHIGSQPKHLCVYLEAGKVTASMSDAGGIST 1608
QY 840 SITPKQSLCDGQWHSVAVSIKORILHL 866
Db 1609 SVTPKQSLCDGQWHSVAVTIKOHILHL 1635

RESULT 10
ADR87606 standard; protein; 1713 AA.
XX

AC ADR87606;
 XX 02-DEC-2004 (first entry)
 XX
 DE Human laminin alpha 3 (nicein), SEQ ID 10.
 XX
 XX Cytostatic; Gene Therapy; renal cell carcinoma; Wilms tumour; human;
 KM Laminin alpha 3, nicein.
 XX
 OS Homo sapiens.
 XX
 PN WO2004075835-A2.
 XX
 PD 10-SEP-2004.
 XX
 PF 20-FEB-2004; 2004WO-US005042.
 XX
 PR 21-FEB-2003; 2003US-00372683.
 XX
 PA (GETH) GENENTECH INC.
 XX
 PI Gerltzen ME, Peale FV, Wu TD;
 DR WPI; 2004-676901/66.
 DR N-PSDB; ADR87605.
 XX
 PT New anti-EDNRA antibody, useful in preparing a composition for diagnosing
 PT or inhibiting the growth of renal cell carcinoma or Wilms tumor.
 XX
 PS Example 1; SEQ ID NO 10; 257pp; English.
 XX
 CC The present invention relates to novel antibodies which bind to proteins
 CC which are overexpressed in renal cell carcinomas or Wilms tumor. The
 CC antibody can bind to a protein comprising CXCR4 (ADR87598), Laminin alpha
 CC 4 (ADR87600), TIMP1 (ADR87602), Type IV collagen alpha 1 (ADR87604),
 CC Laminin alpha 3 (nicein) (ADR87606), Adrenomedullin (ADR87608), Type IV
 CC collagen alpha 2 (ADR87610), Thrombospondin 2 (ADR87612), Type I collagen
 CC alpha 2 (ADR87614), Type VI collagen alpha 3 (ADR87616), Latent TGFbeta
 CC inhibiting protein 2 (LTBP2) (ADR87618), Serine or cysteine protease
 CC inhibitor heat shock protein 47 (HSP47) (ADR87620), Procollagen-lysine, 2
 CC -oxoglutarate 5-dioxygenase (ADR87622), connexin 43 (ADR87624), Type IV
 CC collagen alpha 2 (ADR87626), Connexin 37 (ADR87628), Ephrin A1
 CC (ADR87630), Laminin beta 2 (ADR87632), Integrin alpha 1, hevin
 CC (ADR87633), Stannocalcin 1 (ADR87637), Thrombospondin 4 (ADR87639), CD36
 CC polypeptide (ADR87641), Endothelin receptor A (EDNRA, ADR87643) or
 CC Endothelin receptor B (EDNRB ADR87645). The proteins of ADR87598-ADR87641
 CC and ADR87645 are all overexpressed in renal cell carcinoma, and ADR87643
 CC (EDNRA) is overexpressed in Wilms tumour. The antibodies are useful in
 CC preparing a composition for diagnosing or inhibiting the growth of renal
 CC cell carcinoma or Wilms tumour. The present sequence is one such protein
 CC of the invention.
 CC
 XX
 XX
 SQ Sequence 1713 AA;
 Query Match 79.3%; Score 3560.5; DB 8; Length 1713;
 Best Local Similarity 78.4%; Pred. No. 2.9e-307;
 Matches 680; Conservative 86; Mismatches 98; Indels 3; Gaps 2;
 QY 1 MRFNGSGVEVRLPNDELDKGYTSLPFLORPDLRNGGTEDMFVYLNKDKASKQYIG 60
 DB 771 MRFNGSGVEVRLPNDELDKGYTSLPFLORPDLRNGGTEDMFVYLNKDKASKQYIG 830
 QY 61 MAVVDGQLTCVYNLGDREAEVQIDVLTSESGOAVNDRYKFORIYOPAKLNTYKATSN 120
 DB 831 MAVVDGQLTCVYNLGDREAEVQIDVLTSESGOAVNDRYKFORIYOPAKLNTYKATSN 890
 QY 121 KPRAPAYLDEGGSSNTLNLNDEPDAPFYVGYGVPDPBELSRLLAPPKYKCIERLDINEN 180
 DB 891 KPRAPAYLDEGGSSNTLNLNDEPDAPFYVGYGVPDPBELSRLLAPPKYKCIERLDINEN 950
 QY 181 VLSTLYNFKTTFNLTTEVEPCRRKESDKNYFEGTGYARIPTOPNAPFPNFIOFTIOTYV 240
 DB 951 VLSTLYNFKTTFNLTTEVEPCRRKESDKNYFEGTGYARIPTOPNAPFPNFIOFTIOTYV 1010

241 DRGLFPAENQDNFISLNTEDGNLAVRYKLNSEPPKEKGIKDTINDKSHLITIGKQ 300
 1011 DRGLFPAENQDNFISLNTEDGNLAVRYKLNSEPPKEKGIKDTINDKSHLITIGKQ 1070
 QY 301 KRMWVNERSVRIEIEIPDFTYVYLGIPAIARERNISTPAPOGCMKMLKKTSGVRL 360
 DB 1071 KRMWVNERSVRIEIEIPDFTYVYLGIPAIARERNISTPAPOGCMKMLKKTSGVRL 1130
 QY 361 NDTVGVTKKCSSEWKLVRTASFSRGGOMSTNIDVSTDFOLSPFGQTQPSGTLNMQ 420
 DB 1131 NDTVGVTKKCSSEWKLVRTASFSRGGOMSTNIDVSTDFOLSPFGQTQPSGTLNMQ 1190
 QY 421 TRTSLLVLTEDGHIESTDINSIPIFKSGTMDGLHHVSYISDPSGLRLIIDQVLR 480
 DB 1191 TRTSLLVLTEDGHIESTDINSIPIFKSGTMDGLHHVSYISDPSGLRLIIDQVLR 1250
 QY 481 RNORLPSPNAQOQLRGGHFEGCISNVLYQFSPQSEVYLDLASKSTKDAISLGGCSLN 540
 DB 1251 RNORLPSPNAQOQLRGGHFEGCISNVLYQFSPQSEVYLDLASKSTKDAISLGGCSLN 1310
 QY 541 KPPFLMLFKSPKPKFNKGRIFNVNQLMODAPQAT-RSTEWQDGRSCLPINTKASHRALQ 599
 DB 1311 KPPFLMLFKSPKPKFNKGRIFNVNQLMODAPQAT-RSTEWQDGRSCLPINTKASHRALQ 1368
 QY 600 FGDSPTSHLLKLPQELIKRSGPSLIDICTTSFKGLVFGTQDSPLALVADGRVVAL 659
 DB 1369 FGDSPTSHLLKLPQELIKRSGPSLIDICTTSFKGLVFGTQDSPLALVADGRVVAL 1428
 QY 660 GAGGKQLRSLKSRHYDGMKHTVVFGLNGSKALVVDGLRQBSLPGNSTISPREQVYL 719
 DB 1429 GAGGKQLRSLKSRHYDGMKHTVVFGLNGSKALVVDGLRQBSLPGNSTISPREQVYL 1488
 QY 720 GLPLSRPKSLPQHSFVGCILRDPQLNSKPLDPSAPRGVSPCLGGSLIKGITYRSGGSHV 779
 DB 1489 GLPLSRPKSLPQHSFVGCILRDPQLNSKPLDPSAPRGVSPCLGGSLIKGITYRSGGSHV 1548
 QY 780 ILANSVSLGELCLTISRSLITGYLIRHSGSGQRLSYMMARKYTSVSSDAGGSYV 839
 DB 1549 ILANSVSLGELCLTISRSLITGYLIRHSGSGQRLSYMMARKYTSVSSDAGGSYV 1608
 QY 840 SITPKOSLCDGQMSHVAVSIRKILMH 866
 DB 1609 SITPKOSLCDGQMSHVAVSIRKILMH 1635
 RESULT 11
 AAB48456
 ID AAB48456 standard; protein; 1724 AA.
 AC AAB48456;
 XX
 XX
 DT 02-MAR-2001 (first entry)
 XX
 DE Human laminin 5 polypeptide, SEQ ID NO: 2.
 XX
 KM Human, laminin 5; vulnery; antiulcer; antiinflammatory; antidiabetic;
 KM cell adhesion promoter; wound healing; ulcers; burn; skin graft;
 KM periodontitis; gingivitis; Type I diabetes; angiogenesis regulation.
 OS Homo sapiens.
 XX
 PN WO200066731-A2.
 XX
 PD 09-NOV-2000.
 XX
 PF 28-APR-2000; 2000WO-US011459.
 XX
 PR 30-APR-1999; 99US-0131720P.
 PR 21-AUG-1999; 99US-0149738P.
 PR 24-SEP-1999; 99US-0155945P.
 XX
 PA (BIOS-) BIOSTATUM INC.

XX Boutaud A;
 PI WPI: 2000-687538/67.
 DR N-PSDB; AAC83717.
 XX
 PT Laminin 5-expressing cells, used to accelerate wound healing associated
 with diabetic foot ulcers, venous ulcers, pressure sores, skin surgery,
 PT burns, acute wounds and skin grafts.
 XX
 PS Claim 3; Page 53-59; 232pp; English.
 CC The present sequence is a laminin 5 chain polypeptide. Recombinant
 CC laminin 5-expressing cells are used to accelerate wound healing, skin
 CC especially diabetic foot ulcers, venous ulcers, pressure sores, skin
 CC surgery, burns, acute wounds, skin grafts, corneal ulcerations, gastro-
 CC intestinal ulcers, periodontitis, and gingivitis. They are also used to
 CC improve the biocompatibility of medical devices, and to promote cell
 CC adhesion to a surface. They can be used for the ex vivo treatment of Type
 CC I diabetes. Laminin can also be used to regulate angiogenesis. The cell
 CC line produces and secretes recombinant heterotrimeric laminin, whereas
 CC prior art cell lines have been created that produce but do not secrete
 CC only one or two chain laminins
 XX
 SQ Sequence 1724 AA;
 Query Match 79.3%; Score 3560.5; DB 3; Length 1724;
 Best Local Similarity 78.4%; Pred. No. 3e-307;
 Matches 680; Conservative 86; Mismatches 98; Indels 3; Gaps 2;
 QY 1 MRNGSGGVRLPNDLEDKGTSLSLFLQRPDLRENGTDMFVYLGKNDASDYIG 60
 DB 782 MRNGSGGVRLPNDLEDKGTSLSLFLQRPDSRENGTDMFVYLGKNDASDYIG 841
 QY 61 MAVVDQQLTCVNLGSPREAVQIDVLTSESEQAVMDRPRQRIOPALNTKATSN 120
 DB 842 MAVVDQQLTCVNLGSPREAVQIDVLTSESEQAVMDRPRQRIOPALNTKATSN 901
 QY 121 KPRAPAVYDLGSSNTLNLDPEDAVFYVGYPPFELPSRLRPPYKCIELDLNEN 180
 DB 902 KPRTPGVYDMGNSNTLNLDPENVFYVGYPPFELPSRLRPPYKCIELDLNEN 961
 QY 181 VLSLVNFKTTPNLTTEVEPCRRKESDKNYEGTGAVIPIQPNAPFPNFQITQTV 240
 DB 962 VLSLVNFKTTPNLTTEVEPCRRKESDKNYEGTGAVIPIQPNAPFPNFQITQTV 1021
 QY 241 DRGLFPAENQDFISLNTEDGLMRYKLNSEPRKEGRDRIINGKHSILITGKQ 300
 DB 1022 DRGLFPAENQDFISLNTEDGLMRYKLNSEPRKEGRDRIINGKHSILITGKQ 1081
 QY 301 KRWMINVRSVRIEGSIPSTYVYAGIPIAIRERFNISTPAFOGCMKYLKTSGVRL 360
 DB 1082 KRWMINVRSVRIEGSIPSTYVYAGIPIAIRERFNISTPAFOGCMKYLKTSGVRL 1141
 QY 361 NDTVGVTKKCESEDMKLVRTASFSRGGQMSFTNLDPSTDRFQSPFGOTFQPSGTLINQ 420
 DB 1142 NDTVGVTKKCESEDMKLVRTASFSRGGQMSFTNLDPSTDRFQSPFGOTFQPSGTLINQ 1201
 QY 421 TRTSSLLVLTEDGHILSTDSNIPFKSRGTMDGLHNVYISDTSGLRLIIDQVLR 480
 DB 1202 TRTSSLLVLTEDGHILSTDSNIPFKSRGTMDGLHNVYISDTSGLRLIIDQVLR 1261
 QY 481 RNQRLSPFSAQSLRLGSGHFEGCISNVLVQRFOSQPEVLDAKSTKDAISGCSLN 540
 DB 1262 NSRRLHGISSRSLSLGGSNFEGCISNVLVQSLSPVLDLTSKRDVSLGGCSLN 1321
 QY 541 KPPFLMLFKSPKRFNKGRIFNVLQMODAPQAT-RSTEAWQDSRSCPLPNTYASHRALQ 599
 DB 1322 KPPFLMLFKSTFNTKTFRIQLQDTPVASPRSVKWD--ACSPLEKTOANHALQ 1379
 QY 600 FGDSPTSHLLKLPOELKRPQPSLIDQTSFKGLVFGYAGTOSPLALVADGRVPL 659
 DB 1380 FGDIPTSHLLKLPOELKRPQPSLIDQTSFKGLVFGYAGTOSPLALVADGRVPL 1439

QY 660 GAGKKRLRLSRKRYHDKMTVPGLNGKARLVVDGILRAQSGSLPGNSTISPREQVYL 719
 DB 1440 GTDGKKRLRLSKRKXKNDGMHVTVFGRHGEKRLVVDGILRAQSGSLPGNSTISAPVYL 1499
 QY 720 GLPLSRKPKSLPQHSFVGLRDPLNLSKPLDPSAPFVSPCLGSLKGIYFSGGGHV 779
 DB 1500 GSPSGKPKSLPTNSFVGLKPLDPSKPLVTPSSSFGVSLGGLPKGIYFSEGGHV 1559
 QY 780 ILANSVLSGPELKLFPSTIRPRLTGVLTHVSGSGQRLSYVWEAKVTTSVSDAGGSVT 839
 DB 1560 VLAHSVLSGPELKLFPSTIRPRLTGVLTHVSGSGQRLSYVWEAKVTTSVSDAGGSVT 1619
 QY 840 SITPKQSLCDGQMSVAVSIRKRIHL 866
 DB 1620 SITPKQSLCDGQMSVAVSIRKRIHL 1646
 RESULT 12
 ADE08094
 ID ADE08094 standard; protein; 3332 AA.
 XX
 AC ADE08094;
 XX
 DT 29-JAN-2004 (first entry)
 XX
 DE Novel protein (useful for identifying genetic disorders) #249.
 XX
 KW novel gene; novel protein; tissue marker; molecular weight marker;
 KW chromosome marker; genetic disorder.
 XX
 OS Undefined.
 XX
 PN MO2003054152-A2.
 XX
 PD 03-JUL-2003.
 XX
 PF 10-DEC-2002; 2002WO-US039555.
 XX
 PR 10-DEC-2001; 2001US-0339739P.
 PR 11-DEC-2001; 2001US-0339453P.
 PR 14-MAR-2002; 2002US-0365091P.
 PR 14-MAR-2002; 2002US-0365384P.
 PR 12-APR-2002; 2002US-0372381P.
 PR 12-APR-2002; 2002US-0372615P.
 PR 22-APR-2002; 2002US-0012855P.
 PR 24-APR-2002; 2002US-0376045P.
 XX
 PA (HYSE-) HYSEQ INC.
 XX
 PI Tang YT, Asundi V, Goodrich RW, Ren F, Zhang J, Zhao QA, Wang J;
 PI Ghosh M, Xue AJ, Wehrman T, Weng G, Zhou P, Dmanac RT, Wang Z;
 PI Ma Y, Wang D, Chen R, Xu C, Boyle B;
 XX
 DR WPI: 2003-569235/53.
 DR N-PSDB; ADB07183.
 XX
 PT New polynucleotides, useful for expressing recombinant proteins for
 PT analysis, characterization or therapeutic use, or as markers for tissues
 PT in which the corresponding protein is preferentially expressed.
 XX
 PS Claim 20; SEQ ID NO 1160; 1177pp; English.
 CC The invention comprises the amino acid and coding sequences of novel
 CC proteins. The DNA and protein sequences of the invention are useful as:
 CC markers for tissues in which the corresponding protein is preferentially
 CC expressed; as molecular weight markers on gels; as chromosome markers or
 CC tags; to identify chromosomes or to map related gene positions; and to
 CC compare with endogenous DNA sequences in patients to identify potential
 CC genetic disorders. The present amino acid sequence represents a protein
 CC of the invention.
 XX
 SQ Sequence 3332 AA;

Query Match 79.3%; Score 3560.5; DB 7; Length 3332;
 Best Local Similarity 78.4%; Pred. No. 8.8e-307; Indels 3; Gaps 2;
 Matches 680; Conservative 86; Mismatches 98; Indels 3; Gaps 2;

QY 1 MRNFGSGVEVRLPNLEDELDKGYTSLPLQRPDLRENGTDMFVYLVGNKASRDYIG 60
 DB 2390 MRNFGSGVEVRLPNLEDELDKGYTSLPLQRPDLRENGTDMFVYLVGNKASRDYIG 2449
 QY 61 MAVVDQQLTCVYVNGDRBAEVOIDVLTSEESQOAVMDRYKFORIYQFALNTTKATSN 120
 DB 2450 MAVVDQQLTCVYVNGDRBAEVOIDVLTSEESQOAVMDRYKFORIYQFALNTTKATSN 2509
 QY 121 KPRAPAVYDLEGGSSNTLNLDPEDAVFYVGYPPDFELSRRLRPPYKGCIELDLNEN 180
 DB 2510 KPRAPAVYDLEGGSSNTLNLDPEDAVFYVGYPPDFELSRRLRPPYKGCIELDLNEN 2569
 QY 181 VLSLVNFKTFTNLTTEVEPCRRRKESDKNYFEGTGYARIPTQPNAPFPNFQITQTV 240
 DB 2570 VLSLVNFKTFTNLTTEVEPCRRRKESDKNYFEGTGYARIPTQPNAPFPNFQITQTV 2629
 QY 241 DRGLFFPAENQDNFISLINEDGNLMVYKLNSEPPKEKIRDTINDGKHSILITGKIQ 300
 DB 2630 DRGLFFPAENQDNFISLINEDGNLMVYKLNSEPPKEKIRDTINDGKHSILITGKIQ 2689
 QY 301 KRWMINNERSVAVIEGIFDPFSTYYLGGIPAIARERNISTPAFQCGMKLTKTSGVRL 360
 DB 2690 KRWMINNERSVAVIEGIFDPFSTYYLGGIPAIARERNISTPAFQCGMKLTKTSGVRL 2749
 QY 361 NDVGVYTKKCESEMDKLVRTASFRSGQMSFTNLDPVSTDRFQSGFQTPQSGTLNHO 420
 DB 2750 NDVGVYTKKCESEMDKLVRTASFRSGQMSFTNLDPVSTDRFQSGFQTPQSGTLNHO 2809
 QY 421 TRTSSLVLTLEDGHIELSTDSNIPFKSGTYMDGLHNVYSIDTSGRLRIDQVLR 480
 DB 2810 TRTSSLVLTLEDGHIELSTDSNIPFKSGTYMDGLHNVYSIDTSGRLRIDQVLR 2869
 QY 481 RNRRLSPSNAQSLRGGHFRGICISNVLYQRPSPFVLDLASKTKDASLGGSIN 540
 DB 2870 RNRRLSPSNAQSLRGGHFRGICISNVLYQRPSPFVLDLASKTKDASLGGSIN 2929
 QY 541 KPPFLMLFKSPKPKGRIFNVNOMODAPQAT-RSTBAWODGRSCCLPPLTKASHRALQ 599
 DB 2930 KPPFLMLFKSPKPKGRIFNVNOMODAPQAT-RSTBAWODGRSCCLPPLTKASHRALQ 2987
 QY 600 FGDSPTSHLLKLPOELIKERSQFSLDIQTSFKGLVFAGTQDSFLATLVADGRVVAL 659
 DB 2988 FGDSPTSHLLKLPOELIKERSQFSLDIQTSFKGLVFAGTQDSFLATLVADGRVVAL 3047
 QY 660 GAGGKRLRLSKRYHDGKMTYVFGANGKARLVYDGLRAQSGSLFGNSTISPREOYL 719
 DB 3048 GAGGKRLRLSKRYHDGKMTYVFGANGKARLVYDGLRAQSGSLFGNSTISPREOYL 3107
 QY 720 GLPLSRPKSLPOHSPFGCLRDFOVNSKPLDSPARPGVSPCLGSGLEKGIYSPGSGHY 779
 DB 3108 GLPLSRPKSLPOHSPFGCLRDFOVNSKPLDSPARPGVSPCLGSGLEKGIYSPGSGHY 3167
 QY 780 ILANSVSLGPELKLTFESIRPSRLTGVLIHVSGSGGRLSYVMEAGKVTTSVSSDAGSVT 839
 DB 3168 ILANSVSLGPELKLTFESIRPSRLTGVLIHVSGSGGRLSYVMEAGKVTTSVSSDAGSVT 3227
 QY 840 SITPKQSLCPGQWHSVAVSTIKORILHL 866
 DB 3228 SITPKQSLCPGQWHSVAVSTIKORILHL 3254

RESULT 13
 AAR70148 standard; protein; 1713 AA.
 AC AAR70148;
 XX XX
 DT 25-MAR-2003 (revised)

QY 05-OCT-1995 (first entry)
 XX Deduced sequence of cDNA corresp. to the alpha-3Bpa transcript.
 DB E170; epithelial ligand glycoprotein; epiligrin complex;
 KW epithelial cell binding.
 OS Homo sapiens.
 XX W09506660-A1.
 PN 09-MAR-1995.
 PD 02-SEP-1994; 94MO-US010261.
 PE 02-SEP-1993; 93US-00115918.
 PR (HUTC-) HUTCHINSON CANCER RES CENT FRED.
 PA Carter WG, G11 SG, Ryan MC,
 PI WPI, 1995-115398/15.
 DR N-PSDB; AA083236.
 PS New nucleic acid encoding epiligrin, an epithelial ligand complex - also
 XX related vectors, transformed cells, proteins and antibodies, useful
 PT therapeutically and diagnostically, e.g., in cases of inflammation and to
 PT induce cancer cell differentiation.
 XX
 PS Claim 12; Fig 15A-F; 187pp; English.
 XX
 CC AA083235 depicts the nt. sequence compiled from sequencing cDNA clones
 CC corresp. to the alpha-3 Bpa transcript. The invention includes nt
 CC sequences in the gp. comprising the nt sequence shown in AA083235, the
 CC cDNA clone Ep-1 (ATCC No. 75540) shown in AA083234, the cDNA clone 1-1
 CC (ATCC No. 75539), and the cDNA clone 8-6 (ATCC No. 75538), or the nt.
 CC sequences shown in AA083236. The entire nt. region encoding E170 is
 CC depicted in AA083236, and corresp. to the SQ of alpha-3. AA083236
 CC consists of a composite sequence derived from several overlapping clones.
 CC A synthetic polypeptide of at least 5 AAs that corresp. to part or all of
 CC the nt. sequence shown in AA083236 is claimed. (Updated on 25-MAR-2003 to
 CC correct PN field.)
 XX
 SQ Sequence 1713 AA;

Query Match 79.1%; Score 3552.5; DB 2; Length 1713;
 Best Local Similarity 78.3%; Pred. No. 1.5e-306;
 Matches 679; Conservative 86; Mismatches 99; Indels 3; Gaps 2;

QY 1 MRNFGSGVEVRLPNLEDELDKGYTSLPLQRPDLRENGTDMFVYLVGNKASRDYIG 60
 DB 771 MRNFGSGVEVRLPNLEDELDKGYTSLPLQRPDLRENGTDMFVYLVGNKASRDYIG 830
 QY 61 MAVVDQQLTCVYVNGDRBAEVOIDVLTSEESQOAVMDRYKFORIYQFALNTTKATSN 120
 DB 831 MAVVDQQLTCVYVNGDRBAEVOIDVLTSEESQOAVMDRYKFORIYQFALNTTKATSN 890
 QY 121 KPRAPAVYDLEGGSSNTLNLDPEDAVFYVGYPPDFELSRRLRPPYKGCIELDLNEN 180
 DB 891 KPRAPAVYDLEGGSSNTLNLDPEDAVFYVGYPPDFELSRRLRPPYKGCIELDLNEN 950
 QY 181 VLSLVNFKTFTNLTTEVEPCRRRKESDKNYFEGTGYARIPTQPNAPFPNFQITQTV 240
 DB 951 VLSLVNFKTFTNLTTEVEPCRRRKESDKNYFEGTGYARIPTQPNAPFPNFQITQTV 1010
 QY 241 DRGLFFPAENQDNFISLINEDGNLMVYKLNSEPPKEKIRDTINDGKHSILITGKIQ 300
 DB 1011 DRGLFFPAENQDNFISLINEDGNLMVYKLNSEPPKEKIRDTINDGKHSILITGKIQ 1070
 QY 301 KRWMINNERSVAVIEGIFDPFSTYYLGGIPAIARERNISTPAFQCGMKLTKTSGVRL 360
 DB 1071 KRWMINNERSVAVIEGIFDPFSTYYLGGIPAIARERNISTPAFQCGMKLTKTSGVRL 1130

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QY 361 NDTVGVTKKCSDEMDKLVKTASFSGGQMSFTNIDVSTDRFQLSFGFQTFQPSGTLINQ 420
DB 1131 NDTVGVTKKCSDEMDKLVKTASFSGGQMSFTNIDVSTDRFQLSFGFQTFQPSGTLINQ 1190
QY 421 TTTSSLVLTLEDHILSTRDSNIPFKSPGTYMDGLHHVSYISTSGRLIIDQVLR 480
DB 1191 TWRNLTQVLTLEDHILSTRDSNIPFKSPGTYMDGLHHVSYISTSGRLIIDQVLR 1250
QY 481 RNQRLSPFNAQOGLSLGSGHFEGLCSNVLVQRFQSPSEVLDLASKSTKQDASLGCSN 540
DB 1251 NSGRKLHHISSRQSLGSGHFEGLCSNVLVQRFQSPSEVLDLASKSTKQDASLGCSN 1310
QY 541 KPPFLMLFKSPKPKFNKRIENVNQLMODAPQAT-RSTEAMQDGRSCLPLANTKASHRALQ 599
DB 1311 KPPFLMLFKSGSTFNKTKTFRIQLQDPFVAPRPAVKWQD--ACSPLEPKTQANNGALQ 1368
QY 600 FGQSPFSSHLLKLPQBLKLRPSQPSLIDQTSFKGIYPAAGTQSLALYVADGRVPL 659
DB 1369 FGQSPFSSHLLKLPQBLKLRPSQPSLIDQTSFKGIYPAAGTQSLALYVADGRVPL 1428
QY 660 GAGGKTLRLSKRYHDGKWHYVFGANGKARLVYDGLRAQSGSLPGNSTISPREQVYL 719
DB 1429 GTDGKTLRKSKKCKMDGKMHYVFGHDEKGRHLYVDGLRAQSGSLPGNSTISIRAPVYL 1488
QY 720 GLPLSRKPKSLPQHSFVGCILRDFOLNSKPLDSPSARFVSPCLGSLKGIYPSQGGH 779
DB 1489 GSPSPKPKSLPTNSFVGCILKPNFOLDKPLTYTSSFGVSSCLGPLEKGIYPSSEGGHY 1548
QY 780 ILANSYSLGPELKLTVTSIRPSLTGYLHHVSGSGORLSYMEAGKYTTSVSSDAGGSYT 839
DB 1549 VLHASYVLGPEFLVLSIRPSLTGYLHHVSGSGORLSYMEAGKYTTSVSSDAGGSYT 1608
QY 840 SITPKOSLDCQWHSAVSIKQRIHL 866
DB 1609 SITPKOSLDCQWHSAVSIKQRIHL 1635

RESULT 14
AAG75103
ID AAG75103 standard; protein; 469 AA.
XX
AC AAG75103;
XX
DT 03-SEP-2001 (first entry)
XX
DE Human colon cancer antigen protein SEQ ID NO:5867.
XX
KW Human; colon cancer; colon cancer antigen; diagnosis; detection;
  colorectal carcinoma; chromosome 18.
XX
OS Homo sapiens.
XX
PN MO200122920-A2.
XX
PD 05-APR-2001.
XX
PF 28-SEP-2000; 2000MO-US026524.
XX
PR 29-SEP-1999; 99US-0157137P.
  PR 03-NOV-1999; 99US-0163280P.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI Ruben SM, Barash SC, Birse CE, Rosen CA;
  DR WPI, 2001-235357/24.
  DR N-PSDB; AAB34508.
XX
PT Nucleic acids encoding 4277 human colon cancer-associated polypeptides,
  useful for preventing, diagnosing and/or treating colorectal cancers.
XX
PS Claim 11; Page 7385-7387; 9803P; English.
XX
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CC AAH32943 to AAH37195 and AAG73514 to AAG77788 represent human colon
CC cancer-associated nucleic acid molecules (N) and proteins (P), where the
CC proteins are collectively known as colon cancer antigens. The colon
CC cancer antigens have cytostatic activity and can be used in gene therapy
CC and vaccine production. N and P may be used in the prevention, diagnosis
CC and treatment of diseases associated with inappropriate P expression. For
CC example, N and P may be used to treat disorders associated with decreased
CC expression by rectifying mutations or deletions in a patient's genome
CC that affect the activity of P by expressing inactive proteins or to
CC supplement the patient's own production of P. Additionally, N may be used
CC to produce the colon cancer-associated P8, by inserting the nucleic acids
CC into a host cell and culturing the cell to express the proteins. N and P
CC can be used in the prevention, diagnosis and treatment of colorectal
CC carcinomas and cancers. AAH37196 to AAH37204 and AAB7789 represent
CC sequences used in the exemplification of the present invention. N.B.
CC Pages 666 to 682 and page 7053 of the sequence listing were missing at
CC time of publication, meaning no sequences are present for SEQ ID NO:1027
CC to 1052, 7921 and 7922
XX
SQ Sequence 469 AA;
XX
Query Match 35 6%; Score 1599; DB 4; Length 469;
Best Local Similarity 65.9%; Pred. No.3.6e-133; Indels 30; Gaps 5;
Matches 323; Conservative 55; Mismatches 82;
XX
QY 379 TASFERGQMSFTNIDVSTDRFQLSFGFQTFQPSGTLINQRTSSLVLTLEDHILS 438
DB 1 SASFERGQMSFTNIDVSTDRFQLSFGFQTFQPSGTLINQRTSSLVLTLEDHILS 60
QY 439 TRDSNIPFKSPGTYMDGLHHVSYISTSGRLIIDQVLRNRORLSPFNAQOGLSLG 498
DB 61 TSDSXGPIFKSPQTYMDGLHHVSYISTSGRLIIDQVLRNRORLSPFNAQOGLSLG 120
QY 499 GGHFGGCSNVLVQRFQSPSEVLDLASKSTKQDASLGCSNKPFLMLFKSPKPKNGR 558
DB 121 GSNFEGCISNVVQRLSPSEVLDLTSNSLRKDVSLGCSNKPFLMLFKSGTRFNKTK 180
QY 559 IFNVNQLMODAPQAT-RSTEAMQDGRSCLPLANTKASHRALQFGDSPTSHLLKLPQEL 617
DB 181 TFRINQLQDPFVAPRPAVKWQD--ACSPLEPKTQANNGALQFGDIPFSSHLLKLPQEL 238
QY 618 KPSQPSLIDQTSFKGIYPAAGTQSLALYVADGRVPLVAGGKTLRLSKRYHDG 677
DB 239 KPSQPSLIDQTSFKGIYPAAGTQSLALYVADGRVPLVAGGKTLRLSKRYHDG 298
QY 678 KHTVVPFGANGKARLVYDGLRAQSGSLPGNSTISPREQVYLGPLSRKPKSLPQHSFV 737
DB 299 KHTVVPFGANGKARLVYDGLRAQSGSLPGNSTISIRAPVYLGSPSPKPKSLPTNSFV 358
QY 738 CLRDFOGLNSKPLDSPSARFVSPCLGSLKGIYPSQGGHYILANSYSLGPELKLTVTSI 797
DB 359 CLKNFQDLSKPLTYTSSFGVSSCLGPLEKGIYPSSEGGHYVLHASYVLGPEFLVPSI 418
QY 798 RPRSLTGYLHHVSGSGORLSYMEAGKYTTSVSSDAGGSYTSITPKOSLDCQWH 852
DB 419 RPRSLTGYLHHVSGSGORLSYMEAGKYTTSVSSDAGGSYTSITPKOSLDCQWH 459
QY 853 ---HSAVSI 859
DB 460 NVGHTKAVSV 469

RESULT 15
AAH26584
ID AAH26584 standard; protein; 770 AA.
XX
AC AAH26584;
XX
DT 25-MAR-2003 (revised)
  DT 21-JAN-1998 (first entry)
XX
DE Rat hemidesmosome formation inducing protein 154 kDa subunit.
XX
```

KW Hemidesmosome; laminin; epithelial cell; cell attachment; adhesion;
KM bladder carcinoma; 804G; NBT-II; rat; dental implant.

XX
XX
OS Rattus sp.

PN US5658789-A.

PD 19-AUG-1997.

PF 19-MAY-1995; 95US-00445135.

PR 12-NOV-1993; 93US-00151134.

PA (DESM-) DESMOS INC.

PI Hormia M, Quaranta V;

XX WPI; 1997-424242/39.

PT Soluble protein that induces hemidesmosome formation in epithelial cells
PT - useful for stimulating epithelial cell attachment, e.g. to dental
implants or teeth.

PS Claim 2; Col 21-26; 20P; English.

CC This polypeptide comprises the 154 kDa alpha chain of an isolated soluble
CC protein that induces hemidesmosome formation in epithelial cells normally
CC unable to form hemidesmosomes. The 146 kD gamma chain (see AAW26584) and
CC the N-terminal portion (see AAW26585) of the 139 kDa beta chain sequence
CC were also determined. The protein has properties including: (a)
CC solubility in aqueous media; (b) binding by antibodies present in the
CC serum of rabbits inoculated with an extracellular matrix deposited by
CC 804G rat bladder carcinoma cells or NBT-II rat bladder carcinoma cells;
CC (c) being bound by monoclonal antibodies generated against extracellular
CC matrix; (d) promoting rapid epithelial cell adhesion to substrates coated
CC with at least one of the three protein chains; and (e) being obtainable
CC from 804G rat bladder carcinoma cells or NBT-II rat bladder carcinoma
CC cells. The protein (secreted laminin) is used to induce hemidesmosome
CC formation in epithelial cells and to facilitate their growth (claimed).
CC It may be used to promote cell attachment to solid surfaces, e.g. to
CC dental implants, and may also be of use in studies concerning
CC hemidesmosome morphogenesis and alpha 6 beta 4 integrin interactions with
CC the epithelial extracellular matrix. (Updated on 25-MAR-2003 to correct
CC PP field.)

XX
XX
SQ Sequence 770 AA;

Query Match 29.2%; Score 1310; DB 2; Length 770;

Best Local Similarity 90.9%; Pred. No. 4.9e-107; Mismatches 13; Indels 10; Gaps 4;

Matches 259; Conservative 3; Mismatches 13; Indels 10; Gaps 4;

QY 1 MRFNGKSGVEVRLPNDLEDKGYTSLFLQRPDLRENGTDMFVYLGAKDASKDYIG 60

DB 491 MRFNGKSGVEVRLPNDLEDKGYTSLFLQRPDLRENGTDMFVYLGAKDASKDYIG 550

QY 61 MA---VVDGQLTGVNLCGRBAFVQIDV-LTSESQBAVMDRVKQRIYQPAKLNYYTK 115

DB 551 IGGCRWPA---VCLQPGGR--SVSSDRSGLTSESQBAVMDRVKQRIYQPAKLNYYTK 605

QY 116 EATSNKPKAPAVVDLEGGSSNTLTLNLPDAVFVGVGYPDPFELPSRLRFPYKCTELD 175

DB 606 EATSNKPKAPAVVDLEGGSSNTLTLNLPDAVFVGVGYPDPFELPSRLRFPYKCTELD 665

QY 176 DLNENVLSTLYNFKTTFNLTTEVPCRRRKEESDKNYFEGTGYARIPTOPNAPPNFIQT 235

DB 666 DLNENVLSTLYNFKTTFNLTTEVPCRRRKEESDKNYFEGTGYARIPTOPNAPPNFIQT 725

QY 236 IQTTVARGLLFPANQDNFISLNTEDGNLWRYRYKLANSPPKCKGI 280

DB 726 IQTTVARGLLFPANQDNFISLNTEDGNLWRYRYKLANSPPKCKGI 770

Search completed: February 22, 2005, 08:18:44

Job time : 164.651 secs

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GenCore version 5.1.6
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OM protein - protein search, using SW model

Run on: February 22, 2005, 08:19:00 ; Search time 116.062 Seconds
(without alignments)
2441.722 Million cell updates/sec

Title: US-10-817-423-2

Perfect score: 4491

Sequence: 1 MRFNGKSGVGVRLPNDLEDL.....LDDGQMSVAVSXIKRIHL 866

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 1380268 seqs, 327241040 residues

Total number of hits satisfying chosen parameters: 1380268

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications AA:
1: /cgn2_6/prodata/2/pubppaa/US07_PUBCOMB.pep.*
2: /cgn2_6/prodata/2/pubppaa/PCT_NEW_PUB.pep.*
3: /cgn2_6/prodata/2/pubppaa/US06_NEW_PUB.pep.*
4: /cgn2_6/prodata/2/pubppaa/US06_PUBCOMB.pep.*
5: /cgn2_6/prodata/2/pubppaa/US07_NEW_PUB.pep.*
6: /cgn2_6/prodata/2/pubppaa/PCTUS_PUBCOMB.pep.*
7: /cgn2_6/prodata/2/pubppaa/US08_NEW_PUB.pep.*
8: /cgn2_6/prodata/2/pubppaa/US08_PUBCOMB.pep.*
9: /cgn2_6/prodata/2/pubppaa/US09_PUBCOMB.pep.*
10: /cgn2_6/prodata/2/pubppaa/US09C_PUBCOMB.pep.*
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12: /cgn2_6/prodata/2/pubppaa/US10_NEW_PUB.pep.*
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19: /cgn2_6/prodata/2/pubppaa/US60_NEW_PUB.pep.*
20: /cgn2_6/prodata/2/pubppaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	4491	100.0	1694	US-10-603-725-12	Sequence 12, Appl
2	4491	100.0	1725	US-10-603-725-10	Sequence 10, Appl
3	3560.5	79.3	1693	US-10-603-725-4	Sequence 4, Appl
4	3560.5	79.3	1693	US-10-603-725-8	Sequence 8, Appl
5	3560.5	79.3	1713	US-10-171-311-113	Sequence 113, Appl
6	3560.5	79.3	1713	US-10-372-683-10	Sequence 10, Appl
7	3560.5	79.3	1713	US-10-603-725-6	Sequence 6, Appl
8	3560.5	79.3	1724	US-10-603-725-2	Sequence 2, Appl
9	1599	35.6	469	US-10-106-698-5877	Sequence 5877, Ap
10	1198	26.7	1816	US-10-372-683-4	Sequence 4, Appl
11	1192	26.5	1823	US-10-363-616-457	Sequence 457, App
12	1190	26.5	1581	US-10-408-765A-154	Sequence 154, App
13	1187	26.4	1816	US-10-299-058-2	Sequence 2, Appl

14	1185	26.4	1816	US-10-299-058-4	Sequence 4, Appl
15	1045.5	23.3	1634	US-10-037-417-49	Sequence 49, Appl
16	1045.5	23.3	1677	US-10-112-944-801	Sequence 801, App
17	1045.5	23.3	1675	US-10-312-352-22	Sequence 22, Appl
18	1045.5	23.3	1696	US-10-312-088-31	Sequence 31, Appl
19	1045.5	23.3	1695	US-10-312-088-30	Sequence 30, Appl
20	1042.5	23.2	1695	US-10-037-182-2	Sequence 2, Appl
21	1042	23.2	1640	US-10-037-417-8	Sequence 8, Appl
22	1041	23.2	1640	US-10-112-944-347	Sequence 347, App
23	1015.5	22.6	953	US-09-845-583-4	Sequence 4, Appl
24	1015.5	22.6	953	US-10-037-417-50	Sequence 50, Appl
25	948	21.1	1635	US-09-845-583-2	Sequence 2, Appl
26	948	21.1	1635	US-10-037-182-4	Sequence 4, Appl
27	948	21.1	1635	US-10-037-417-47	Sequence 47, Appl
28	943	21.0	1635	US-10-037-417-6	Sequence 6, Appl
29	943	21.0	1635	US-10-037-417-2	Sequence 2, Appl
30	908	20.2	908	US-10-037-417-4	Sequence 4, Appl
31	636.5	14.2	3712	US-10-108-605-103	Sequence 103, App
32	636.5	14.2	3712	US-10-037-417-48	Sequence 48, Appl
33	636.5	14.2	3712	US-10-037-417-51	Sequence 51, Appl
34	600.5	13.4	3672	US-10-369-493-6146	Sequence 6146, Ap
35	545	12.1	3084	US-09-938-275-4	Sequence 4, Appl
36	545	12.1	3084	US-10-262-670-2	Sequence 2, Appl
37	529.5	11.8	3075	US-09-938-275-5	Sequence 5, Appl
38	484.5	10.8	3070	US-09-961-403-7	Sequence 7, Appl
39	323.5	7.2	1514	US-10-336-603A-36	Sequence 36, Appl
40	322.5	7.2	286	US-10-299-058-5	Sequence 5, Appl
41	322.5	7.2	286	US-10-299-058-6	Sequence 6, Appl
42	321	7.1	289	US-10-299-058-13	Sequence 13, Appl
43	316	7.0	463	US-10-264-049-3039	Sequence 3039, Ap
44	314.5	7.0	342	US-10-264-049-3068	Sequence 3068, Ap
45	313.5	7.0	1399	US-10-187-975-26	Sequence 26, Appl

ALIGNMENTS

RESULT 1
US-10-603-725-12
; Sequence 12, Application US/10603725
; Publication No. US20040014665A1
; GENERAL INFORMATION:
; APPLICANT: Bontand, Arlet
; TITLE OF INVENTION: Recombinant Laminin 5
; FILER REFERENCE: 99-274-C
; CURRENT APPLICATION NUMBER: US/10/603,725
; CURRENT FILING DATE: 2003-06-25
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: Patentn Ver. 2.0
; SEQ ID NO 12
; LENGTH: 1694
; TYPE: PRT
; ORGANISM: Rattus norvegicus
US-10-603-725-12

Query Match 100.0%; Score 4491; DB 15; Length 1694;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 866; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRFNGKSGVGVRLPNDLEDKGYTSLFLQRLDRENGGTEDMFVYVLGNKQASKOYIG 60
|||||
DB 751 MRFNGKSGVGVRLPNDLEDKGYTSLFLQRLDRENGGTEDMFVYVLGNKQASKOYIG 810
QY 61 MAVVDQQLTCVYVNLGDRREAVQIDQVLTSESGEAVMDRVKFORIYQFAFNTYKATSN 120
|||||
DB 811 MAVVDQQLTCVYVNLGDRREAVQIDQVLTSESGEAVMDRVKFORIYQFAFNTYKATSN 870
QY 121 KPRAPAVYDLGGSSNTLNLDPEDAVFYVYGVPDPPELPSRLRPFPYKCIETLDINEN 180
|||||
DB 871 KPRAPAVYDLGGSSNTLNLDPEDAVFYVYGVPDPPELPSRLRPFPYKCIETLDINEN 930
QY 181 VLSLYPKTFENLNTTEVEPRCRRKESDKNYEGTGAYARIPTQNPAPFNFQIOTIQTIV 240
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Db      931 VLSYNFKTTFNLTTEVEPCRRRKEESDKNYEGTGVAIPTQPNAPFPNF1QTIQTV 990
QY      241 DGLLFFAENQDNFISLNIEDGNLAVRYKLNSEPPKEKGRDITNDGKHSLITIGKQ 300
Db      991 DGLLFFAENQDNFISLNIEDGNLAVRYKLNSEPPKEKGRDITNDGKHSLITIGKQ 1050
QY      301 KKMWINNERSVRIEGBIFDSTYYLGGIPAIIRERFNISTPAFGCKMNLKKTSGVRL 360
Db      1051 KKMWINNERSVRIEGBIFDSTYYLGGIPAIIRERFNISTPAFGCKMNLKKTSGVRL 1110
QY      361 NDTVGVTKKCSBDMKLVRTASFSRGQMSFTNLDVSTDRFQLSRFGQTFQPSGTLNMQ 420
Db      1111 NDTVGVTKKCSBDMKLVRTASFSRGQMSFTNLDVSTDRFQLSRFGQTFQPSGTLNMQ 1170
QY      421 TRTSSLVLTLEDGHIELSTDSNIP1FKSPGTMDGLAHVSVISDTSGLRLIIDQVLR 480
Db      1171 TRTSSLVLTLEDGHIELSTDSNIP1FKSPGTMDGLAHVSVISDTSGLRLIIDQVLR 1230
QY      481 RNQRLPSFSNAQOSLRIGGHEGCI SNVLVORFSQSPVLDLASKSTKQDASLGCSLN 540
Db      1231 RNQRLPSFSNAQOSLRIGGHEGCI SNVLVORFSQSPVLDLASKSTKQDASLGCSLN 1290
QY      541 KPPFLMLFKSPKPKFKGRIFNVNQLMODAPQATRSSTEAMODGRSCPLPLNTKASHRALQ 600
Db      1291 KPPFLMLFKSPKPKFKGRIFNVNQLMODAPQATRSSTEAMODGRSCPLPLNTKASHRALQ 1350
QY      601 GDSPTSHLLKLPQELKPRSQFSLDIQTSPKGLVFAGTQDSFLALVYADGRVVPALG 660
Db      1351 GDSPTSHLLKLPQELKPRSQFSLDIQTSPKGLVFAGTQDSFLALVYADGRVVPALG 1410
QY      661 AGGKRLRLSKERYHDGKHTVVFGLNGKARLVVDGLRAQEGSLPGNSTISPREQVYLQ 720
Db      1411 AGGKRLRLSKERYHDGKHTVVFGLNGKARLVVDGLRAQEGSLPGNSTISPREQVYLQ 1470
QY      721 LPLSRKPKSLPOHSFVGCCLRDPLNSKPLDSPSARFVSPCLGSLBKGIYFSGGCHYI 780
Db      1471 LPLSRKPKSLPOHSFVGCCLRDPLNSKPLDSPSARFVSPCLGSLBKGIYFSGGCHYI 1530
QY      781 LANSVSLGPELKLTFESIRPSRLTGVLIHVGSQSGQRLSVYMEAGKVTTSVSSDAGSVTS 840
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Db      1591 ITPKQSLCDGQMSVAVS1KQRIIHL 1616

RESULT 2
US-10-603-725-10
; Sequence 10, Application US/10603725
; Publication No. US20040014655A1
; GENERAL INFORMATION:
; APPLICANT: Boudand, Arlet
; TITLE OF INVENTION: Recombinant Laminin 5
; FILE REFERENCE: 99-274-C
; CURRENT APPLICATION NUMBER: US/10/603,725
; CURRENT FILING DATE: 2003-06-25
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 10
; LENGTH: 1725
; TYPE: PR
; ORGANISM: Rattus norvegicus
US-10-603-725-10

Query Match 100.0%; Score 4491; DB 15; Length 1725;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 866; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY      1 MRFNGSGVEVRLPNLEDEIKGYTSLFLQRPDLRENGTDEMFWVYLGKNDASDYIG 60
Db      782 MRFNGSGVEVRLPNLEDEIKGYTSLFLQRPDLRENGTDEMFWVYLGKNDASDYIG 841

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QY      61 MAVVDGQLTCVYNIADREAEVQIDQVLTSSBSQBAVMDRVKORYQAKNTYTEATSN 120
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QY      121 KEKAAVYDLBSGSSNTLNLNDPEDAVYVGGYPPDFELBSRLRPPFKGCIELDDLEN 180
Db      902 KEKAAVYDLBSGSSNTLNLNDPEDAVYVGGYPPDFELBSRLRPPFKGCIELDDLEN 961
QY      181 VLSYNFKTTFNLTTEVEPCRRRKEESDKNYEGTGVAIPTQPNAPFPNF1QTIQTV 240
Db      962 VLSYNFKTTFNLTTEVEPCRRRKEESDKNYEGTGVAIPTQPNAPFPNF1QTIQTV 1021
QY      241 DGLLFFAENQDNFISLNIEDGNLAVRYKLNSEPPKEKGRDITNDGKHSLITIGKQ 300
Db      1022 DGLLFFAENQDNFISLNIEDGNLAVRYKLNSEPPKEKGRDITNDGKHSLITIGKQ 1081
QY      301 KKMWINNERSVRIEGBIFDSTYYLGGIPAIIRERFNISTPAFGCKMNLKKTSGVRL 360
Db      1082 KKMWINNERSVRIEGBIFDSTYYLGGIPAIIRERFNISTPAFGCKMNLKKTSGVRL 1141
QY      361 NDTVGVTKKCSBDMKLVRTASFSRGQMSFTNLDVSTDRFQLSRFGQTFQPSGTLNMQ 420
Db      1142 NDTVGVTKKCSBDMKLVRTASFSRGQMSFTNLDVSTDRFQLSRFGQTFQPSGTLNMQ 1201
QY      421 TRTSSLVLTLEDGHIELSTDSNIP1FKSPGTMDGLAHVSVISDTSGLRLIIDQVLR 480
Db      1202 TRTSSLVLTLEDGHIELSTDSNIP1FKSPGTMDGLAHVSVISDTSGLRLIIDQVLR 1261
QY      481 RNQRLPSFSNAQOSLRIGGHEGCI SNVLVORFSQSPVLDLASKSTKQDASLGCSLN 540
Db      1262 RNQRLPSFSNAQOSLRIGGHEGCI SNVLVORFSQSPVLDLASKSTKQDASLGCSLN 1321
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Db      1322 KPPFLMLFKSPKPKFKGRIFNVNQLMODAPQATRSSTEAMODGRSCPLPLNTKASHRALQ 1381
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Db      1382 GDSPTSHLLKLPQELKPRSQFSLDIQTSPKGLVFAGTQDSFLALVYADGRVVPALG 1441
QY      661 AGGKRLRLSKERYHDGKHTVVFGLNGKARLVVDGLRAQEGSLPGNSTISPREQVYLQ 720
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QY      721 LPLSRKPKSLPOHSFVGCCLRDPLNSKPLDSPSARFVSPCLGSLBKGIYFSGGCHYI 780
Db      1502 LPLSRKPKSLPOHSFVGCCLRDPLNSKPLDSPSARFVSPCLGSLBKGIYFSGGCHYI 1561
QY      781 LANSVSLGPELKLTFESIRPSRLTGVLIHVGSQSGQRLSVYMEAGKVTTSVSSDAGSVTS 840
Db      1562 LANSVSLGPELKLTFESIRPSRLTGVLIHVGSQSGQRLSVYMEAGKVTTSVSSDAGSVTS 1621
QY      841 ITPKQSLCDGQMSVAVS1KQRIIHL 866
Db      1622 ITPKQSLCDGQMSVAVS1KQRIIHL 1647

RESULT 3
US-10-603-725-4
; Sequence 4, Application US/10603725
; Publication No. US20040014655A1
; GENERAL INFORMATION:
; APPLICANT: Boudand, Arlet
; TITLE OF INVENTION: Recombinant Laminin 5
; FILE REFERENCE: 99-274-C
; CURRENT APPLICATION NUMBER: US/10/603,725
; CURRENT FILING DATE: 2003-06-25
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 1693
; TYPE: PR
; ORGANISM: Homo sapiens

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QY      1 MRFNGSGVEVRLPNLEDEIKGYTSLFLQRPDLRENGTDEMFWVYLGKNDASDYIG 60
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US-10-603-725-4

Query Match 79.3%; Score 3560.5; DB 15; Length 1693;
Best Local Similarity 78.4%; Pred. No. 5.1e-283;
Matches 680; Conservative 86; Mismatches 98; Indels 3; Gaps 2;

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DB 751 MRNNGSGVEVRLPNDLEDKGYTSLFLQRPDLRENGTEGDMFVYLGNDKASDXYIG 810
QY 61 MAVVDQQLTCVYMLGDRBAELQVDQILTKSETEKAVMDRYKQRIYQFARLANTYKATSN 120
DB 811 MAVVDQQLTCVYMLGDRBAELQVDQILTKSETEKAVMDRYKQRIYQFARLANTYKATSN 870
QY 121 KKPAPAVYDLBEGSSNTLNLDPEDAVFYVGYPPDFBLPSRLRPPYKGCIELDLNEN 180
DB 871 KKPAPAVYDLBEGSSNTLNLDPEDAVFYVGYPPDFBLPSRLRPPYKGCIELDLNEN 930
QY 181 VSLVNFKTFNLTTEVEPCRRRKESSDKNYEGGYARIPQPNAPPNFIQTIQTV 240
DB 931 VSLVNFKTFNLTTEVEPCRRRKESSDKNYEGGYARIPQPNAPPNFIQTIQTV 990
QY 241 DRGLFFAENQDNFISLINEDGNLAVRYKLNSEPPKEKIRDTINDKHSILITIGKQ 300
DB 991 DRGLFFAENQDNFISLINEDGNLAVRYKLNSEPPKEKIRDTINDKHSILITIGKQ 1050
QY 301 KRWIVNRSVRIEGBIFDFTYTYGGIPAIAREFNISTPAPOGCMKUKKTSGVRL 360
DB 1051 KRWIVNRSVRIEGBIFDFTYTYGGIPAIAREFNISTPAPOGCMKUKKTSGVRL 1110
QY 361 NDVGVYTKCSBEMKLVRTASFSRGQMSFTNLDPVSTDRFOLSPFGOTQPSGTLINQ 420
DB 1111 NDVGVYTKCSBEMKLVRTASFSRGQMSFTNLDPVSTDRFOLSPFGOTQPSGTLINQ 1170
QY 421 TRTSLSLVLEDDHIELSTRDSNIPFKSPGYMDGLLHVSVISDPSGRLIIDQVLR 480
DB 1171 TRTSLSLVLEDDHIELSTRDSNIPFKSPGYMDGLLHVSVISDPSGRLIIDQVLR 1230
QY 481 RNQRLPSFNAQOSLRLGGHPEGCISNVLVORFSOSPEVLDLASKSTKDAISLGGCSLN 540
DB 1231 RNQRLPSFNAQOSLRLGGHPEGCISNVLVORFSOSPEVLDLASKSTKDAISLGGCSLN 1290
QY 541 KRPFLMLFKSPKRFNKGRIFFNVNQLMODAPQAT-RSTEAMODGRSCPLPLNTASRAHQ 599
DB 1291 KRPFLMLFKSPKRFNKGRIFFNVNQLMODAPQAT-RSTEAMODGRSCPLPLNTASRAHQ 1348
QY 600 FGDSPTSHLLKLPQELILKPSQFSLDIQTSPEKLVFVAGTOSFALTYVADGRVFL 659
DB 1349 FGDSPTSHLLKLPQELILKPSQFSLDIQTSPEKLVFVAGTOSFALTYVADGRVFL 1408
QY 660 GAGGKRLRLSKERHYDGMHTVVFGLNGKARLVVDGLRAOGSLPGNSTISIPREOVYL 719
DB 1409 GAGGKRLRLSKERHYDGMHTVVFGLNGKARLVVDGLRAOGSLPGNSTISIPREOVYL 1468
QY 720 GLPLSRKPKSLPQHSFVGCILRDQOLNSKPLDPSARFVSPCCGSLKGIYFSOGGSHV 779
DB 1469 GLPLSRKPKSLPQHSFVGCILRDQOLNSKPLDPSARFVSPCCGSLKGIYFSOGGSHV 1528
QY 780 ILANSVSLGPELKLTSIRPRSLTGVLHYVGSOGSLSYMEAGKYTTSVSDAGGSVT 839
DB 1529 ILANSVSLGPELKLTSIRPRSLTGVLHYVGSOGSLSYMEAGKYTTSVSDAGGSVT 1588
QY 840 SITPKQSLCDGQWHSVAVSIKRIHL 866
DB 1589 SITPKQSLCDGQWHSVAVSIKRIHL 1615

RESULT 4
US-10-603-725-8
; Sequence 8, Application US/10603725
; Publication No. US20040014665A1
; GENERAL INFORMATION:
; APPLICANT: Boudand, Ariel

TITLE OF INVENTION: Recombinant Laminin 5
FILE REFERENCE: 99-274-C
CURRENT APPLICATION NUMBER: US/10/603,725
CURRENT FILING DATE: 2003-06-25
NUMBER OF SEQ ID NOS: 36
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 8
LENGTH: 1693
; ORGANISM: Homo sapiens
; TYPE: PRT
US-10-603-725-8

Query Match 79.3%; Score 3560.5; DB 15; Length 1693;
Best Local Similarity 78.4%; Pred. No. 5.1e-283;
Matches 680; Conservative 86; Mismatches 98; Indels 3; Gaps 2;

1 MRNNGSGVEVRLPNDLEDKGYTSLFLQRPDLRENGTEGDMFVYLGNDKASDXYIG 60
DB 751 MRNNGSGVEVRLPNDLEDKGYTSLFLQRPDLRENGTEGDMFVYLGNDKASDXYIG 810
QY 61 MAVVDQQLTCVYMLGDRBAELQVDQILTKSETEKAVMDRYKQRIYQFARLANTYKATSN 120
DB 811 MAVVDQQLTCVYMLGDRBAELQVDQILTKSETEKAVMDRYKQRIYQFARLANTYKATSN 870
QY 121 KKPAPAVYDLBEGSSNTLNLDPEDAVFYVGYPPDFBLPSRLRPPYKGCIELDLNEN 180
DB 871 KKPAPAVYDLBEGSSNTLNLDPEDAVFYVGYPPDFBLPSRLRPPYKGCIELDLNEN 930
QY 181 VSLVNFKTFNLTTEVEPCRRRKESSDKNYEGGYARIPQPNAPPNFIQTIQTV 240
DB 931 VSLVNFKTFNLTTEVEPCRRRKESSDKNYEGGYARIPQPNAPPNFIQTIQTV 990
QY 241 DRGLFFAENQDNFISLINEDGNLAVRYKLNSEPPKEKIRDTINDKHSILITIGKQ 300
DB 991 DRGLFFAENQDNFISLINEDGNLAVRYKLNSEPPKEKIRDTINDKHSILITIGKQ 1050
QY 301 KRWIVNRSVRIEGBIFDFTYTYGGIPAIAREFNISTPAPOGCMKUKKTSGVRL 360
DB 1051 KRWIVNRSVRIEGBIFDFTYTYGGIPAIAREFNISTPAPOGCMKUKKTSGVRL 1110
QY 361 NDVGVYTKCSBEMKLVRTASFSRGQMSFTNLDPVSTDRFOLSPFGOTQPSGTLINQ 420
DB 1111 NDVGVYTKCSBEMKLVRTASFSRGQMSFTNLDPVSTDRFOLSPFGOTQPSGTLINQ 1170
QY 421 TRTSLSLVLEDDHIELSTRDSNIPFKSPGYMDGLLHVSVISDPSGRLIIDQVLR 480
DB 1171 TRTSLSLVLEDDHIELSTRDSNIPFKSPGYMDGLLHVSVISDPSGRLIIDQVLR 1230
QY 481 RNQRLPSFNAQOSLRLGGHPEGCISNVLVORFSOSPEVLDLASKSTKDAISLGGCSLN 540
DB 1231 RNQRLPSFNAQOSLRLGGHPEGCISNVLVORFSOSPEVLDLASKSTKDAISLGGCSLN 1290
QY 541 KRPFLMLFKSPKRFNKGRIFFNVNQLMODAPQAT-RSTEAMODGRSCPLPLNTASRAHQ 599
DB 1291 KRPFLMLFKSPKRFNKGRIFFNVNQLMODAPQAT-RSTEAMODGRSCPLPLNTASRAHQ 1348
QY 600 FGDSPTSHLLKLPQELILKPSQFSLDIQTSPEKLVFVAGTOSFALTYVADGRVFL 659
DB 1349 FGDSPTSHLLKLPQELILKPSQFSLDIQTSPEKLVFVAGTOSFALTYVADGRVFL 1408
QY 660 GAGGKRLRLSKERHYDGMHTVVFGLNGKARLVVDGLRAOGSLPGNSTISIPREOVYL 719
DB 1409 GAGGKRLRLSKERHYDGMHTVVFGLNGKARLVVDGLRAOGSLPGNSTISIPREOVYL 1468
QY 720 GLPLSRKPKSLPQHSFVGCILRDQOLNSKPLDPSARFVSPCCGSLKGIYFSOGGSHV 779
DB 1469 GLPLSRKPKSLPQHSFVGCILRDQOLNSKPLDPSARFVSPCCGSLKGIYFSOGGSHV 1528
QY 780 ILANSVSLGPELKLTSIRPRSLTGVLHYVGSOGSLSYMEAGKYTTSVSDAGGSVT 839
DB 1529 ILANSVSLGPELKLTSIRPRSLTGVLHYVGSOGSLSYMEAGKYTTSVSDAGGSVT 1588
QY 840 SITPKQSLCDGQWHSVAVSIKRIHL 866

Db 1589 SVTPKQSLCDGQWHSVAVTIKOHILHL 1615

RESULT 5

US-10-171-311-113
; Sequence 113, Application US/10171311
; Publication No. US20030087270A1
; GENERAL INFORMATION:
; APPLICANT: Schlegel, Robert
; APPLICANT: Chen, Yan
; APPLICANT: Zhao, Xumei
; APPLICANT: Monahan, John
; APPLICANT: Kamackar, Shubhangi
; APPLICANT: Ghatt, Karen
; APPLICANT: Ganavaram, Manjula
; APPLICANT: Hoerh, Sebastian
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
; TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND THERAPY
; TITLE OF INVENTION: OF CERVICAL CANCER
; FILE REFERENCE: MRI-035
; CURRENT APPLICATION NUMBER: US/10/171,311
; PRIOR FILING DATE: 2002-06-12
; PRIOR FILING DATE: 2001-06-13
; PRIOR FILING DATE: 2001-06-13
; PRIOR FILING DATE: 2001-06-13
; PRIOR FILING DATE: 2001-06-13
; PRIOR FILING DATE: 2001-11-14
; NUMBER OF SEQ ID NOS: 238
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 113
; LENGTH: 1713
; TYPE: PRF
; ORGANISM: Homo sapiens
US-10-171-311-113

Query Match 79.3%; Score 3560.5; DB 14; Length 1713;
Best Local Similarity 78.4%; Pred. No. 5.2e-283;
Matches 680; Conservative 86; Mismatches 98; Indels 3; Gaps 2;

QY 1 MRNNGSGVVRRLPNDLEDKGYTSLFLQRPDLRENGTDEMFMVMTLGNDAKSDYIG 60
DB 771 MRNNGSGVVRRLPNDLEDKGYTSLFLQRPDLRENGTDEMFMVMTLGNDAKSDYIG 830
QY 61 MAVVDGQLTCVYNLGDREARLQVDILTSRTEKAVMDRVKFORIYQPARLNTTKATSN 120
DB 831 MAVVDGQLTCVYNLGDREARLQVDILTSRTEKAVMDRVKFORIYQPARLNTTKATSN 890
QY 121 KPRAPAVYDLGEGSSNTLNLDPEDAVFYVGGYPPDFELPSRLRPPYKGCIELDLNN 180
DB 891 KPRAPAVYDLGEGSSNTLNLDPEDAVFYVGGYPPDFELPSRLRPPYKGCIELDLNN 950
QY 181 VSLNFKTTEFLNTTVEPCRRRKEESDKNYFEGGYARIPTQNPAPFPNFIQTITQTV 240
DB 951 VSLNFKTTEFLNTTVEPCRRRKEESDKNYFEGGYARIPTQNPAPFPNFIQTITQTV 1010
QY 241 DRGLLFFAENQDNFTSLNIEDGNLWVRKYKLNSEPRKEGIRDTINDKXHSILITGKQ 300
DB 1011 DRGLLFFAENQDNFTSLNIEDGNLWVRKYKLNSEPRKEGIRDTINDKXHSILITGKQ 1070
QY 301 KRWMINNERSVRIEGLIPDFSTYLLGGLPIAIRERFNISTPAFOGCMKULKKTSGVNL 360
DB 1071 KRWMINNERSVRIEGLIPDFSTYLLGGLPIAIRERFNISTPAFOGCMKULKKTSGVNL 1130
QY 361 NDTFVGTAKCSBDWKLVRTASPSRGQMSFTNLDPBETDFOLSPFGQTFQPSGTLINQ 420
DB 1131 NDTFVGTAKCSBDWKLVRTASPSRGQMSFTNLDPBETDFOLSPFGQTFQPSGTLINQ 1190
QY 421 TRTSLLVLTLEDHIELSTDSNIPTEKSGTMDGLHIVSVISDTSGLRLIIDQVLR 480
DB 1191 TRTSLLVLTLEDHIELSTDSNIPTEKSGTMDGLHIVSVISDTSGLRLIIDQVLR 1250

QY 481 RNORLSPFSMAQSLRLGQGHFEGCISNVLYVORPSQSEPEVLDLASKTRKQASLGGCSLN 540
DB 1251 RNORLSPFSMAQSLRLGQGHFEGCISNVLYVORPSQSEPEVLDLASKTRKQASLGGCSLN 1310
QY 541 KPPFLMLKSGTRFKTKTTFRINOLQDTPVAPSPSVFWOD--ACSLPRTQANHGLQ 599
DB 1311 KPPFLMLKSGTRFKTKTTFRINOLQDTPVAPSPSVFWOD--ACSLPRTQANHGLQ 1368
QY 600 FGDSPSTSHLLKLPOLKLPSPQFSLDIQTSPKGLVYAGTKOSFLALVYADGVNPL 659
DB 1369 FGDSPSTSHLLKLPOLKLPSPQFSLDIQTSPKGLVYAGTKOSFLALVYADGVNPL 1428
QY 660 GAGGKRLRSKRYTHDKMHTVVGNGKARLVVDGJRAQBSGLPNSNISTPREQYLL 719
DB 1429 GAGGKRLRSKRYTHDKMHTVVGNGKARLVVDGJRAQBSGLPNSNISTPREQYLL 1488
QY 720 GLPLSRKRSKLPQHSFVGLADPOLNLSRPLDPSKARFVSPCLGSLERKGIYFSGGSHV 779
DB 1489 GLPLSRKRSKLPQHSFVGLADPOLNLSRPLDPSKARFVSPCLGSLERKGIYFSGGSHV 1548
QY 780 ILANSVSLQPELKLTFPSIRPSRLTGVLLHVSQSGQRLSYVMEAGKVTTSVSDAGSVT 839
DB 1549 ILANSVSLQPELKLTFPSIRPSRLTGVLLHVSQSGQRLSYVMEAGKVTTSVSDAGSVT 1608
QY 840 SITPKQSLCDGQWHSVAVSIRKQRIHL 866
DB 1609 SITPKQSLCDGQWHSVAVSIRKQRIHL 1635

RESULT 6

US-10-372-683-10
; Sequence 10, Application US/10372683
; Publication No. US20040009171A1
; GENERAL INFORMATION:
; APPLICANT: GERRITSEN, MARY E.
; APPLICANT: BEALE JR., FRANKLIN V.
; TITLE OF INVENTION: METHODS FOR THE TREATMENT OF CARCINOMA
; FILE REFERENCE: P1928R1P1
; CURRENT APPLICATION NUMBER: US/10/372,683
; PRIOR FILING DATE: 2003-02-21
; PRIOR FILING DATE: 2002-10-16
; PRIOR FILING DATE: 2002-10-16
; PRIOR FILING DATE: 2001-10-18
; NUMBER OF SEQ ID NOS: 49
; SEQ ID NO 10
; LENGTH: 1713
; TYPE: PRF
; ORGANISM: Homo sapien
US-10-372-683-10

Query Match 79.3%; Score 3560.5; DB 15; Length 1713;
Best Local Similarity 78.4%; Pred. No. 5.2e-283;
Matches 680; Conservative 86; Mismatches 98; Indels 3; Gaps 2;

QY 1 MRNNGSGVVRRLPNDLEDKGYTSLFLQRPDLRENGTDEMFMVMTLGNDAKSDYIG 60
DB 771 MRNNGSGVVRRLPNDLEDKGYTSLFLQRPDLRENGTDEMFMVMTLGNDAKSDYIG 830
QY 61 MAVVDGQLTCVYNLGDREARLQVDILTSRTEKAVMDRVKFORIYQPARLNTTKATSN 120
DB 831 MAVVDGQLTCVYNLGDREARLQVDILTSRTEKAVMDRVKFORIYQPARLNTTKATSN 890
QY 121 KPRAPAVYDLGEGSSNTLNLDPEDAVFYVGGYPPDFELPSRLRPPYKGCIELDLNN 180
DB 891 KPRAPAVYDLGEGSSNTLNLDPEDAVFYVGGYPPDFELPSRLRPPYKGCIELDLNN 950
QY 181 VSLNFKTTEFLNTTVEPCRRRKEESDKNYFEGGYARIPTQNPAPFPNFIQTITQTV 240
DB 951 VSLNFKTTEFLNTTVEPCRRRKEESDKNYFEGGYARIPTQNPAPFPNFIQTITQTV 1010
QY 241 DRGLLFFAENQDNFTSLNIEDGNLWVRKYKLNSEPRKEGIRDTINDKXHSILITGKQ 300

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Db 1011 DRGLLFAENGDRFISINIDGKLMVRYKLNSELPKERGVDALNNRGDHSIQIKIGLQ 1070
Qy 301 KRMINNERSVRIEGIFDPSTYYLGGIPAIHERNISTPAPQCGMKLKTSGVRL 360
Db 1071 KRMINVNDVNTIIDGEVFPSTYYLGGIPAIHERNISTPAPRGCKMKLKTSGVRL 1130
Qy 361 NDTVGYTKKCSBDMKLVRTASFSRGQMSFTNLDVSTDRFOLSPFGQTFQPSGTLNMQ 420
Db 1131 NDTVGYTKKCSBDMKLVRTASFSRGQMSFTNLDVSTDRFOLSPFGQTFQPSGTLNMQ 1190
Qy 421 TRTSLLVLTLEDGHIESTRDSNIPFKSPQTYMDGLLHHVSI SDTSGRLIIDQVLR 480
Db 1191 TWTRNLQVTLLEDGYIELSTDSGGPIFKSPQTYMDGLLHHVSI SDTSGRLIIDQVLR 1250
Qy 481 RNQRLBFSNAQSLRIGGHPGECISNVLYORPSQPEYLDASKSTKQDASIGGCSLN 540
Db 1251 NSKRLKHIISSRSQSLRIGGHPGECISNVLYORPSQPEYLDASKSTKQDASIGGCSLN 1310
Qy 541 KPPLMLFKSPKRNKRIFNVNQMDAPQAT-RSTEAMODGRSCCLPPLNTRKASHRALQ 599
Db 1311 KPPLMLFKSSTRNKTKTFRINQLODTPVASRPSVKWQD-ACSPLEPTQANHQAQ 1368
Qy 600 FGDSPYTHLLKLPOELIKERSQPSLDIQTTSPKGLVFACTKDSFLALYVADGRVVEAL 659
Db 1369 FGDIPYTHLLKLPOELIKERSQPSLDIQTTSPKGLVFACTKDSFLALYVADGRVVEAL 1428
Qy 660 GAGGKRLRLSKRYHDGKMTVYVGLNGSKALVYDGLRAQBSLFGNSTISPREOYL 719
Db 1429 GTDGKRLRIKSKCKNDGKMTVYVGLNGSKALVYDGLRAQBSLFGNSTISPREOYL 1488
Qy 720 GLPLSRPKSLPOHSFVGCRLDPOLNSKPLDSPARPGVSPCLGSGLEKGIYFSQGGHV 779
Db 1489 GSPSPGPKSLPLPNSFVGCRLDPOLNSKPLDSPARPGVSPCLGSGLEKGIYFSQGGHV 1548
Qy 780 ILANSVSLGPELKLTPSIRPSRLTGVLIHVSGSGQRLSYVMEAGKTYTSVSDAGSVT 839
Db 1549 VLHNSVTLGPEFLVFSIRPSRLTGVLIHVSGSGQRLSYVMEAGKTYTSVSDAGSVT 1608
Qy 840 SITPKQSLCDGQWHSVAVSIKQRIHL 866
Db 1609 SITPKQSLCDGQWHSVAVSIKQRIHL 1635

RESULT 7
US-10-603-725-6
; Sequence 6, Application US/10603725
; Publication No. US20040014665A1
; GENERAL INFORMATION:
; APPLICANT: Bouland, Ariel
; TITLE OF INVENTION: Recombinant Laminin 5
; FILE REFERENCE: 99-274-C
; CURRENT APPLICATION NUMBER: US/10/603,725
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 6
; LENGTH: 1713
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-603-725-6

Query Match 79.3%; Score 3560.5; DB 15; Length 1713;
Best Local Similarity 78.4%; Pred. No. 5.2e-283;
Matches 680; Conservative 86; Mismatches 98; Indels 3; Gaps 2;
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Qy 121 KPRAPAYDLEGGSSNTLNLDPEDAVFYVGYGPPDFELPSRLRFPPEYKCIETLDLNN 180
Db 891 KPEPFGYDMDGKNSNTLNLDPEDAVFYVGYGPPDFELPSRLRFPPEYKCIETLDLNN 950
Qy 181 VLSIYNKTYFNNTTEVEBCRRRKESDKNYEGTGYARIPTOPNAPFPNFIOTIOTTV 240
Db 951 VLSIYNKTYFNNTTEVEBCRRRKESDKNYEGTGYARIPTOPNAPFPNFIOTIOTTV 1010
Qy 241 DRGLLFAENGDRFISINIDGKLMVRYKLNSEPPKRGIRDTINDGKHSILITIGLQ 300
Db 1011 DRGLLFAENGDRFISINIDGKLMVRYKLNSEPPKRGIRDTINDGKHSILITIGLQ 1070
Qy 301 KRMINNERSVRIEGIFDPSTYYLGGIPAIHERNISTPAPQCGMKLKTSGVRL 360
Db 1071 KRMINVNDVNTIIDGEVFPSTYYLGGIPAIHERNISTPAPRGCKMKLKTSGVRL 1130
Qy 361 NDTVGYTKKCSBDMKLVRTASFSRGQMSFTNLDVSTDRFOLSPFGQTFQPSGTLNMQ 420
Db 1131 NDTVGYTKKCSBDMKLVRTASFSRGQMSFTNLDVSTDRFOLSPFGQTFQPSGTLNMQ 1190
Qy 421 TRTSLLVLTLEDGHIESTRDSNIPFKSPQTYMDGLLHHVSI SDTSGRLIIDQVLR 480
Db 1191 TWTRNLQVTLLEDGYIELSTDSGGPIFKSPQTYMDGLLHHVSI SDTSGRLIIDQVLR 1250
Qy 481 RNQRLBFSNAQSLRIGGHPGECISNVLYORPSQPEYLDASKSTKQDASIGGCSLN 540
Db 1251 NSKRLKHIISSRSQSLRIGGHPGECISNVLYORPSQPEYLDASKSTKQDASIGGCSLN 1310
Qy 541 KPPLMLFKSPKRNKRIFNVNQMDAPQAT-RSTEAMODGRSCCLPPLNTRKASHRALQ 599
Db 1311 KPPLMLFKSSTRNKTKTFRINQLODTPVASRPSVKWQD-ACSPLEPTQANHQAQ 1368
Qy 600 FGDSPYTHLLKLPOELIKERSQPSLDIQTTSPKGLVFACTKDSFLALYVADGRVVEAL 659
Db 1369 FGDIPYTHLLKLPOELIKERSQPSLDIQTTSPKGLVFACTKDSFLALYVADGRVVEAL 1428
Qy 660 GAGGKRLRLSKRYHDGKMTVYVGLNGSKALVYDGLRAQBSLFGNSTISPREOYL 719
Db 1429 GTDGKRLRIKSKCKNDGKMTVYVGLNGSKALVYDGLRAQBSLFGNSTISPREOYL 1488
Qy 720 GLPLSRPKSLPOHSFVGCRLDPOLNSKPLDSPARPGVSPCLGSGLEKGIYFSQGGHV 779
Db 1489 GSPSPGPKSLPLPNSFVGCRLDPOLNSKPLDSPARPGVSPCLGSGLEKGIYFSQGGHV 1548
Qy 780 ILANSVSLGPELKLTPSIRPSRLTGVLIHVSGSGQRLSYVMEAGKTYTSVSDAGSVT 839
Db 1549 VLHNSVTLGPEFLVFSIRPSRLTGVLIHVSGSGQRLSYVMEAGKTYTSVSDAGSVT 1608
Qy 840 SITPKQSLCDGQWHSVAVSIKQRIHL 866
Db 1609 SITPKQSLCDGQWHSVAVSIKQRIHL 1635

RESULT 8
US-10-603-725-2
; Sequence 2, Application US/10603725
; Publication No. US20040014665A1
; GENERAL INFORMATION:
; APPLICANT: Bouland, Ariel
; TITLE OF INVENTION: Recombinant Laminin 5
; FILE REFERENCE: 99-274-C
; CURRENT APPLICATION NUMBER: US/10/603,725
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 1724
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-603-725-2

Query Match 79.3%; Score 3560.5; DB 15; Length 1724;
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Best Local Similarity 78.4%; Pred. No. 5.3e-283;
Matches 660; Conservative 86; Mismatches 98; Indels 3; Gaps 2;

QY 1 MRRNGSGVEVRLPNDLEDKGYTSLFLQRPDLRENGTDEMFMVYLGAKQASDYIG 60
Db 782 MRRNGSGVEVRLPNDLEDKGYTSLFLQRPDLRENGTDEMFMVYLGAKQASDYIG 841
QY 61 MAVVDQQLTCVYVLPGRBAVQIDQVLTSESGOAVMDRYKFORIYQPAKNTTKATSN 120
Db 842 MAVVDQQLTCVYVLPGRBAVQIDQVLTSESGOAVMDRYKFORIYQPAKNTTKATSN 901
QY 121 KKPAPAVYDLEGGSSNTLNLDEDAVFYVGYGPPDELSRLRFPYKCIELDLNEN 180
Db 902 KKPAPAVYDLEGGSSNTLNLDEDAVFYVGYGPPDELSRLRFPYKCIELDLNEN 961
QY 181 VLSLVNFKTTFNLNTEVEVERCRRKESDKNYFEGTGYARIPTQAPAPFPFIQTIQTV 240
Db 962 VLSLVNFKTTFNLNTEVEVERCRRKESDKNYFEGTGYARIPTQAPAPFPFIQTIQTV 1021
QY 241 DRGLFPAENQDNFISLNIEDGNLMVRYKLNSEPPKEKIRDTINDKSHLITIGKQ 300
Db 1022 DRGLFPAENQDNFISLNIEDGNLMVRYKLNSEPPKEKIRDTINDKSHLITIGKQ 1081
QY 301 KRWIVNRSVARIIEBIEIDFSTYYVIGTPIAIRBNSTIRAFQCMKTKTSGSVRL 360
Db 1082 KRWIVNRSVARIIEBIEIDFSTYYVIGTPIAIRBNSTIRAFQCMKTKTSGSVRL 1141
QY 361 NDTVGYTKCSBDMKLVRTASFSGQMSFTNLDVSTDRFQSLFSGTQFQSGTLLNHQ 420
Db 1142 NDTVGYTKCSBDMKLVRTASFSGQMSFTNLDVSTDRFQSLFSGTQFQSGTLLNHQ 1201
QY 421 TRTSLLVLTEDGHIELSTRDNIPIPKSPGYMDGLHHVSVISDTSGRLIIDQVLR 480
Db 1202 TRTSLLVLTEDGHIELSTRDNIPIPKSPGYMDGLHHVSVISDTSGRLIIDQVLR 1261
QY 481 RNORLFSFNAOQSLRLGGHFEKGSNTLVORFSGSPRYLDLASKSTKQDSLGGCSLN 540
Db 1262 RNORLFSFNAOQSLRLGGHFEKGSNTLVORFSGSPRYLDLASKSTKQDSLGGCSLN 1321
QY 541 KPPFLMLFKSPKPKFNKRIFFNVQMODAPQAT-RSTEAMQDGRSCLPPLNTKASHRALQ 599
Db 1322 KPPFLMLFKSPKPKFNKRIFFNVQMODAPQAT-RSTEAMQDGRSCLPPLNTKASHRALQ 1379
QY 600 FGDSPFSLHLKLPQBLKPKRSQPSLDIQTTSFKGLVFYAGTDSPLALVYADGRVVAL 659
Db 1380 FGDSPFSLHLKLPQBLKPKRSQPSLDIQTTSFKGLVFYAGTDSPLALVYADGRVVAL 1439
QY 660 GAGGKTLRLSKRKRYHDGKKHTVYFGLNGKALVYDGLPAQSGSLPGNSTISIRAPVYL 719
Db 1440 GAGGKTLRLSKRKRYHDGKKHTVYFGLNGKALVYDGLPAQSGSLPGNSTISIRAPVYL 1499
QY 720 GLPLSRKPKSLPOHSFVGLCLRDFOQLNSKPLDPSARFVSPCLGGSLEKGIYPSOGGSHV 779
Db 1500 GLPLSRKPKSLPOHSFVGLCLRDFOQLNSKPLDPSARFVSPCLGGSLEKGIYPSOGGSHV 1559
QY 780 ILANSVSLGEBELKLTFSIRPSRLTGVLIHVSGSGQRLSYVMEAGKVTTSVSSDAGSVY 839
Db 1560 ILANSVSLGEBELKLTFSIRPSRLTGVLIHVSGSGQRLSYVMEAGKVTTSVSSDAGSVY 1619
QY 840 SITPKQSLCDGQNHSAVAVSIKORILHL 866
Db 1620 SITPKQSLCDGQNHSAVAVSIKORILHL 1646

RESULT 9
US-10-106-698-5877
; Sequence 5877, Application US/10106698
; Publication No. US20030109690A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Colon and Colon Cancer Associated Polynucleotides and Polypeptide
; FILE REFERENCE: PA005P1
; CURRENT APPLICATION NUMBER: US/10/106,698
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; CURRENT FILING DATE: 2002-03-27
; PRIOR APPLICATION NUMBER: PCT/US00/26524
; PRIOR FILING DATE: 2000-09-28
; PRIOR APPLICATION NUMBER: US 60/157,137
; PRIOR FILING DATE: 1999-09-29
; PRIOR APPLICATION NUMBER: US 60/163,280
; PRIOR FILING DATE: 1999-11-03
; NUMBER OF SEQ ID NOS: 8564
; SOFTWARE: PatentIn Ver. 3.0
; SEQ ID NO 5877
; LENGTH: 469
; TYPE: prf
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: MISC_FEATURE
; LOCATION: (8)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: MISC_FEATURE
; LOCATION: (47)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: MISC_FEATURE
; LOCATION: (65)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: MISC_FEATURE
; LOCATION: (436)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-10-106-698-5877
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Query Match 35.6%; Score 1599; DB 14; Length 469;

Best Local Similarity 65.9%; Pred. No. 1.7e-122;
Matches 333; Conservative 55; Mismatches 82; Indels 30; Gaps 5;

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QY 379 TASFSRGGQMSFTNLDVSTDRFQSLFSGTQFQSGTLLNHQTRTSLLVLTEDGHIELS 438
Db 1 SASFSRGGQMSFTNLDVSTDRFQSLFSGTQFQSGTLLNHQTRTSLLVLTEDGHIELS 60
QY 439 TRDSNIPPIKSPGYMDGLHHVSVISDTSGRLIIDQVLRNRORLFSFNAOQSLRLG 498
Db 61 TRDSNIPPIKSPGYMDGLHHVSVISDTSGRLIIDQVLRNRORLFSFNAOQSLRLG 120
QY 499 GGHFEKGSNTLVORFSGSPRYLDLASKSTKQDSLGGCSLNKPPFLMLFKSPKFNKGR 558
Db 121 GGHFEKGSNTLVORFSGSPRYLDLASKSTKQDSLGGCSLNKPPFLMLFKSPKFNKGR 180
QY 559 IFNVNQMODAPQAT-RSTEAMQDGRSCLPPLNTKASHRALQFGDPSFSLHLKLPQBL 617
Db 181 IFNVNQMODAPQAT-RSTEAMQDGRSCLPPLNTKASHRALQFGDPSFSLHLKLPQBL 238
QY 618 KERSQPSLDIQTTSFKGLVFYAGTDSPLALVYADGRVVALGAGGKTLRLSKRKRYHDG 677
Db 238 KERSQPSLDIQTTSFKGLVFYAGTDSPLALVYADGRVVALGAGGKTLRLSKRKRYHDG 298
QY 678 KHTVYFGLNGKALVYDGLPAQSGSLPGNSTISIRAPVYVSPCLGGSLEKGIYPSOGGSHV 737
Db 299 KHTVYFGLNGKALVYDGLPAQSGSLPGNSTISIRAPVYVSPCLGGSLEKGIYPSOGGSHV 358
QY 738 CLRDFOQLNSKPLDPSARFVSPCLGGSLEKGIYPSOGGSHVILANSVSLGEBELKLTFSI 797
Db 358 CLRDFOQLNSKPLDPSARFVSPCLGGSLEKGIYPSOGGSHVILANSVSLGEBELKLTFSI 418
QY 798 RPRSLTGVLIHVSGSGQRLSYVMEAGKVTTSVSSDAGSVTSITPKQSLCDGQNHSAVAVSI 852
Db 418 RPRSLTGVLIHVSGSGQRLSYVMEAGKVTTSVSSDAGSVTSITPKQSLCDGQNHSAVAVSI 852
QY 853 ---HSAVAVSI 859
Db 460 NVGHKTAHSV 469

RESULT 10
US-10-372-683-4
; Sequence 4, Application US/10372683
; Publication No. US20040009171A1
```

```

; GENERAL INFORMATION:
; APPLICANT: GERRITSEN, MARY E.
; APPLICANT: PEARL JR., FRANKLIN V.
; APPLICANT: WU, THOMAS D.
; TITLE OF INVENTION: METHODS FOR THE TREATMENT OF CARCINOMA
; FILE REFERENCE: P1928R1P1
; CURRENT APPLICATION NUMBER: US/10/372,683
; CURRENT FILING DATE: 2003-02-21
; PRIOR APPLICATION NUMBER: US 10/271,690
; PRIOR FILING DATE: 2002-10-16
; PRIOR APPLICATION NUMBER: US 60/344,534
; PRIOR FILING DATE: 2001-10-18
; NUMBER OF SEQ ID NOS: 49
; SEQ ID NO 4
; LENGTH: 1816
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-372-683-4

```

```

Query Match      26.7%; Score 1198; DB 15; Length 1816;
Best Local Similarity 33.1%; Pred. No. 1.5e-88;
Matches 309; Conservative 161; Mismatches 373; Indels 90; Gaps 26;

```

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1 MRFNKSGVAVRLPNDLEDKGYTSLSLFL---QRDLRENGGTEDMFVYVYAGNKDASK 56
229 MMTDGGSAVAVHRTSMDDLKAFSLSLYKPKPKBELTE---TADQFLLYLSKNAKK 885
57 DYIGMAVVDQQLTCVYNLGDREAEVQIDQVLTSESGEAVMDRYKFORIQAFKANTYKE 116
886 EYNGALIKNDNLVYVYNLGTKDVEIPLDS--KPVSSWPAYFSYIKIRVGHGKVFLLVP 943
117 AITNKPAPAVYDLEGGSSNTLNLDPEDAVFYGYGPPDFELSRKRPYKGCIELDD 176
944 SLSTAEKRTIKGEGSGDLSLDLDEPDVIFYGVGPSFKLPTSLNLGPGVCELELAT 1003
177 LNEVNLVYNFKTPTNLNTEVEPCRRRK-----EESDKNYFEGTGYARLPTQPN---A 227
1004 LNDVLSLVNFKHLYNMDPSTVPCARDKLAFTOSRAASYFPDGSYAVVVDITRRGKFG 1063
228 PPNFIOTIOTYVDKGLLFAENQDNFISINIEDNLMVRY-----KLNSEPKKGI 280
1064 QVTRFDEIVRTPADNGILLMNVGSMFRLERNGYLHVFDYDFGSSGRVHLEDTLKKA- 1122
281 RDTINDKHSILITIGLQKRMINVERSVRI---EGELFDPSTYLLGIP-----I 331
1123 --QINDAKYHEISL-IYHNDKMTLVDRHVKSMDEKMKIPTDIIYIGAPPEILQSR 1179
332 AIRERFNISTPAFOGCKMNL---KKTSGVRLNDTVGTYKKCSBDMCLVRTASPRGGM 388
1180 ALRAHLPLDI-NFRGCKMGFQPKKDFNLLEQETITLGVGCPEDSLISRPAFVN--GQS 1236
389 SFTNLD-VPSIDRQLSPFQOTFQPSGTLNHOQRTSLVLTLEDGHELESTRDSNPIF 447
1237 FIASIQKISFPDGEFGFNRTLOPNGLLFTYASGSVPSISLNDGVIMDVK--GIKVG 1284
448 KSPETMDGLAHVSVISDTSGLR--LLID-DQVLRNQRLLPSFSNAQSLR---LGG-- 499
1295 SVDKQYNDGLSHF--VISVSVPTRYELIVDSRVGSKNPTGKLEQTAKEKKYFGGSP 1352
500 -----GHEGCGISVAVVQFSQSPEDVLDASKSTKQDASLOGCSLNPPLMLFKSKRF 554
1353 ISAOYAFITGICISAVYTRVDRVDEDFQRYTEKHVTSLEYCEPIESSPLFLAKKKNL 1412
555 NKGRIFVNVQ--LMQAPQATSTRAWQDGRSCPLPLNT-----KASHRALQF 600
1413 SKPRAQNKKGKSKDAP-----SWDPVALKLPENTPRNSHCHLSNBPRAIEHAUY 1465
601 GDSPTSHLLKLPBELKRSQSLDQTTSPKGLVYAAKGD--SFLALVYADGRVFA 658
1466 GGTNSHQEFELHGLDGAQSOFISIRLTRSSHGMITFYSDQEBNDPMTLFLAAGRLVYM 1525
659 LGAGGKTLRSKRYHDKWHTVVFGLNGKARLVVDGLAAGSL--PGNSTSPREOV 717

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Db      1526 FNVGHKKLIRSQEKNDGLMHDVIFIRERSGRLVIDGLVLEESLPTEATWIKI 1585
Qy      718 YLGLPLSRKXSLPQ-----HSFVGLRDPQNLNKPDSPPARGVSPCLGSLKGYFS 773
Db      1586 YLGGVAPGKAVKVVQINSIYFSFGCLSNQDNGASTISASQTSVTCFEGMETGYFS 1645
Qy      774 OGGHVIANSVSLGPELKLTFIRPSRLTGLVLIHWSOGQRLSYVMEAGKYTTSVSD 833
Db      1646 TEGGVVLDSEFNGIKFELAFEVRRSSGTLVHGSUNGEYLIANMKGQVLYKVNNG 1705
Qy      834 AGGSVTSITPKQSLCDQWHSVAVSIKORILH 866
Db      1706 IRDFSTSVTEPKQSLCDGRWERTVIRDSNVQL 1738

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RESULT 11
US-10-363-616-457

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; Sequence 457, Application US/10363616
; Publication No. US20040044181A1

```

```

; GENERAL INFORMATION:

```

```

; APPLICANT: Hysq, Inc

```

```

; TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES

```

```

; FILE REFERENCE: 21272-113 (793)

```

```

; CURRENT APPLICATION NUMBER: US/10/363,616

```

```

; CURRENT FILING DATE: 2003-03-03

```

```

; PRIOR APPLICATION NUMBER: 09/654,935

```

```

; PRIOR FILING DATE: 2000-09-01

```

```

; NUMBER OF SEQ ID NOS: 490

```

```

; SEQ ID NO 457

```

```

; LENGTH: 1823

```

```

; TYPE: PRT

```

```

; ORGANISM: Homo sapiens

```

```

; US-10-363-616-457

```

```

Query Match      26.5%; Score 1192; DB 15; Length 1823;
Best Local Similarity 33.5%; Pred. No. 4.7e-88;
Matches 312; Conservative 158; Mismatches 374; Indels 88; Gaps 28;

```

```

1 MRFNKSGVAVRLPNDLEDKGYTSLSLFL---QRDLRENGGTEDMFVYVYAGNKDASK 56
836 MMTDGGSAVAVHRTSMDDLKAFSLSLYKPKPKBELTE---TADQFLLYLSKNAKK 892
57 DYIGMAVVDQQLTCVYNLGDREAEVQIDQVLTSESGEAVMDRYKFORIQAFKANTYKE 116
893 EYNGALIKNDNLVYVYNLGTKDVEIPLDS--KPVSSWPAYFSYIKIRVGHGKVFLLVP 950
117 AITNKPAPAVYDLEGGSSNTLNLDPEDAVFYGYGPPDFELSRKRPYKGCIELDD 176
951 SLSTAEKRTIKGEGSGDLSLDLDEPDVIFYGVGPSFKLPTSLNLGPGVCELELAT 1010
893 EYNGALIKNDNLVYVYNLGTKDVEIPLDS--KPVSSWPAYFSYIKIRVGHGKVFLLVP 950
117 AITNKPAPAVYDLEGGSSNTLNLDPEDAVFYGYGPPDFELSRKRPYKGCIELDD 176
951 SLSTAEKRTIKGEGSGDLSLDLDEPDVIFYGVGPSFKLPTSLNLGPGVCELELAT 1010
1011 LNDVLSLVNFKHLYNMDPSTVPCARDKLAFTOSRAASYFPDGSYAVVVDITRRGKFG 1070
228 PPNFIOTIOTYVDKGLLFAENQDNFISINIEDNLMVRYKLN--SEPPKKGIRDT--- 283
1071 QVTRFDEIVRTPADNGILLMNVGSMFRLERNGYLHVFDYDFGSSGPVH--LEDTLK 1128
284 --INDKHSILITIGLQKRMINVERSVRI---EGELFDPSTYLLGIP-----IA 332
1129 AQINDAKYHEISL-IYHNDKMTLVDRHVKSMDEKMKIPTDIIYIGAPPEILQSR 1187
333 IRERFNISTPAFOGCKMNL---KKTSGVRLNDTVGTYKKCSBDMCLVRTASPRGGM 389
1188 LRAHLPLDI-NFRGCKMGFQPKKDFNLLEQETITLGVGCPEDSLISRPAFVN--GQS 1244
390 FTMND-VPSIDRQLSPFQOTFQPSGTLNHOQRTSLVLTLEDGHELESTRDSNPIF 448
1245 IASIQKISFPDGEFGFNRTLOPNGLLFTYASGSVPSISLNDGVIMDVK--GIKVG 1302
449 SPTGYMDGLAHVSVISDTSGLR--LLID-DQVLRNQRLLPSFSNAQSLR---LGG-- 499
1303 VDKQYNDGLSHF--VISVSVPTRYELIVDSRVGSKNPTGKLEQTAKEKKYFGGSP 1360

```


OTHER INFORMATION: X in position 1112 = Arg/Pro
US-10-299-058-2

Query Match	26.4%	Score 1187	DB 14	Length 1816
Best Local Similarity	33.2%	Pred. No. 1.2e-87		
Matches 310, Conservative	160	Mismatches 373	Indels 90	Gaps 27

Qy	MRPFGKSGVEVR.LJNDJED.LKGYTSL.FL-----QRPLRENGGJEDMFVWYLLGNQDASK	56
Dd	829 MAFGQGSANVEHSTSMDDRAFTSLSLYMKPVRPELTLT---TADPFIYLYLSSKNKKK	895
Qy	57 DYIGMAVVDGQJTCVYNLIGDREAEVQIDQVLTSESQCEAVMDRYKFORIYOPALANTYKE	116
Dd	886 EYMGJALKNQDLVYYVNLGTQDVEILPLDS--KXPSSWPAHYPSYKLEBVGHGAVPLTVR	943
Qy	117 ATSNKPKAPAVYDLBGGSSNTLLMLDPEDAVYGYGPPDELP.SRLRFPFYKCCIBLD	176
Dd	944 SLSTSTAEKFKPKGHSFSDSDILDLDPEDTIVFYGVGVSNPKLPTSLNLPFGVCLBIAT	1003
Qy	177 LNEVNL.SLYNKKTJFNLTNTVEPRRRK-----EEDXN.FEGGVA--RIPQPN--A	227
Dd	1004 LNNVDLSLYNKHLYNMDPSTSVPCARDKLAFQTSRASTYFPDGSYAUVDDITRRKFG	1063
Qy	228 PFPPIQTIQTVNRCGLLFAENODNFISLIEDGNLMVRY-----KLNSEPPKEGJ	280
Dd	1064 QVTFPDLIEVR.PPALNGLILLMVNGSMFRLRMNGYLHVFDPRGSSXVHLEDTLKKA-	11222
Qy	281 RDTJNDGKHSILITTGLOKRMNINERSVRI---EGEIPDSTYYLGGIP-----I	331
Dd	1123 --QINDAKYHEISI-IYHNDKMLLVDRRHVKSMDNEKMKI.PFDIYIGAPPEILQSR	1179
Qy	332 AIBREFNSTPAFGCKMNL---KKTSGVYVNLNTVGYTKKCSBDMKLVRASSRGQM	388
Dd	1180 ALRHLPLDIT-NFNGCKMGFOFOKKDFNLJQTEFLGVCYCPESLISRAVYFN--GQS	1236
Qy	389 SFTMLD-VPSYDRQLSGFQTFQPSGTYLHNOTRSLVTLIEDGHEILSTRSNPIF	447
Dd	1237 FIASIQKISFDPGREGFNFRITLQNGLLFYAAGSDVPSISLNDGYIMOVK--GIKVQ	1294
Qy	448 KSPGTWMDGLAHVSVISDTSGLR--LIID-DQVLRNQRLLPSPNMQSLR---LGS-	499
Dd	1295 SVDRQYNDGLSHF--VISVSPTRYELIVDKSRVGSKNPTGKJLEQTQASKEKVFQGS	1352
Qy	500 -----GHEEGISNVLVORFSGSPBYVLDLASKTJKDASLGGCGLNKPPLMLKSPRF	554
Dd	1353 ISAOYANTGGISNMYFTRVDRDVEBEPORYTEVHTSLYCEPLSSPLFLHKKGKNL	1412
Qy	555 NKGBIFNVNQ--LMODAPQATRSTEAWODGRSLPLNT-----KASHRALQF	600
Dd	1413 SKPRAQNKKGKGSKDAP-----SNQPVALKLPERTTPNNSHCLNSRRLA.EHAYQ	1465
Qy	601 GDSPTSHLLKLPOELLKPRSQFSLDIQTTSPKGLVFFAAGTKD--SPLALVADGRVVFA	658
Dd	1466 GGTANSRQEFHKLKGDFAKSOFSIRLRTSSHGMIFFVSDQEBENDFWTLFLAHLRLVYM	1525
Qy	659 LGAGGKDLRLASKERYHDKKHTVYVPLGANGKARLYVDGLFAQGBSL-PGNSITSPREQV	717
Dd	1526 FNVGHKKLKIKTSQEKTYNDGLMHWDIYFIRERSGRLVYDGLVLEBSLPTPTATYKIKPI	1585
Qy	718 YLGLPLSRKPSLPO---HSFVGLCLRPOLANSKPLDSPSARFGVPCPLGSLSEKGIYFS	773
Dd	1586 YLGGVAPRKAVXNQYINSYFSGCLSMYOLGNGASITBASQTFVYTPPEFBPMETGIYFS	1645
Qy	774 QGGGHVILANSVSLGPELKLTPSIRPSRLTGVLLIHVSQSGQRLSVYMEAGVTTVSSD	833
Dd	1646 TEGGVVYVDESPNIGLKEFIEAFRYVPRSSGTLVGHGSVNGEYLVHMKNGQVIVKXVNG	1705
Qy	834 AGGSVTSLTPKOSLCDGQSHVAVASIKRRIIHL	866
Dd	1706 IRDSTSTVTPKOSLCDGRMHRITVYIRDSNVVQL	1738

US-10-299-058-4
Sequence 4, Application US/10299058
Publication No. US20030103975A1
ATTORNEY: TWISS, HARRISON & ASSOCIATES, P.C.

```

; GENERAL INFORMATION:
;
; APPLICANT: JONES, JONATHAN C.R.
;
; APPLICANT: GONZALES, MEREDITH
;
; TITLE OF INVENTION: MODULATION OF ANGIOGENESIS AND ENDOTHELIALIZATION

```

```

; FILE REFERENCE: 1720-1-002 CIP
; CURRENT APPLICATION NUMBER: US/10/299,058
; CURRENT FILING DATE: 2002-11-18
; PRIOR APPLICATION NUMBER: 09/706,235
; PRIOR FILING DATE: 2000-11-03
; PRIOR APPLICATION NUMBER: 60/163,199
; PRIOR FILING DATE: 1999-11-03
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 1816
; TYPE: PRT
; ORGANISM: Homo sapien
; FEATURES:
; OTHER INFORMATION: X in position 1112 = R/P
US-10-299-058-4

```

Query Match	26.4%;	Score 1185;	DB 14;	Length 1816;
Best Local Similarity	33.2%;	Pred. No. 1.7e-87;		
Matches 310;	Conservative 160;	Mismatches 373;	Indels 90;	Gaps 27;
Qy	1	MRFNKSGVGEVRLPNLDELDKGYTSLFL-----QRDLRENGSTEDMFVYILGNKQASK	56	
Db	829	MMFPGQGANVEHSTSTMDLKAFITSLBYNKKPKPKRELT---TLAQFIYILGSKAKK	885	
Qy	57	DYIGMAVVDGLTCVNYILGDBAEVQIDQVLTSESQSEAVMDRYKFORIQYAFKLTATKE	116	
Db	886	EYMGALIKNDLVYVNYLGTQDVEIPLDS--KPGSWPAYSPYIKIIRVVGKGVFLTPV	943	
Qy	117	ATSKKPKAPAVYIDEGSSNTLNLDEPDVAVFYGTGPRDPBELSRKLPFYKCTILD	176	
Db	944	SLSTAEKPKFKGKFSQGDLSLLDLDEBDTVFYGVGVPNSFKLPTSLNLPFGVCELTAT	1003	
Qy	177	LNENVLSLYNKTETENLTTEVBCRRK-----ESSDKVYFEGTGYA--RIPQPN--A	227	
Db	1004	LNDVIVISLYNFKHLYNNDPSTSVPCADKLAFQSRASLYFDQSSGYAVVDRITRRKFG	1063	
Qy	228	PFPNFQITQITVDRGLLFAENODNEISLTIEDGNLWRY-----KLNSEPKKGI	280	
Db	1064	QVTFPDEVRPRADNGILLMVNGSMFRLMRNGYLHVFDQFSSGXVHLBDTLKKA-	1122	
Qy	281	RDITNDGKHSILITIGKLQKRMKINVBESVRI---EGEFPDSTYLLGSI-----I	331	
Db	1123	--QINDAKYHEISI-IYHNDKKMILVYDRHRYKSMDBKKKIPITDIYIGAPPELLQSR	1179	
Qy	332	AIIRFPMISTPAPCGCKNL---KCTSGVVRINDTVGVTKKCSMDKLVRPASRGGM	388	
Db	1180	ALRHLPLDI-NFPGCKMKGFQFOQKDKFNLLQETETLVGICGCPEDSLISRAYFN--GQS	1236	
Qy	389	SFTMLD--VPSTDRFQLSFGFQTFQPGSGLTLNHQRTSLTLVLTLDGHEIESTRDSNIPIF	447	
Db	1237	PIASIQKISFPDGGEGGNRRTLOPNGLIFVYASGSDVPSISLNDGVIMDYK--GIKVG	1294	
Qy	448	KSPETMDGLIHVSVISDTSGLR--LIID-DQYLRRNQRLLPSFNSAQQSLR--LGS-	499	
Db	1295	SVDCQYNDGSLHF--VLISSVSPTEYELIVKSKRVGSKNKPTEGKLEQTOASKEKFPFGSP	1352	
Qy	500	-----GHPEGICSNVLVQRPQSQSEVYLDLASKSKTKQDASIGCGSLNKPPLMLFKSPRF	554	
Db	1353	ISAOYANFTGTSINAYFTRDRDVEVEDPQRYTEKVTLSLEYCEFISSPFLFLKKGNLT	1412	
Qy	555	NKGRIFWVNO--LMQDAPQATRSYEAQDGRSCLEPLANT-----KASHRALQF	600	
Db	1413	SKPRAQNKKGKSKQAP-----SMDPVAKLKLPEKNTPRNHSCHLSNRPRAIEHAYQY	1465	
Qy	601	GDSPSTHLLKLPOELLKPRSQSLDIQITSPKGLVIFYAGTKD--SEFLALVYADGRVFA	658	

Db 1466 GGTANRROFEBHUKDPEAKSOPSIRLRTSSHGIMFYVSDQENDFMTLFLAHGLVYM 1525
QY 659 LGAGKRLRLRSKERYHDKMHTVFGNLNGKARLVVDGLRAQEGSL-EGNSTISPREQY 717
Db 1526 FNVGHKKLIRSOBKINDGIMHVIPIRBSGRLVIDGLRVLBESLPPEATWKIKGPI 1585
QY 718 YLGLPSRRKSLPQ-----HSFVGLRDPQLNSKPLDPSAPRGVSPCLGSLKGIYFS 773
Db 1586 YLGVAAPKAVKVVQINSIYFSGCLSNLQNLNGASITSAQTSVTPCFEGPMEGTIYFS 1645
QY 774 QGGHVIILANSVSLGEBLKTESIRPSRLTGVLIHYGSGGRLSYMEAKYTTSSSD 833
Db 1646 TEGGYVLDSEFNIKGFLAFEPVRPRSSGTLVHGHSYGEYLVAMKGVIVKXNNG 1705
QY 834 AGGSVTSITPKOSLCDGWHSAVSIKORILHL 866
Db 1706 IRDFTSVTPKOSLCDGRMRHRTIVIRDSNVQL 1738

RESULT 15
US-10-037-417-49
; Sequence 49, Application US/10037417
; Publication No. US20040052806A1
; GENERAL INFORMATION:
; APPLICANT: Kekuda, Ramesh
; APPLICANT: Alsobrook II, John P
; APPLICANT: Tchernev, Velizar T
; APPLICANT: Liu, Xiaohong
; APPLICANT: Spytek, Kimberly A
; APPLICANT: Raturajan, Meera
; APPLICANT: Grose, William M
; APPLICANT: Lepley, Denise M
; APPLICANT: Burgess, Catherine B
; APPLICANT: Vernet, Corine A.M.
; APPLICANT: Li, Li
; APPLICANT: Gorman, Linda
; APPLICANT: Edinger, Shlomit R
; APPLICANT: Sciore, Paul
; APPLICANT: Billeman, Karen
; APPLICANT: Malvanek, Uriel M
; APPLICANT: Rothenberg, Mark
; APPLICANT: Stone, David J
; APPLICANT: Boldog, Ferenc L
; APPLICANT: Guo, Xiaojia
; APPLICANT: Shenoy, Suresh G
; APPLICANT: Anderson, David W
; APPLICANT: Padigaru, Muralidhara
; APPLICANT: Taupier Jr, Raymond J
; APPLICANT: Bisen, Andrew J
; APPLICANT: Miller, Charles E
; TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same
; FILE REFERENCE: 21402-235
; CURRENT APPLICATION NUMBER: US/10/037,417
; CURRENT FILING DATE: 2002-09-20
; PRIOR APPLICATION NUMBER: 60/260,018
; PRIOR FILING DATE: 2001-01-05
; PRIOR APPLICATION NUMBER: 60/260,360
; PRIOR FILING DATE: 2001-01-08
; PRIOR APPLICATION NUMBER: 60/272,411
; PRIOR FILING DATE: 2001-02-28
; PRIOR APPLICATION NUMBER: 60/272,817
; PRIOR FILING DATE: 2001-03-02
; PRIOR APPLICATION NUMBER: 60/291,186
; PRIOR FILING DATE: 2001-05-15
; PRIOR APPLICATION NUMBER: 60/303,231
; PRIOR FILING DATE: 2001-07-05
; PRIOR APPLICATION NUMBER: 60/305,060
; PRIOR FILING DATE: 2001-07-12
; PRIOR APPLICATION NUMBER: 60/318,405
; PRIOR FILING DATE: 2001-09-10
; PRIOR APPLICATION NUMBER: 60/318,700
; PRIOR FILING DATE: 2001-09-12

; NUMBER OF SEQ ID NOS: 227
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 49
; LENGTH: 1634
; TYPE: prt
; ORGANISM: Homo sapiens
US-10-037-417-49

Query Match 23.3%; Score 1045.5; DB 15; Length 1634;
Best Local Similarity 31.6%; Pred. No. 4.4e-76;
Matches 294; Conservative 159; Mismatches 367; Indels 109; Gaps 32;

QY 1 MRFNKGVEVRLPNDLEDKGYTSLSLPQRPDLRENGGTEDEMEVYLGNKDKASKEYIG 60
Db 676 MKEFGSGVQJRTPRDLADLAAYTALKXYLQGPBEPCQGTEDRVRVMYMGSRQATGYMG 735
QY 61 MAVVDGQLTCVYNGDR-BAEVQIDQVLTESBSQAVNDKRYFQRTIYPAKILNTYKE--- 116
Db 736 VSLRDKKVMYVQLDEAGPAVLSIDEDIGEQ-----PAAVSLDRTLQFGHMSVYVERQM 789
QY 117 --ATSNKDKAPAVYDLEGSSVTLNLPEDAVFYVGGYPPDFELPSRLRPPYKGTIEL 174
Db 790 IQETKGDVYAPGA---EG-----LNLKRPDDVFYVGGYPTFTPTPLIRFPFGYCIEM 841
QY 175 DDLNENSVLYNFKTTFMNLTEVEPCRRRKE-----SDKNYFEGTGYARIPTQPN-AP 228
Db 842 DTLNEBVSFLVYFERTFQDTRAVDRPCARSKSTGDPMLTDGSLYLDGTGFARISPDQIST 901
QY 229 PNFNFIQTITVDRRLPAENQDNFISLNEEDGMLRYKLS-----EPP----- 275
Db 902 TTRFQDELRLVSYSGLVFPFLKQSQFLCLAVQEGSLVLLYFGAELKKAVALPQPPPLTS 961
QY 276 KEKGIKRTINDKDSILITTKLOKRMIMVNER---SVRLEGIFPFSYYLAGI--- 329
Db 962 ASKAIQ-----VPLGSKRKYLVYERATVYSVEDNDLELADAYLGGVPEPD 1010
QY 330 --PLAIRRPNISTPAPQCMKNLK--KTSGVANLNDTVGYTKKCSBDMKLVRTASFSR 384
Db 1011 QLPPLRLRFP-TGGSVRCGVYKALGKYVDLKRLL-TTGVSACTADLLVGRAMTFHG 1068
QY 385 GG--QMSFTNLDVETDRFQLSFGQTFQPSGTLNHOQTRSSSLVLTEDGHIESTDS 442
Db 1069 HGFRLRLALSNV-APLTGNVYSGFGHSAQDSALVYRASPDGLCVSLQGGVSLQLART 1127
QY 443 NIPFKSPQYMDGLHHVSVISDTSGLRLYLDQV--LRNRQRPSSNAQOS---LR 496
Db 1128 EV---KTQAGPADGAPHYAFISNATGWLYVDQDQMKHRKRPPELQRPBEPRL 1184
QY 497 LGG-----GHFEGCISNVLVQRPQSPDEVLDLASKSTKQDASLGGCSLNNKPPFLMEFK 549
Db 1185 LGGLPESGTYVFGSCISNVFQRLGQRYVLDLQNLGSVVST-GCA---PALQA-Q 1238
QY 550 SPKRNRKRIENVNOLMODAPQATSTEAWDGNSCLPPLTKASHRLQRPDSFTSHL 609
Db 1239 TPELPRG-----LOATYARKASRSRQPARNHPACMLPPIHRTTRDYQFQFGSLSSH- 1289
QY 610 LKLPEELKPRS--QFSLDIQTSPKGLVFAAG---TDSFLAVVADGRVVFALGAGSK 664
Db 1290 LEPFVGLLAHNRMBPLSMHVLPRSRGGLFLFARLRPSPSLALSLNGHFAQEGSLGT 1349
QY 665 KLRLSKERYHDKMHTVFGNLNGKARLVVDGLRA-QEG---SLPQNSTISPREQVYL 719
Db 1350 RLRAQSRQSRGRNHNKYSVRNEKRIILVTDGAAMQBEGRHQGAENHQPITLTVG 1409
QY 720 GLPLSRKPKSLP-QHSFVGLRDPQLNSKPLDPSAPRGVSPCLGSLKGIYFSQGGGH 778
Db 1410 GLPASHSKCLPVTVTGFGSCVVRRLHGRPLGAPFRMGAVTPTCIGPLPEAGIFFPGSGGV 1469
QY 779 VILANSVSLGEBLKTFSIRPSRLTGVLIHYG-SQSGRLSYMEAKYTTSSSDAGGS 837
Db 1470 ITLDPGATLPVGLGLEVRPLAVTGLIFHLQQAARTPYLQLOVTEKOVLLRADDAGERF 1529
QY 838 VTSITPKOSLCDGWHSAVSIKORILHL 866

Db 1530 STSVTRPSVLCDCGQWHRHIAVMKSGNVLRL 1558

Search completed: February 22, 2005, 08:44:39
Job time : 119.062 secs

This Page Blank (uspto)

GenCore version 5.1.6
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OM protein - protein search, using SW model

Run on: February 22, 2005, 08:13:40 ; Search time 40.4378 Seconds
(without alignments)
1598.653 Million cell updates/sec

Title: US-10-817-423-2

Perfect score: 4491

Sequence: 1 MRFNGKSGVEVRLPNDLEDL.....LCDGQMSVAVSIKRIILHL 866

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Issued Patents AA:*
1: /cgn2_6/prodata/1/iaa/5A COMB pep:*
2: /cgn2_6/prodata/1/iaa/5B COMB pep:*
3: /cgn2_6/prodata/1/iaa/6A COMB pep:*
4: /cgn2_6/prodata/1/iaa/6B COMB pep:*
5: /cgn2_6/prodata/1/iaa/6C COMB pep:*
6: /cgn2_6/prodata/1/iaa/backfillseq1 pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	4491	100.0	1694	4 US-09-560-385A-12	Sequence 12, App1
2	4491	100.0	1725	4 US-09-560-385A-10	Sequence 10, App1
3	3560.5	79.3	1693	4 US-09-560-385A-4	Sequence 4, App1
4	3560.5	79.3	1693	4 US-09-560-385A-8	Sequence 8, App1
5	3560.5	79.3	1713	3 US-08-600-982-24	Sequence 24, App1
6	3560.5	79.3	1713	4 US-09-560-385A-24	Sequence 24, App1
7	3560.5	79.3	1713	4 US-09-538-092-1359	Sequence 1359, Ap
8	3560.5	79.3	1713	5 PCT-US94-10261A-24	Sequence 24, App1
9	3560.5	79.3	1724	4 US-09-560-385A-2	Sequence 2, App1
10	1310	29.2	770	1 US-08-445-135-2	Sequence 2, App1
11	1198	26.7	1792	4 US-09-561-818A-4	Sequence 4, App1
12	1198	26.7	1800	4 US-09-561-818A-2	Sequence 8, App1
13	1198	26.7	1816	4 US-09-561-818A-8	Sequence 8, App1
14	1198	26.7	1824	4 US-09-561-818A-6	Sequence 6, App1
15	1183	26.3	1792	4 US-09-561-818A-12	Sequence 12, App1
16	1183	26.3	1816	4 US-09-561-818A-10	Sequence 10, App1
17	1015.5	22.6	953	4 US-09-845-583A-4	Sequence 4, App1
18	948	21.1	3635	4 US-09-845-583A-2	Sequence 2, App1
19	925	20.6	3647	4 US-09-949-016-10932	Sequence 10932, A
20	534.5	11.9	1130	6 5444158-2	Patent No. 5444158
21	534.5	11.8	3075	2 US-08-460-309-5	Sequence 5, App1
22	530.5	11.8	3075	2 US-08-460-309-5	Sequence 5, App1
23	526.5	11.7	1130	2 US-08-460-309-2	Sequence 2, App1
24	526.5	11.7	1130	2 US-08-125-077-2	Sequence 2, App1
25	526.5	11.7	3088	4 US-09-562-702A-8	Sequence 8, App1
26	526.5	11.7	3088	4 US-09-562-702A-8	Sequence 8, App1
27	526.5	11.7	3089	4 US-09-562-702A-4	Sequence 4, App1

28	526.5	11.7	3110	4 US-09-562-702A-2	Sequence 2, App1
29	526.5	11.7	3110	4 US-09-562-702A-6	Sequence 6, App1
30	526.5	11.7	3110	4 US-09-561-709B-7	Sequence 7, App1
31	526.5	11.7	3110	4 US-09-917-254-86	Sequence 86, App1
32	526.5	11.7	3110	4 US-09-949-016-5937	Sequence 5937, Ap
33	526.5	11.7	3111	2 US-08-460-309-4	Sequence 4, App1
34	526.5	11.7	3111	2 US-08-125-077-4	Sequence 4, App1
35	516.5	11.5	3084	4 US-09-562-702A-12	Sequence 12, App1
36	516.5	11.5	3106	4 US-09-562-702A-10	Sequence 10, App1
37	484.5	10.8	3070	4 US-09-961-403-7	Sequence 7, App1
38	294	6.5	1384	4 US-09-949-016-7814	Sequence 7814, Ap
39	220.5	4.9	1331	4 US-09-949-016-6861	Sequence 6861, Ap
40	205	4.6	1384	4 US-08-826-134-2	Sequence 2, App1
41	205	4.6	1384	4 US-09-949-016-6395	Sequence 6395, Ap
42	183	4.1	4391	4 US-10-006-011A-2	Sequence 2, App1
43	180	4.0	705	4 US-10-006-011A-3	Sequence 3, App1
44	176.5	3.9	1058	4 US-09-949-016-11457	Sequence 11457, A
45	174	3.9	1381	4 US-08-826-134-4	Sequence 4, App1

ALIGNMENTS

RESULT 1
US-09-560-385A-12

Sequence 12, Application US/09560385A

Patent No. 6703363

GENERAL INFORMATION:

APPLICANT: Bouland, Arlet

TITLE OF INVENTION: Recombinant Laminin 5

FILE REFERENCE: 99-274-C

CURRENT APPLICATION NUMBER: US/09/560,385A

CURRENT FILING DATE: 2000-04-28

NUMBER OF SEQ ID NOS: 36

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 12

LENGTH: 1694

TYPE: PRT

ORGANISM: Rattus norvegicus

US-09-560-385A-12

Query Match 100.0%; Score 4491; DB 4; Length 1694;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 866; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	MRFNGKSGVEVRLPNDLEDLKGYSLSLFLQRPDLRENGGTEDMFVYLGAKDASKDYIG	60
DB	751	MRFNGKSGVEVRLPNDLEDLKGYSLSLFLQRPDLRENGGTEDMFVYLGAKDASKDYIG	810
QY	61	MAVVDQQLTCVYVLGGRBAVQIDQVLTSESGEAVMDVKKPQRIYQPAKLNTTKATSN	120
DB	811	MAVVDQQLTCVYVLGGRBAVQIDQVLTSESGEAVMDVKKPQRIYQPAKLNTTKATSN	870
QY	121	KPAPAVYDLGGSSNTLNLDPEDAVFYVGGVPDPFELPSRLRFPYKGCIELDLNEN	180
DB	871	KPAPAVYDLGGSSNTLNLDPEDAVFYVGGVPDPFELPSRLRFPYKGCIELDLNEN	930
QY	181	VLSLVFKTTFNLTVEVPCRRRKESDKNYEGTGVARIPQPNAPPNFIQTITQTV	240
DB	931	VLSLVFKTTFNLTVEVPCRRRKESDKNYEGTGVARIPQPNAPPNFIQTITQTV	990
QY	241	DRLGLPFAENQNFISLNTBDGMLMRYKLNSPPPKGKIRDTINDGKHSIIITIGKQ	300
DB	991	DRLGLPFAENQNFISLNTBDGMLMRYKLNSPPPKGKIRDTINDGKHSIIITIGKQ	1050
QY	301	KRMWVWNSVRIEIEIFDFTYVGGIPAIAREPNISTPAFQGMKRLKKTSGVRL	360
DB	1051	KRMWVWNSVRIEIEIFDFTYVGGIPAIAREPNISTPAFQGMKRLKKTSGVRL	1110
QY	361	NDTVGVTKCSSEDMKLVRTASFSRGQMSFTNIDVSTDRFQLSFGPQTFQPSGTLINQ	420
DB	1111	NDTVGVTKCSSEDMKLVRTASFSRGQMSFTNIDVSTDRFQLSFGPQTFQPSGTLINQ	1170


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QY 421 TTTSSLVLTLEBGIHIELSTRDSNIPFKSPGYMDGLHHVSVISDTSGLRLIIDQVLR 480
DB 1171 TTTSSLVLTLEBGIHIELSTRDSNIPFKSPGYMDGLHHVSVISDTSGLRLIIDQVLR 1230
QY 481 RNORLPSFSNAOQSLRLGGHPEGCSNVLVORFSGSPVLDLASKSTKXASLGCCSLN 540
DB 1231 RNORLPSFSNAOQSLRLGGHPEGCSNVLVORFSGSPVLDLASKSTKXASLGCCSLN 1290
QY 541 KPPFLMLFKSPKRFNKGRIFFNVNQLMODAPQATRSTTEAMODGRSCPLPLNTKASHRALQF 600
DB 1291 KPPFLMLFKSPKRFNKGRIFFNVNQLMODAPQATRSTTEAMODGRSCPLPLNTKASHRALQF 1350
QY 601 GDSPTSHLLKLPOBLKPRSQFSLDIQTTSPPKGLVFYAGTKDSFLALYVADGRVVFALG 660
DB 1351 GDSPTSHLLKLPOBLKPRSQFSLDIQTTSPPKGLVFYAGTKDSFLALYVADGRVVFALG 1410
QY 661 AGGKRLRLSKERYHDGKMTTVFGLNGKARLVVDGLAQBESLPGNSTISPREQVYLQ 720
DB 1411 AGGKRLRLSKERYHDGKMTTVFGLNGKARLVVDGLAQBESLPGNSTISPREQVYLQ 1470
QY 721 LPLSRKPKSLPQHSFVGCRLDPOLNSKPLDSPSARFVSPCLGSLKGIYFSGGGHVI 780
DB 1471 LPLSRKPKSLPQHSFVGCRLDPOLNSKPLDSPSARFVSPCLGSLKGIYFSGGGHVI 1530
QY 781 LANSVSLGPELKLTFISIRPSRLTGVLIVHGSQSGRLSYVMEAGKVTTSVSDAGSVTS 840
DB 1531 LANSVSLGPELKLTFISIRPSRLTGVLIVHGSQSGRLSYVMEAGKVTTSVSDAGSVTS 1590
QY 841 ITPKQSLCDGQMHSAVSIKORILHL 866
DB 1591 ITPKQSLCDGQMHSAVSIKORILHL 1616

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RESULT 2

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US-09-560-385A-10
; Sequence 10, Application US/09560385A
; Patent No. 6703363
; GENERAL INFORMATION:
; APPLICANT: Boudand, Ariel
; TITLE OF INVENTION: Recombinant Laminin 5
; FILE REFERENCE: 99-274-C
; CURRENT APPLICATION NUMBER: US/09/560,385A
; CURRENT FILING DATE: 2000-04-28
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 10
; LENGTH: 1725
; TYPE: PR1
; ORGANISM: Rattus norvegicus
US-09-560-385A-10

```

```

Query Match 100.0%; Score 4491; DB 4; Length 1725;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 866; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MRFNGSGVEVRLPNDLEDKGYTSLFLQRPDLRENGTDEMFVMTLGNKDSKDYIG 60
DB 782 MRFNGSGVEVRLPNDLEDKGYTSLFLQRPDLRENGTDEMFVMTLGNKDSKDYIG 841
QY 61 MAVVDGQLTCVYNLGDREAVQIDQVLTSEBSQDAVMRVKFORIYQPAKNTYKATSN 120
DB 842 MAVVDGQLTCVYNLGDREAVQIDQVLTSEBSQDAVMRVKFORIYQPAKNTYKATSN 901
QY 121 KPPAPAVYDLEGGSSNTLNLDPEDAVFYVGVPPPELPSRLRFPYKGCIELDLNEN 180
DB 902 KPPAPAVYDLEGGSSNTLNLDPEDAVFYVGVPPPELPSRLRFPYKGCIELDLNEN 961
QY 181 VLSLVNFKTFNLTTEVEPCRRKKESSDKNYFEGTGAYARIPTQNPAPFPNFIQTQTVY 240
DB 962 VLSLVNFKTFNLTTEVEPCRRKKESSDKNYFEGTGAYARIPTQNPAPFPNFIQTQTVY 1021
QY 241 DRGLLFAENQDNFISLNIEDGNLMVRYKLNSEPPKXGIRDTINDGKHSILITIGKLO 300

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DB 1022 DRGLLFAENQDNFISLNIEDGNLMVRYKLNSEPPKXGIRDTINDGKHSILITIGKLO 1081
QY 301 KKMVINVERSVRIEGEIFDEFTYVLGGIPAIHERFNISTPAQCCAKNKKTSGVVRL 360
DB 1082 KKMVINVERSVRIEGEIFDEFTYVLGGIPAIHERFNISTPAQCCAKNKKTSGVVRL 1141
QY 361 NDTGVATKCSBDMKLVETASFSRGGQMSFTNLDPVSTDRPOLSPGOTPOPGSTLNLHQ 420
DB 1142 NDTGVATKCSBDMKLVETASFSRGGQMSFTNLDPVSTDRPOLSPGOTPOPGSTLNLHQ 1201
QY 421 TTTSSLVLTLEBGIHIELSTRDSNIPFKSPGYMDGLHHVSVISDTSGLRLIIDQVLR 480
DB 1202 TTTSSLVLTLEBGIHIELSTRDSNIPFKSPGYMDGLHHVSVISDTSGLRLIIDQVLR 1261
QY 481 RNORLPSFSNAOQSLRLGGHPEGCSNVLVORFSGSPVLDLASKSTKXASLGCCSLN 540
DB 1262 RNORLPSFSNAOQSLRLGGHPEGCSNVLVORFSGSPVLDLASKSTKXASLGCCSLN 1321
QY 541 KPPFLMLFKSPKRFNKGRIFFNVNQLMODAPQATRSTTEAMODGRSCPLPLNTKASHRALQF 600
DB 1322 KPPFLMLFKSPKRFNKGRIFFNVNQLMODAPQATRSTTEAMODGRSCPLPLNTKASHRALQF 1381
QY 601 GDSPTSHLLKLPOBLKPRSQFSLDIQTTSPPKGLVFYAGTKDSFLALYVADGRVVFALG 660
DB 1382 GDSPTSHLLKLPOBLKPRSQFSLDIQTTSPPKGLVFYAGTKDSFLALYVADGRVVFALG 1441
QY 661 AGGKRLRLSKERYHDGKMTTVFGLNGKARLVVDGLAQBESLPGNSTISPREQVYLQ 720
DB 1442 AGGKRLRLSKERYHDGKMTTVFGLNGKARLVVDGLAQBESLPGNSTISPREQVYLQ 1501
QY 721 LPLSRKPKSLPQHSFVGCRLDPOLNSKPLDSPSARFVSPCLGSLKGIYFSGGGHVI 780
DB 1502 LPLSRKPKSLPQHSFVGCRLDPOLNSKPLDSPSARFVSPCLGSLKGIYFSGGGHVI 1561
QY 781 LANSVSLGPELKLTFISIRPSRLTGVLIVHGSQSGRLSYVMEAGKVTTSVSDAGSVTS 840
DB 1562 LANSVSLGPELKLTFISIRPSRLTGVLIVHGSQSGRLSYVMEAGKVTTSVSDAGSVTS 1621
QY 841 ITPKQSLCDGQMHSAVSIKORILHL 866
DB 1622 ITPKQSLCDGQMHSAVSIKORILHL 1647

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RESULT 3

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US-09-560-385A-4
; Sequence 4, Application US/09560385A
; Patent No. 6703363
; GENERAL INFORMATION:
; APPLICANT: Boudand, Ariel
; TITLE OF INVENTION: Recombinant Laminin 5
; FILE REFERENCE: 99-274-C
; CURRENT APPLICATION NUMBER: US/09/560,385A
; CURRENT FILING DATE: 2000-04-28
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 4
; LENGTH: 1693
; TYPE: PR1
; ORGANISM: Homo sapiens
US-09-560-385A-4

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Query Match 79.3%; Score 3560.5; DB 4; Length 1693;
Best Local Similarity 78.4%; Pred. No. 0;
Matches 660; Conservative 86; Mismatches 99; Indels 3; Gaps 2;
QY 1 MRFNGSGVEVRLPNDLEDKGYTSLFLQRPDLRENGTDEMFVMTLGNKDSKDYIG 60
DB 751 MRFNGSGVEVRLPNDLEDKGYTSLFLQRPDLRENGTDEMFVMTLGNKDSKDYIG 810
QY 61 MAVVDGQLTCVYNLGDREAVQIDQVLTSEBSQDAVMRVKFORIYQPAKNTYKATSN 120
DB 811 MAVVDGQLTCVYNLGDREAVQIDQVLTSEBSQDAVMRVKFORIYQPAKNTYKATSN 870

```

[illegible]

NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
ADDRESSEE: Christensen, O'Connor, Johnson, and Kindness
STREET: 1420 Fifth Avenue
CITY: Seattle
STATE: WA
COUNTRY: USA
ZIP: 98101-8100
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: IBM PC compatible
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/600,982
FILING DATE: 02-SEP-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Shelton, Dennis K.
REGISTRATION NUMBER: 26,997
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 682-8100
TELEFAX: (206) 224-0779
INFORMATION FOR SEQ ID NO: 24:
SEQUENCE CHARACTERISTICS:
LENGTH: 1713 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
DESCRIPTION: E170 protein as translated from sequence
of FIGURES 15A-15F, and as shown also in FIGURES
15-08-600-982-24

Query Match 79.3%; Score 3560.5; DB 3; Length 1713;

Best Local Similarity 78.4%; Pred. No. 0; Matches 680; Conservative 86; Mismatches 98; Indels 3; Gaps 2;

QY 1 MRFNGSGVGVRLPNDLEDKGYTSLFLQRPDLRENGTDMFVYLGNDKASDXYIG 60
DB 771 MRFNGSGVGVRLPNDLEDKGYTSLFLQRPDLRENGTDMFVYLGNDKASDXYIG 830
QY 61 MAVVDQQLTCVYNLGDREAEVQIDVLTBSSEQEAVMDRVKQRIYQPAKLNTYKATSN 120
DB 831 MAVVDQQLTCVYNLGDREAEVQIDVLTBSSEQEAVMDRVKQRIYQPAKLNTYKATSN 890
QY 121 KKPAPVYDLEGGSSNTLNLDPEDAVFYVGGYPPDPFLPSRLRPYKGCIELDLNEN 180
DB 891 KKPAPVYDLEGGSSNTLNLDPEDAVFYVGGYPPDPFLPSRLRPYKGCIELDLNEN 950
QY 181 VLSVNFKTFNLTTEVEPCRRRKESDKNYFEGTGVARIPQPNAPFPNFIQTITQTV 240
DB 951 VLSVNFKTFNLTTEVEPCRRRKESDKNYFEGTGVARIPQPNAPFPNFIQTITQTV 1010
QY 241 DRGLLFPANQDNFISLNIEDGNLWRYKLNSEPPYEKGIPTINDGKHSILITIGKIQ 300
DB 1011 DRGLLFPANQDNFISLNIEDGNLWRYKLNSEPPYEKGIPTINDGKHSILITIGKIQ 1070
QY 301 KRWMIIVNERSVRIIEGIPDSTYYLGGIPAIIRERNISTPAFGCKMNLKKTSGVRL 360
DB 1071 KRWMIIVNERSVRIIEGIPDSTYYLGGIPAIIRERNISTPAFGCKMNLKKTSGVRL 1130
QY 361 NDTVGVTKKCSBDMKLVRTASFSRGQMSFTNLDPSTDRFQLSFGFQTPQSGTLLNHQ 420
DB 1131 NDTVGVTKKCSBDMKLVRTASFSRGQMSFTNLDPSTDRFQLSFGFQTPQSGTLLNHQ 1190
QY 421 TRTSSLVLTLEDGHIILSTRDSNIPFKSPGTYMDGLLHHVYSIDTSGRLLLIDQVLA 480
DB 1191 TRTSSLVLTLEDGHIILSTRDSNIPFKSPGTYMDGLLHHVYSIDTSGRLLLIDQVLA 1250
QY 481 RNRRLSFSMAQOSLNLGGHFEKGCISNVLVQFSPQSPFVLDLASKTKDASLGGCSLN 540
DB 1251 RNRRLSFSMAQOSLNLGGHFEKGCISNVLVQFSPQSPFVLDLASKTKDASLGGCSLN 1310

QY 541 KPPPLMLFKSPYKFKGRIFVYVQLOMDAPQAT-RSTEAMODGRSLPPLNTKASHRALQ 599
DB 1311 KPPPLMLFKSPYKFKGRIFVYVQLOMDAPQAT-RSTEAMODGRSLPPLNTKASHRALQ 1368
QY 600 FQDSPTSHLLKLPOLLKPRSQPSLDIQTSSPKGLVYAGTQSPFLALYVADGVFVAL 659
DB 1369 FQDSPTSHLLKLPOLLKPRSQPSLDIQTSSPKGLVYAGTQSPFLALYVADGVFVAL 1428
QY 660 GAGGKKLRIRSKERVHDGWHVVFVGLNGKRLVVDGRLAQEGSLPGNSTISPEQVYL 719
DB 1429 GAGGKKLRIRSKERVHDGWHVVFVGLNGKRLVVDGRLAQEGSLPGNSTISPEQVYL 1488
QY 720 GLPLSRKPKSLPQHSFVGLCLRDPLQNSKPLDPSARFVSPCLGSLKGIYFSQGGHY 779
DB 1489 GLPLSRKPKSLPQHSFVGLCLRDPLQNSKPLDPSARFVSPCLGSLKGIYFSQGGHY 1548
QY 780 ILANSVSLAPBLKLTFSIRPRSLTVLTHVGSQSQRLSVYMEAGKVTTSVSSDAGSVT 839
DB 1549 ILANSVSLAPBLKLTFSIRPRSLTVLTHVGSQSQRLSVYMEAGKVTTSVSSDAGSVT 1608
QY 840 SITPKQSLCDGQWMSVAVSIKORILHL 866
DB 1609 SITPKQSLCDGQWMSVAVSIKORILHL 1635

RESULT 6

US-09-560-385A-6

Sequence 6, Application US/09560385A

Patent No. 6703363

GENERAL INFORMATION:

APPLICANT: Bouland, Arjel

TITLE OF INVENTION: Recombinant Lamtin 5

CURRENT APPLICATION NUMBER: US/09/560,385A

CURRENT FILING DATE: 2000-04-28

NUMBER OF SEQ ID NOS: 36

SOFTWARE: Patentin Ver. 2.0

SEQ ID NO 6

LENGTH: 1713

TYPE: PRT

ORGANISM: Homo sapiens

US-09-560-385A-6

Query Match 79.3%; Score 3560.5; DB 4; Length 1713;

Best Local Similarity 78.4%; Pred. No. 0; Matches 680; Conservative 86; Mismatches 98; Indels 3; Gaps 2;

QY 1 MRFNGSGVGVRLPNDLEDKGYTSLFLQRPDLRENGTDMFVYLGNDKASDXYIG 60
DB 771 MRFNGSGVGVRLPNDLEDKGYTSLFLQRPDLRENGTDMFVYLGNDKASDXYIG 830
QY 61 MAVVDQQLTCVYNLGDREAEVQIDVLTBSSEQEAVMDRVKQRIYQPAKLNTYKATSN 120
DB 831 MAVVDQQLTCVYNLGDREAEVQIDVLTBSSEQEAVMDRVKQRIYQPAKLNTYKATSN 890
QY 121 KKPAPVYDLEGGSSNTLNLDPEDAVFYVGGYPPDPFLPSRLRPYKGCIELDLNEN 180
DB 891 KKPAPVYDLEGGSSNTLNLDPEDAVFYVGGYPPDPFLPSRLRPYKGCIELDLNEN 950
QY 181 VLSVNFKTFNLTTEVEPCRRRKESDKNYFEGTGVARIPQPNAPFPNFIQTITQTV 240
DB 951 VLSVNFKTFNLTTEVEPCRRRKESDKNYFEGTGVARIPQPNAPFPNFIQTITQTV 1010
QY 241 DRGLLFPANQDNFISLNIEDGNLWRYKLNSEPPYEKGIPTINDGKHSILITIGKIQ 300
DB 1011 DRGLLFPANQDNFISLNIEDGNLWRYKLNSEPPYEKGIPTINDGKHSILITIGKIQ 1070
QY 301 KRWMIIVNERSVRIIEGIPDSTYYLGGIPAIIRERNISTPAFGCKMNLKKTSGVRL 360
DB 1071 KRWMIIVNERSVRIIEGIPDSTYYLGGIPAIIRERNISTPAFGCKMNLKKTSGVRL 1130
QY 361 NDTVGVTKKCSBDMKLVRTASFSRGQMSFTNLDPSTDRFQLSFGFQTPQSGTLLNHQ 420

Db 1131 NDVGVATKCSSEMDKLVRSASFSGQLSTFDGLPPTDHLQASFGQTQPSGILLDHQ 1190
 QY 421 TRTSSLVLTLEDGHIESTRDSNIPFKSPGTMDGLHHRVYSIDTSGRLIIDQVLR 480
 Db 1191 TWTRNLQVTLBEDGYIELSTSDSGPIFKSPQTYMDGLHHRVYSIDNSGRLIIDQVLR 1250
 QY 481 RNORLPSFNAOQSLGCGHFGGCTSNVTVORFSGSPETLDLASKSTKDDALGCGSLN 540
 Db 1251 NSRRLKHISRSRSLRGSGSNFEGCISNVFORLSLSPVLDLTSNLKRDVSLGCGSLN 1310
 QY 541 KPEPLMLFKSPKPKFKRIFNVNQLMODAPQAT-RSTEAMODGRSCLPPLNTKASHRALQ 599
 Db 1311 KPEPLMLKSGSTFKNTKTRINQLODTPVASPRVYKQWD--ACSPLEKTOANHCALQ 1368
 QY 600 FGDSPTSHLLKLPQELKPKRSQPSLDIQTSPKGLVFYAGTOSFLATLVADGRVVAL 659
 Db 1369 FGDIPTSHLLFKLPQELKPKRSQFAVDMQTTSSRGVLFHTGTNKSFMALYLSKRLVVAL 1428
 QY 660 GAGGKTLRLSKRYNDGKHTVYVFGANGKARLVYDGLRAOGSLPFGNSTISPREVYL 719
 Db 1429 GTDGKTLRLSKRYNDGKHTVYVFGANGKARLVYDGLRAOGSLPFGNSTISIRAVYL 1488
 QY 720 GLPLSRKPKSLPOHSFVGLRDFOQLNSKPLDSPARFVSPCLGSLKGIYFSOGGSHV 779
 Db 1489 GSPSPGPKSLPNTNSFVGLCKNFQDSKPLYTSSSFVSSCGGLEKGIYFSBEGSHV 1548
 QY 780 ILANSVSLGPELKLTFESIRPSRLTGVLHVHSGOGRLSYMEAGKVTTSVSSDAGSVT 839
 Db 1549 VLAHSVILGPEFLVFSIRPSRLTGILIHISGQPGKILCYLLEAGKVTTAAMDAGAGTST 1608
 QY 840 SITPKOSLDCQWHSVAVSIKORILHL 866
 Db 1609 SVTPKOSLDCQWHSVAVSIKORILHL 1635

RESULT 7

US-09-538-092-1359
 ; Sequence 1359, Application US/09538092
 ; Patent No. 6753314
 ; GENERAL INFORMATION:
 ; APPLICANT: Menziesfield, Traci A.
 ; TITLE OF INVENTION: Protein-Protein Complexes and Method of Using Same
 ; FILE REFERENCE: 15966-542
 ; CURRENT APPLICATION NUMBER: US/09/538,092
 ; PRIOR FILING DATE: 2000-03-29
 ; PRIOR APPLICATION NUMBER: 60/127,352
 ; PRIOR FILING DATE: 1999-04-01
 ; PRIOR APPLICATION NUMBER: 60/178,965
 ; PRIOR FILING DATE: 2000-02-01
 ; NUMBER OF SEQ ID NOS: 1387
 ; SOFTWARE: CuraParseFormat Version 0.9
 ; SEQ ID NO 1359
 ; LENGTH: 1713
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; NAME/KEY: misc_feature
 ; LOCATION: (0)..(0)
 ; OTHER INFORMATION: Polypeptide Accession Number Q16787
 US-09-538-092-1359

Query Match 79.3%; Score 3560.5; DB 4; Length 1713;
 Best Local Similarity 78.4%; Pred. No. 0;
 Matches 680; Conservative 86; Mismatches 98; Indels 3; Gaps 2;

QY 1 MRFRGSGVAVRLPNDLEDKGYTSLPLQRPDLRNGGHEMFVYVIGNKASKRYIG 60
 Db 771 MRFRGSGVAVRLPNDLEDKGYTSLPLQRPDRSNGGHEMFVYVIGNKASKRYIG 830
 QY 61 MAVVDGQLTCVYNLGDREAEVQIDVLTESQEAAMDVRFQRIYPAKANTYKATSN 120

Db 831 MAVVDGQLTCVYNLGDREAEVQIDVLTESQEAAMDVRFQRIYPAKANTYKATSN 890
 QY 121 KPAKAVYDLEGGSSNTLNTDPEDAVFYVGVPPDPELPSRLRPPPYGCIELDLNEN 180
 Db 891 KPEPBGVYMDGNSNTLNTDPEVAVFYVGVPPDPELPSRLRPPPYGCIELDLNEN 950
 QY 181 VLSLVNFKTTPNLTTEVEPCRRKESDKNYEGGVYARIPTQNPAPFPNFQITQTV 240
 Db 951 VLSLVNFKTTPNLTTEVEPCRRKESDKNYEGGVYARIPTQNPAPFPNFQITQTV 1010
 QY 241 DRGLFPAENQDNFISLNTIEDGNLWRYKLNSEPREKGIQDTINDKHSILITGKLQ 300
 Db 1011 DRGLFPAENQDNFISLNTIEDGNLWRYKLNSEPREKGIQDTINDKHSILITGKLQ 1070
 QY 301 KRWIVNRSVRIEERIDPSTYYIGTPIARREFPNTSTPAFOGCMKLTGTSVYVL 360
 Db 1071 KRWIVNRSVRIEERIDPSTYYIGTPIARREFPNTSTPAFOGCMKLTGTSVYVL 1130
 QY 361 NDVGVATKCSSEMDKLVRTASFSRGGMSFTNLDVSTDRFOLSFGQTFQPSGTLINHQ 420
 Db 1131 NDVGVATKCSSEMDKLVRSASFSGQLSTFDGLPPTDHLQASFGQTQPSGILLDHQ 1190
 QY 421 TRTSSLVLTLEDGHIESTRDSNIPFKSPGTMDGLHHRVYSIDTSGRLIIDQVLR 480
 Db 1191 TWTRNLQVTLBEDGYIELSTSDSGPIFKSPQTYMDGLHHRVYSIDNSGRLIIDQVLR 1250
 QY 481 RNORLPSFNAOQSLGCGHFGGCTSNVTVORFSGSPETLDLASKSTKDDALGCGSLN 540
 Db 1251 NSRRLKHISRSRSLRGSGSNFEGCISNVFORLSLSPVLDLTSNLKRDVSLGCGSLN 1310
 QY 541 KPEPLMLFKSPKPKFKRIFNVNQLMODAPQAT-RSTEAMODGRSCLPPLNTKASHRALQ 599
 Db 1311 KPEPLMLKSGSTFKNTKTRINQLODTPVASPRVYKQWD--ACSPLEKTOANHCALQ 1368
 QY 600 FGDSPTSHLLKLPQELKPKRSQPSLDIQTSPKGLVFYAGTOSFLATLVADGRVVAL 659
 Db 1369 FGDIPTSHLLFKLPQELKPKRSQFAVDMQTTSSRGVLFHTGTNKSFMALYLSKRLVVAL 1428
 QY 660 GAGGKTLRLSKRYNDGKHTVYVFGANGKARLVYDGLRAOGSLPFGNSTISPREVYL 719
 Db 1429 GTDGKTLRLSKRYNDGKHTVYVFGANGKARLVYDGLRAOGSLPFGNSTISIRAVYL 1488
 QY 720 GLPLSRKPKSLPOHSFVGLRDFOQLNSKPLDSPARFVSPCLGSLKGIYFSOGGSHV 779
 Db 1489 GSPSPGPKSLPNTNSFVGLCKNFQDSKPLYTSSSFVSSCGGLEKGIYFSBEGSHV 1548
 QY 780 ILANSVSLGPELKLTFESIRPSRLTGVLHVHSGOGRLSYMEAGKVTTSVSSDAGSVT 839
 Db 1549 VLAHSVILGPEFLVFSIRPSRLTGILIHISGQPGKILCYLLEAGKVTTAAMDAGAGTST 1608
 QY 840 SITPKOSLDCQWHSVAVSIKORILHL 866
 Db 1609 SVTPKOSLDCQWHSVAVSIKORILHL 1635

RESULT 8

PCT-US94-10261A-24
 ; Sequence 24, Application PC/TUS9410261A
 ; GENERAL INFORMATION:
 ; APPLICANT: Carter, William G.
 ; APPLICANT: Gil, Susanna A.
 ; TITLE OF INVENTION: Epitigrin, an Epithelial Ligand for
 ; NUMBER OF SEQUENCES: 30
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Christensen, O'Connor, Johnson, and Kindness
 ; STREET: 1420 Fifth Avenue
 ; CITY: Seattle
 ; STATE: WA
 ; COUNTRY: USA
 ; ZIP: 98101-8100
 ; COMPUTER READABLE FORM:

MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/10261A
FILING DATE: 02-SEP-1994
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Shelton, Dennis K.
REGISTRATION NUMBER: 26,997
TELEPHONE: (206) 682-8100
TELEFAX: (206) 224-0779
INFORMATION FOR SEQ ID NO: 24:
SEQUENCE CHARACTERISTICS:
LENGTH: 1713 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
DESCRIPTION: E170 protein as translated from sequence of
FIGURES 15A-15F, and as shown also in FIGURES 19A-19K
PCT-US94-10261A-24

Query Match 79.3%; Score 3560.5; DB 5; Length 1713;
Best Local Similarity 78.4%; Pred. No. 0;
Matches 680; Conservative 86; Mismatches 98; Indels 3; Gaps 2;

1 MRNGSGVEVRLPNLDELKGYTSLFLQRPDLRENGGTEDMVMYLGNDASRDYIG 60
771 MRNGSGVEVRLPNLDELKGYTSLFLQRPNSRNGGTEDMVMYLGNDASRDYIG 830
61 MAVVDQQLTCVYNLGDREAVQIDQVLTSESQEAVMRVKFORIYQFANLTYTKATS 120
831 MAVVDQQLTCVYNLGDREAVQIDQVLTSESQEAVMRVKFORIYQFANLTYTKATS 890
121 KRPAPAVYDLEGSSNTLNLDPEDAVFYGGYPPDFELPSRLSPPYKGCIELDLNEN 180
891 KRPETGVYDMDGRNSNTLNLDPENVVFFYGGYPPDFELPSRLSPPYKGCIELDLNEN 950
181 VLSLNPFTKFTNLTTEVEPCRRKESDKNYFEGGYARIPQPNAPPNFQITQITV 240
951 VLSLNPFTKFTNLTTEVEPCRRKESDKNYFEGGYARIPQPNAPPNFQITQITV 1010
241 DRGLLFFAENQDNFISLINEDGNLWRYKLNSEPKKGIKDTINDGHSILITIGKQ 300
1011 DRGLLFFAENQDNFISLINEDGNLWRYKLNSEPKKGVGDALNNGRDHSIQIKIGKQ 1070
301 KRMWVNERSVRIEGERIDPSTYYLGGIPAIIRERFNISTPAFQGCCKNLKKTSGVRL 360
1071 KRMWVNERSVRIEGERIDPSTYYLGGIPAIIRERFNISTPAFQGCCKNLKKTSGVRL 1130
361 NDVVGVTKKSEDMKLVRTASFSRGGMSFTNLDPSTDRFQLSFGQTQPSGTLNMQ 420
1131 NDVVGVTKKSEDMKLVRTASFSRGGMSFTNLDPSTDRFQLSFGQTQPSGTLNMQ 1190
421 TRTSSLVLTLEDGHEILSTRDSNIPFKSPGYMDGLLHHVSVISDPSGLRLIIDQVLR 480
1191 TRTSSLVLTLEDGHEILSTRDSNIPFKSPGYMDGLLHHVSVISDPSGLRLIIDQVLR 1250
481 RNQRLPSFNAQSLRLGGHFGGCI SNVLVORFSGSPREVLDAASKSTKKDASLGCCSLN 540
1251 NSKRLKHISRSQSLRLGGHFGGCI SNVLVORFSGSPREVLDAASKSTKKDASLGCCSLN 1310
541 KRPFLMLFKSPKPKRINRVNQLMDAPQAT-RSTFAMQDGRSCIPPLNTAKSHRALQ 599
1311 KRPFLMLFKSPKPKRINRVNQLMDAPQAT-RSTFAMQDGRSCIPPLNTAKSHRALQ 1368
600 FGDPSTSHLLKXPOBELKPKRSQPSLDIOTSPKGVFVAGTQDSFLATLVADGRVVEAL 659
1369 FGDPSTSHLLKXPOBELKPKRSQPSLDIOTSPKGVFVAGTQDSFLATLVADGRVVEAL 1428
660 GAGGKKLRLSKRYHDKMHTVVFGLNGKARLVVDGLRAQEGSLPGNSTISPREQVYL 719

1429 GTDGGKLLIKSKREKCNCKMHTVVGHDGEGRLVVDGLRAREGSLPGNSTISIRAPYLL 1488
720 GLPLSRKPSLQPSFVGLCLDPOLNSKPLDPSARFVSPCLDGLSKGYFSGGGHHV 779
1489 GSPGPKPSLPTNSFVGLKPLDPSARFVSPCLDGLSKGYFSGGGHHV 1548
780 ILANSVSLPELKLFTSIRPSLTVGLIHVSGSGQRLSVYMAKVTTSVSSDAGSVT 839
1549 VLAHSVGLPEKLVFSIRPSLTVGLIHVSGSGQRLSVYMAKVTTSVSSDAGSVT 1608
840 SITPKQSLCDGQMSVANSIKORIIHL 866
1609 SITPKQSLCDGQMSVANSIKORIIHL 1635

RESULT 9
US-09-560-385A-2
Sequence 2, Application US/09560385A
Patent No. 6703363
GENERAL INFORMATION:
APPLICANT: Bouffard, Ariel
TITLE OR INVENTION: Recombinant Laminin 5
FILE REFERENCE: 99-274-C
CURRENT APPLICATION NUMBER: US/09/560,385A
CURRENT FILING DATE: 2000-04-28
NUMBER OF SEQ ID NOS: 36
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 2
LENGTH: 1724
TYPE: PRT
ORGANISM: Homo sapiens
US-09-560-385A-2

Query Match 79.3%; Score 3560.5; DB 4; Length 1724;
Best Local Similarity 78.4%; Pred. No. 0;
Matches 680; Conservative 86; Mismatches 98; Indels 3; Gaps 2;

1 MRNGSGVEVRLPNLDELKGYTSLFLQRPDLRENGGTEDMVMYLGNDASRDYIG 60
782 MRNGSGVEVRLPNLDELKGYTSLFLQRPNSRNGGTEDMVMYLGNDASRDYIG 841
61 MAVVDQQLTCVYNLGDREAVQIDQVLTSESQEAVMRVKFORIYQFANLTYTKATS 120
842 MAVVDQQLTCVYNLGDREAVQIDQVLTSESQEAVMRVKFORIYQFANLTYTKATS 901
121 KRPAPAVYDLEGSSNTLNLDPEDAVFYGGYPPDFELPSRLSPPYKGCIELDLNEN 180
902 KRPETGVYDMDGRNSNTLNLDPENVVFFYGGYPPDFELPSRLSPPYKGCIELDLNEN 961
181 VLSLNPFTKFTNLTTEVEPCRRKESDKNYFEGGYARIPQPNAPPNFQITQITV 240
962 VLSLNPFTKFTNLTTEVEPCRRKESDKNYFEGGYARIPQPNAPPNFQITQITV 1021
241 DRGLLFFAENQDNFISLINEDGNLWRYKLNSEPKKGIKDTINDGHSILITIGKQ 300
1022 DRGLLFFAENQDNFISLINEDGNLWRYKLNSEPKKGVGDALNNGRDHSIQIKIGKQ 1081
301 KRMWVNERSVRIEGERIDPSTYYLGGIPAIIRERFNISTPAFQGCCKNLKKTSGVRL 360
1082 KRMWVNERSVRIEGERIDPSTYYLGGIPAIIRERFNISTPAFQGCCKNLKKTSGVRL 1141
361 NDVVGVTKKSEDMKLVRTASFSRGGMSFTNLDPSTDRFQLSFGQTQPSGTLNMQ 420
1142 NDVVGVTKKSEDMKLVRTASFSRGGMSFTNLDPSTDRFQLSFGQTQPSGTLNMQ 1201
421 TRTSSLVLTLEDGHEILSTRDSNIPFKSPGYMDGLLHHVSVISDPSGLRLIIDQVLR 480
1202 TRTSSLVLTLEDGHEILSTRDSNIPFKSPGYMDGLLHHVSVISDPSGLRLIIDQVLR 1261
481 RNQRLPSFNAQSLRLGGHFGGCI SNVLVORFSGSPREVLDAASKSTKKDASLGCCSLN 540
1262 NSKRLKHISRSQSLRLGGHFGGCI SNVLVORFSGSPREVLDAASKSTKKDASLGCCSLN 1321


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Db      1099 --QINDAKTHEISI-IYHNDKMLVDRRHVKSMDNEKKIIPFTDIYIGAPPEILOGR 1155
Qy      332 AIRERFNISTPAFOGCKMNL---KKTSGVVRINDTVGTTKCSSEDMKLVRTASFSRGGOM 388
      1156 ALRAHILPLDI-NFRGCMKGFOFOKDPNLLEQTEITIGVGCPEDELSIRRAFTN--GQS 1212
Qy      389 SFTNLD-VSTDRFQLSFGHOFQFQPSGTLNHOQRTSSLVLEEDGHIELSTRDSNIPF 447
      1213 PTASIOKISFPDFEGGFNFRITLQPNGLIFYASGSDVPSISLDNGTVIMDVK--GIKVQ 1270
Qy      448 KSPGTMDGLLHVVISDTSGLR--LLID-DQVLRNRQLRPSFNAOQSLR---LGG-- 499
      1271 SYDKQYNDGLSHF--VISSVSPTRYELIVDKSRVSGKNPTKGIQGTQASEKKEFYGGSP 1328
Qy      500 -----GHFEGCISNVLVORFSGQPEVLDLASKSTKDASLGCSLNKPPFLMFKSPKF 554
      1329 ISAOYANFTGCSISNAFTVRDVEVEDFORYTEKHTSLYECPIESSPLFLHKKGNL 1388
Qy      555 NKGRIFNNVQ--LMODAPQATRSTEAMODGRSCLPLNT-----KASHRALOF 600
      1389 SKPKASQNKKGKSKDAP-----SMDPVALKLPERNTPRNSHCHLSNRPALIEHAQY 1441
Qy      601 GDSPTSHLLKLPOELIKRPSQFSLDIQTSPKGLVFIAGTKD--SFLALYVADGRVVA 658
      1442 GGTANRQOEFELHKDPGAKSQFSIRLRTSSHGMIFYVSDQENDFMTLFLAHGRLYVM 1501
Qy      659 LGAGGKCLRLSKERYHDGKMTTVFGLNGKARLVVDGLRAQESL-PGNSTISPREQV 717
      1502 FNVGHKKLIRSEKKNIDGLMHDVIFIRRESSGRLVIDGLRVLEBBLPTEAATWKIGPI 1561
Qy      718 YLGLPLSRKPSLPQ---HSFVGLRDPQLNSKPLDSPARFVSPCLGSGLEKGIYPS 773
      1562 YLGVAAPGAVKVNQINSIYSPSGCLSNQLNGASITSASQTPSVPCFEGPMETGYPS 1621
Qy      774 QGGGHVILANSVSLGPELKLTPSIRPSRLTGVLIVHGSQSGRLSYMEAGKVTTSVSD 833
      1622 TREGVVLDESFNIGLKEPAIEVAPRSSSGTLVHGHSVNGEYLVNHNKGQVIVKVNNG 1681
Db      834 AGGSVTSITPKOSLCDQMHVAVSIIKORILHL 866
Qy      1682 IRDFSTSVTPKOSLCDGRWHRITVIRDSNVQL 1714

RESULT 12
US-09-561-818A-8
; Sequence 8, Application US/09561818A
; Patent No. 6638907
; GENERAL INFORMATION:
; APPLICANT: Korteemaa, Jarkko
; APPLICANT: Tyysvaeson, Karl
; TITLE OF INVENTION: Laminin 8 and Methode For Its Use
; FILE REFERENCE: 99,274-D
; CURRENT APPLICATION NUMBER: US/09/561,818A
; CURRENT FILING DATE: 2000-04-28
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: Patentln Ver. 2.0
; SEQ ID NO 8
; LENGTH: 1800
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-561-818A-8

Query Match      26.7%; Score 1198; DB 4; Length 1800;
Best Local Similarity 33.1%; Pred. No. 1,1e-109;
Matches 309; Conservative 161; Mismatches 373; Indels 90; Gaps 26;
Qy      1 MRFNGSGVEVRLPNLELDIKGYTSLFL---QSPDLRENGTSDMFVYLGNDASK 56
      805 MMEFGSAVEVHRTSMDLKAFTSLSLYKPKPELRE---TADQFILYLSGNAXK 861
Db      57 DYTGMAVVDGQLTCVNNIGDREAEVQIDQVLTSESGEAMVDFQRIYQPAKMYTAE 116
      862 ETYGLAIKDNLVYVNLGTQVEIPLDS--KPVSSMPAFYSIVKIERVGKHKGVFLVVP 919

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Qy      117 ATSNPKAPAVYDLEGGSSNTLNLNDPEDAVFYVGGYPPDFELRRLRPPYKGCIELD 176
      920 SLSTABAEKFKIKGFSGDDSLDLDPEDTVYVGGVSNFGLPFSIMLPGVGLGELAT 979
Db      177 LNEANVLSLNFPTTNNLNTTEVPCRRK-----ESDKNYEGGYARIPQPN-----A 227
      980 LNNVLSLNFPGIINMDPSTSVPCARDKLAFQSGRAAYFGVGGVAVVDRIPRGRKG 1039
Qy      228 PEPNFLOTQTVDRGLLFFAENQDNFTSLNEDGNLWRY-----KLNEEPKEKGI 280
      1040 QVTRFDIEVTRPADGLILAMNGSMFLEKRNGLVHFVDFGSSGRVHLADTLKCA- 1098
Db      281 RDTINDGDHSLITITGKLOKMMINVERSVRI--EGEIFDFSTYIIGGIP-----I 331
Qy      1099 --QINDAKTHEISI-IYHNDKMLVDRRHVKSMDNEKKIIPFTDIYIGAPPEILOGR 1155
      332 AIRERFNISTPAFOGCKMNL---KKTSGVVRINDTVGTTKCSSEDMKLVRTASFSRGGOM 388
      1156 ALRAHILPLDI-NFRGCMKGFOFOKDPNLLEQTEITIGVGCPEDELSIRRAFTN--GQS 1212
Qy      389 SFTNLD-VSTDRFQLSFGHOFQFQPSGTLNHOQRTSSLVLEEDGHIELSTRDSNIPF 447
      1213 PTASIOKISFPDFEGGFNFRITLQPNGLIFYASGSDVPSISLDNGTVIMDVK--GIKVQ 1270
Qy      448 KSPGTMDGLLHVVISDTSGLR--LLID-DQVLRNRQLRPSFNAOQSLR---LGG-- 499
      1271 SYDKQYNDGLSHF--VISSVSPTRYELIVDKSRVSGKNPTKGIQGTQASEKKEFYGGSP 1328
Qy      500 -----GHFEGCISNVLVORFSGQPEVLDLASKSTKDASLGCSLNKPPFLMFKSPKF 554
      1329 ISAOYANFTGCSISNAFTVRDVEVEDFORYTEKHTSLYECPIESSPLFLHKKGNL 1388
Qy      555 NKGRIFNNVQ--LMODAPQATRSTEAMODGRSCLPLNT-----KASHRALOF 600
      1389 SKPKASQNKKGKSKDAP-----SMDPVALKLPERNTPRNSHCHLSNRPALIEHAQY 1441
Qy      601 GDSPTSHLLKLPOELIKRPSQFSLDIQTSPKGLVFIAGTKD--SFLALYVADGRVVA 658
      1213 PTASIOKISFPDFEGGFNFRITLQPNGLIFYASGSDVPSISLDNGTVIMDVK--GIKVQ 1270
Qy      659 LGAGGKCLRLSKERYHDGKMTTVFGLNGKARLVVDGLRAQESL-PGNSTISPREQV 717
      1271 SYDKQYNDGLSHF--VISSVSPTRYELIVDKSRVSGKNPTKGIQGTQASEKKEFYGGSP 1328
Qy      718 YLGLPLSRKPSLPQ---HSFVGLRDPQLNSKPLDSPARFVSPCLGSGLEKGIYPS 773
      1329 ISAOYANFTGCSISNAFTVRDVEVEDFORYTEKHTSLYECPIESSPLFLHKKGNL 1388
Qy      774 QGGGHVILANSVSLGPELKLTPSIRPSRLTGVLIVHGSQSGRLSYMEAGKVTTSVSD 833
      1389 SKPKASQNKKGKSKDAP-----SMDPVALKLPERNTPRNSHCHLSNRPALIEHAQY 1441
Db      834 AGGSVTSITPKOSLCDQMHVAVSIIKORILHL 866
Qy      1442 GGTANRQOEFELHKDPGAKSQFSIRLRTSSHGMIFYVSDQENDFMTLFLAHGRLYVM 1501
      1502 FNVGHKKLIRSEKKNIDGLMHDVIFIRRESSGRLVIDGLRVLEBBLPTEAATWKIGPI 1561
Qy      659 LGAGGKCLRLSKERYHDGKMTTVFGLNGKARLVVDGLRAQESL-PGNSTISPREQV 717
      1502 FNVGHKKLIRSEKKNIDGLMHDVIFIRRESSGRLVIDGLRVLEBBLPTEAATWKIGPI 1561
Qy      718 YLGLPLSRKPSLPQ---HSFVGLRDPQLNSKPLDSPARFVSPCLGSGLEKGIYPS 773
      1562 YLGVAAPGAVKVNQINSIYSPSGCLSNQLNGASITSASQTPSVPCFEGPMETGYPS 1621
Db      774 QGGGHVILANSVSLGPELKLTPSIRPSRLTGVLIVHGSQSGRLSYMEAGKVTTSVSD 833
      1622 TREGVVLDESFNIGLKEPAIEVAPRSSSGTLVHGHSVNGEYLVNHNKGQVIVKVNNG 1681
Qy      834 AGGSVTSITPKOSLCDQMHVAVSIIKORILHL 866
      1682 IRDFSTSVTPKOSLCDGRWHRITVIRDSNVQL 1714
Db      1682 IRDFSTSVTPKOSLCDGRWHRITVIRDSNVQL 1714

RESULT 13
US-09-561-818A-2
; Sequence 2, Application US/09561818A
; Patent No. 6638907
; GENERAL INFORMATION:
; APPLICANT: Korteemaa, Jarkko
; APPLICANT: Tyysvaeson, Karl
; TITLE OF INVENTION: Laminin 8 and Methode For Its Use
; FILE REFERENCE: 99,274-D
; CURRENT APPLICATION NUMBER: US/09/561,818A
; CURRENT FILING DATE: 2000-04-28
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: Patentln Ver. 2.0
; SEQ ID NO 2
; LENGTH: 1816

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; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-561-818A-2

```

Query Match	26.7%;	Score 1198;	DB 4;	Length 1816;
Best Local Similarity	33.1%;	Pred. No. 1.2e-109;		
Matches 309;	Conservative 161;	Mismatches 373;	Indels 90;	Gaps 26;

QY 1 MRPNKSGVAVRPLPNDLBDLKGYSLSLFL-----QRPLRNGGDEMFVWYLLGNKQASK 56

Db 829 MMFPGQSAVYHRSRSHMDLKAFTSLSLTMKPYKRPBLTE---TAQDFILYLSKAKK 885

QY 57 DYIGNAVVDGQLTCVYINLGBREAVQIDQVLTISESOEAVNDRYKFORIYQPAKANTYKE 116

Db 886 EYMGLAIKNDMLVYVYVNLGTROVEIPLDS--KPVSSWPAVPSIYKIERVGGKGVPLTP 943

QY 117 ATSNKPKRPAVYDDEGGSSNTLLNLPEDDAVFYIGYVPPDELPSRLRFPYKXCIELDD 176

Db 944 SLSSTAEKFKTKGEPFSGDSDSLDLDPEDTFFVYGVGVSNNKPLPSSLNLPBFVGCLELAT 1003

QY 177 LNEVNTLSLYNPKTYTNLTNTLTVBPCKRK-----EESDKNFEGBGVARIPTQDN-----A 227

Db 1004 LNDVYLSYANRKHLYNMDPSTSVPAKDKLAFOTSRASYSFDDSGIAVAVDIPRRKFG 1063

QY 228 PEPNFIQTIQTTVDKGLLFPANQDNFISLNIEDGNLWRY-----KLSBPPKEGI 280

Db 1064 QVTRDIEVRRPADNGILLMWNGSMFRLERNGYLHVFDGFSGSRVHLEDTLKKA- 1122

QY 281 RDTINDGKSHLITTGKLOKRMWINVERSRI---EGEIPDSTYYLGSI-----I 331

Db 1123 --QINDAKYHISLI-YHNDKXMLLVDRRHVKSMDNKKMKIPFDIYIGAPPELLQSR 1179

QY 332 AIRERFNSTAFQCMNL---KTSQSVVNLNDVGTGKCSDEMKLVFRASSRGOM 388

Db 1180 ALRAHLPLDT-NFRCKMGFOFOKKDFNLQETELTGVCYCPESDLSIRRAYFN--GQS 1236

QY 389 SFTNLD-VPTSDRFQSGFQTPQPSGYLHNQRTSSLWLTBEDGHIELSTRDSNPIF 447

Db 1237 FIASIQKISPFDPGEGFNFRITLQNGLLFFYASGSDVFSISLNDGYIMDK--GIKVQ 1294

QY 448 KSPGYMDGLHHVSVISDTSGLR--LIID-DQVLRNQRPLPSFMAQOSIR---LGG-- 499

Db 1295 SVDKQYNGLSHF--VISVSPTREYELIYDKSRVGSKNPTGKIEQTQASHEKFEYFGGSP 1352

QY 500 -----GHEGECISNLYVQRFQSPRYVLLAASKTKQDSLGGCSLNKRPFLMLFKSPRF 554

Db 1353 ISAQANFTGCISNVPFTRVDRVDEVPQRYTEKVHTSLYCEPTSESPFLFKHKKGNL 1412

QY 555 NKGRIFENUNO--LMODAPQATRSTEAWODGSCSLPLNT-----KASHRALQF 600

Db 1413 SKPKASQNKKGKSKDAP-----SWPVALKLPBRTTPRNSHCHLSNRPALIEHAYQ 1465

QY 601 GDSPTSHLLKLPOELALPKRQSPSLDITYSPKGLVFFYAGTKD--SFLALYVADGRVFA 658

Db 1466 GGTANSROBEHLKGDGPKAQSGFSIRLTRSSHGMIFFVQSDBEUDFWTLFLAHLGLVYM 1525

QY 659 LGAGGKTRILASKEKHYHNGKWHTVVFGALNGAKALVUDGLAAGBSL-PGNSITSPBEQV 717

Db 1526 FNVGKHKKLKIRQOEKXNDGLMHWDFIIFERSGRLVUIDGLTALBERSLPTFATYKIKPI 1585

QY 718 YLGLPLSRKPKSLPQ-----HSFVGLGRLDPOLNSKXLDPSARFGVSPCLGSLSEKGIYFS 773

Db 1586 YLGGVAPRKAIVGNQVINSIYSPSGCLSNLQNGASITASAQTSFVTPCFEBSPMETGIYFS 1645

QY 774 QGGGHVILLANSVSLGPELKLFTSIRPRSJLTVGLLVHVSQSQORLSVYMEAGKVTTVSDD 833

Db 1646 TEGGYVVLDESFNIGLKEFELIAFEVYPRSSSGTLVGHGSHVNGBEYLVHMKNGQVIVKVNNG 1705

QY 834 AGGSVTSITPKOSLCDGQMHSAVAVSIKQRIILH 866

Db 1706 IRDFSTSVTPKOSLCDGRWHRITVIRDSNVQOL 1738

RESULT 14
US-09-561-818A-6
Sequence 6, Application US/09561818A
Date: 09/09/2007

Query Match	26.7%;	Score 1198;	DB 4;	Length 1824;
Best Local Similarity	33.1%;	Pred. No. 1.2e-109;		
Matches 309;	Conservative 161;	Mismatches 373;	Indels 90;	Gaps 26;

[illegible]

```

Db      1526 FNVGHHKKLKIRSOEKNYDGLMHDVIFIRERSSGRLVIDGLRVLEESLPTEATWKIKGPI 1585
Qy      718 YLGLPLSRKPKSLPQ-----HSFVGLRDLPOLNSKPLDSPAAPGVPCLGSLKGIYFS 773
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      1586 YLGGVAVPGRKAVKVVQINSISYFSFGCLSNQLNGASITSAQTSVFPCBEGMEIGTYS 1645
Qy      774 QGGHVIILANSVSLGELKLTFSIRPSRLTGVLIVHGSQGRSLSYMEAGKTTSSVSD 833
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      1646 TBGGYVVLDESFNIGLKFBIAPFVRPRSSGTLVHGHSVNGEYLVHMKNGQYIVVNNNG 1705
Qy      834 AGGSVTSITPKOSLCDGQMSVAVSIIKORILHL 866
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      1706 IRDFSTSVLPKOSLCDGRWHRIYIRDSNVQL 1738

RESULT 15
US-09-561-818A-12
; Sequence 12, Application US/09561818A
; Patent No. 6638907
; GENERAL INFORMATION:
; APPLICANT: Korteemaa, Jariko
; APPLICANT: Teesgvaason, Karl
; TITLE OF INVENTION: Laminin 8 and Methode For Its Use
; FILE REFERENCE: 99,274-D
; CURRENT APPLICATION NUMBER: US/09/561,818A
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 12
; LENGTH: 1792
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-561-818A-12

```

Query Match 26.3%; Score 1183; DB 4; Length 1792;

Best Local Similarity 32.7%; Pred. No.3.6e-108; Matches 304; Conservative 165; Mismatches 378; Indels 82; Gaps 26;

```

Qy      1 MRENGSGVEVRLPNDLBDLKGYTSLPLQ--RPDLRENGGTEDMFVYVYLGNDKASD 57
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      805 MMEFDGSAVEVHVKHVSVDLKAFTSISLWKPPKAPBPGAVVADQFVILYLSKXAKKE 864
Qy      58 YIGMAVVDGQLTCVYVNLGDBAEVQIDQVLTESESOAVMDRVKFORIYQPAKLNTYKEA 117
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      865 YMGIAIKNDLVVYVNMGMKDVIELDS--KPVSSWPAYFSIVKIERVGEHGVFLVPS 922
Qy      118 TSNKPKAPAVYDLEGSSNTLNLDPEDAVFYVGVPPDELPRLRFPYKGCIELDDL 177
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      923 LSTAEKFKIKKEFPAGDSDLDVTPEDVYFVGVPAVNFKLPSLNLPSYSGCLELATL 982
Qy      178 NENVLSLYNFKTFLNLTTEVEPCRRRK-----EESDKVFBGTGYA--RIPTQPN--AP 228
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      983 NNDVILSYNPKHLYNNDPSKVPKADKLAFTQSRASAYFFDSSAYAVRDIRRKGFPQ 1042
Qy      229 FPNFTIQTITDRCGLLFPANODNFIISLIEGNTMVRKYLN--SEPPKEKGIKDT---- 283
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      1043 VTRFDIEIRPADNGVLVLMVNGSMFSEMRNGYLHVFYDFGFSNGPVH--LEDTLAKKA 1100
Qy      284 -INDGKHSILITIGLQKRMWVNNVRSVRI--EGEIFDFSTYYLGGIPIAIRERFNI 339
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      1101 QINDAKYHEISL--IYNNDKMMILVDDRHHKSTDNKKKLPFTDIYIGAPQEVILQSRTL 1159
Qy      340 STPA-----FOGCMKNL---KKTSGVRLNDIVGVTKKSEMDKLVRTASFSRQMSFT 391
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      1160 RAHLPLDINPRGCMKGFQPKQDNLEQETITLGVGCGPEDSLISRATFN--QGSFTA 1217
Qy      392 NLD--VSTDRPQLSFGFQTFQPSGTLNHQTRTSSLVLTLEDGHIELSTRDSNIPIFKSP 450
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      1218 SIQKISFFPFGFEGGFNRLQPNGLLFYYTSGSDVFSISLNDGTVMVDVK--GIKVMSTD 1275
Qy      451 GTYMDGLLHH--VVISDTSGLRLIDDQVLRNRQRLPSPFNAQOS-----LRLGG----- 499
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      1276 KQYHGDGLPHFVVVISDTR--YELVVDKSRIRLGRN--PTKGKAEQYOTTEKKFYFGGSPIS 1332

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```

Qy      500 ---GHFEGCISNVLVQRESQSBEBVLDLASKSTKQDASLGCSLNKPPFLMLFKSPKRPNK 556
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      1333 PQYANFTGCSISNAVFTRLDRDVEVEDFQRYSEKVTHTSLYECPIESSPLFLHKKGKNSKK 1392
Qy      557 GRIFVNVQLMDAP-----QATRTTEAMQDGRSCLPLNTAQSHRALQFQGSP 604
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      1393 PPTNQGEKSKDAPSWMDIGLKFLEQKAPRDSH-----CHLSSSPRAIIEHAYQYGGTA 1445
Qy      605 TSHLLKLQPOELLKERSQFSLDIOTTSFKGLVFYAGTKD--SFLALVYVADGRVVPALGAG 662
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      1446 NSRQFEHIEQDPRGKSQFAIRLKTSSHGMIFVSDDEBNDFTLFLAHGRVLVMTFVG 1505
Qy      663 GKGLRLRSKERHYDKMHTVVFGLNGGARLVVDGLRAQEGSL--PGNSTIIPREQVYL--G 720
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      1506 HKKLKIRSOEKNYDGLMHDVIFIREKSSGRLVIDGLRVLEERLPDGAAMKIKGPIYILGG 1565
Qy      721 LPLSRKPKSL--PQHSFVGLRDLPOLNSKPLDSPAAPGVPCLGSLKGIYFSQGG 777
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      1566 VAPGRVAVKVVQITSVYFSFGCLSNQLNGASITSAQTSVFPCBEGMEIGTYSFTEGG 1625
Qy      778 HVIILANSVSLGELKLTFSIRPSRLTGVLIVHGSQGRSLSYMEAGKTTSSVSDAGS 837
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      1626 YVVLDESFNIGLKFBIAPFVRPRSSGTLVHGHSVNGEYLVHMKNGQYIVVNNNGVADF 1685
Qy      838 VTSITPKOSLCDGQMSVAVSIIKORILHL 866
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      1686 STSVTPKQNLCDGRWHRIYIRDSNVQL 1714

```

Search completed: February 22, 2005, 08:40:52
Job time : 44.4378 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: February 22, 2005, 08:05:49 ; Search time 15.0758 Seconds

(without alignments)
3605.942 Million cell updates/sec

Title: US-10-817-423-4

Perfect score: 2940
Sequence: 1 MRFNGKSGVEVRLPNDLEDL.....MLFKSPKRFKGRIFVNVQL 565

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*

Prod. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2439	83.0	1713	2 A55347	adhesive ligand ep
2	686	23.3	1816	1 S68960	laminin alpha-4 ch
3	681	23.2	3635	2 T10053	laminin alpha-5 ch
4	395	13.4	3712	2 S18253	laminin alpha-1 ch
5	302	10.3	3106	1 S53868	laminin alpha-2 ch
6	298.5	10.2	3672	2 T23433	hypothetical prote
7	298.5	10.2	3704	2 T37316	probable laminin a
8	294	10.0	1751	1 MMHDMH	laminin alpha-2 ch
9	280	9.5	3084	1 MMSA	laminin alpha-1 ch
10	270	9.2	3075	2 S14458	laminin alpha-1 ch
11	247	8.4	3102	2 T43281	laminin alpha ch
12	222.5	7.6	2823	2 F87908	protein T22A3.8 [1
13	222.5	7.6	2823	2 T23064	hypothetical prote
14	212.5	7.2	1438	2 A48216	neurexin III-alpha
15	212.5	7.2	1471	2 B48218	neurexin III-alpha
16	212.5	7.2	1578	2 T48216	neurexin III-alpha
17	199.5	6.8	1530	2 T45944	neurexin I-alpha
18	199	6.8	1507	2 A40228	neurexin I-alpha
19	175	6.0	1715	2 C40228	neurexin II-alpha
20	170	5.8	1283	2 T13799	neurexin IV - frut
21	160.5	5.5	1264	2 T19545	hypothetical prote
22	159	5.4	3707	2 S18252	heparan sulfate pr
23	153	5.2	4391	2 A38096	perlecan precursor
24	147.5	5.0	281	2 T33466	hypothetical prote
25	143.5	4.9	1955	1 AGCH	agrin precursor -
26	142	4.8	1523	2 T13953	MEGF5 protein - ra
27	140	4.8	2610	2 T20968	hypothetical prote
28	138.5	4.7	1381	2 T31083	paranodin - rat
29	138	4.7	1025	2 T42626	secreted leucine-r

30	137.5	4.7	1385	2 T14158	neurexin IV - mous
31	135.5	4.6	1328	2 T43060	agrin - electric r
32	128.5	4.4	3034	2 T14119	seven-pass transme
33	128	4.4	637	2 F83839	myo-inositol catab
34	128	4.4	1531	2 T42218	slit-1 protein hom
35	125	4.3	403	2 T22025	sex steroid-bindin
36	124.5	4.2	601	2 T22025	hypothetical prote
37	124.5	4.2	601	2 D89711	protein P40B10.4 [
38	124.5	4.2	673	2 A48089	growth arrest-spec
39	122	4.1	2325	2 A61208	chondroitin sulfat
40	121.5	4.1	935	2 A64608	excitoclease ABC c
41	121.5	4.1	2809	2 T30213	G-cadherin - sea u
42	120	4.1	757	2 T34362	hypothetical prote
43	120	4.1	768	2 B97725	outer membrane pro
44	119.5	4.1	627	2 A41609	dnar-type molecula
45	119.5	4.1	1417	2 AG2137	hypothetical prote

ALIGNMENTS

RESULT 1

A55347
adhesive ligand epiligrin, alpha-3 chain form A precursor - human
C:Species: Homo sapiens (man)
C>Date: 06-Feb-1995 #sequence_revision 06-Feb-1995 #text_change 09-Jul-2004
C/Accession: A55347
R/Ryan, M.C.; Tizard, R.; Vandevanter, D.R.; Carter, W.G.
J. Biol. Chem. 269, 22779-22787, 1994
A>Title: Cloning of the lam3 gene encoding the alpha3 chain of the adhesive ligand epi
A/Reference number: A55347, PMID:94357926; PMID:8077230
A/Accession: A55347
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-1713 <R>A>
A/Cross-references: UNIPROT:Q16787; GB:U34155; NID:9551596; PID:9551597
C/Superfamily: laminin alpha-4 chain; laminin G repeat homology; laminin-type EGF-like
C/Keywords: alternative splicing
F/67-114/Domain: laminin-type EGF-like homology <LE2>
F/1392-1534/Domain: laminin G repeat homology <LG4>

Query Match	83.0%	Score 2439;	DB 2;	Length 1713;
Best Local Similarity	81.9%	Prod. No. 5.9e-165;		
Matches 463;	Conservative 47;	Mismatches 55;	Indels 0;	Gaps 0;
QY	1	MRFNGKSGVEVRLPNDLEDLKGYSLSLFLQRPDLRNGTDMFVYILGNKDSKDYIG	60	
DB	771	MRFNGKSGVEVRLPNDLEDLKGYSLSLFLQRPDLRNGTDMFVYILGNKDSKDYIG	830	
QY	61	MAVVDGQLTCVYVNLGDBAEVQIDQVLTSESSQAVMDRKYFORIYOPALNTTKATSN	120	
DB	831	MAVVDGQLTCVYVNLGDBAEVQIDQVLTSESSQAVMDRKYFORIYOPALNTTKATSN	890	
QY	121	KPKAPAVYDLGGSSNTLNLDPEDDAVFYVGYPPDELSRLRFPYKGCISLDDNEN	180	
DB	891	KPSTPGVYDMDGNSNTLNLDPEDDAVFYVGYPPDELSRLRFPYKGCISLDDNEN	950	
QY	181	VLSTLVNFKTFENLNTTEVEPCRRRKESDKNVEGTYARIPQPNAPFNFIQTITTV	240	
DB	951	VLSTLVNFKTFENLNTTEVEPCRRRKESDKNVEGTYARIPQPNAPFNFIQTITTV	1010	
QY	241	DRGLLFAENQDNFISLNTIDGNLAVRYKANSPPKRGIRDTINDGKHSILITTKLQ	300	
DB	1011	DRGLLFAENQDNFISLNTIDGNLAVRYKANSPPKRGIRDTINDGKHSILITTKLQ	1070	
QY	301	KRWMINNERSVRIEGEIPDSTYYIGPIAIRBNFISTPAFOGCKMLKKTSGVRL	360	
DB	1071	KRWMINNERSVRIEGEIPDSTYYIGPIAIRBNFISTPAFOGCKMLKKTSGVRL	1130	
QY	361	NDTVGVTKKCSSEMDKLVRTASFSRGGQMSFTNLDVSTDRPOLSGFQTFQPSGTLNMQ	420	
DB	1131	NDTVGVTKKCSSEMDKLVRTASFSRGGQMSFTNLDVSTDRPOLSGFQTFQPSGTLNMQ	1190	

QY 421 TRTSLLVLEDEGHIELSTRDSNIPFKSGPTMGILLHHVSYISPTSGILLIIDQVLR 480
 DB 1191 TWRRNQVLEDEYIELSTSDSGPIFKSPQTMDEGLHHVSYISDNGILRLIIDQLLR 1250
 QY 481 RNORLPSFNAOQSLTLAGGHEPGCSNLYVRFOSPEYLDLASKSTKDDSLGGCSIN 540
 DB 1251 NSGRLLHSSRSQSLTLAGGSEFGCSINFWQRLSLSPVLDLTSNLSKRDVSLGGCSIN 1310
 QY 541 KEPEMLFKSPKAFKGRITFVNQL 565
 DB 1311 KEPEMLFKSGTFRFKTKPRINQL 1335
 RESULT 2
 S68960
 Laminin alpha-4 chain precursor - human
 N:Alternate names: laminin A4
 C:Species: Homo sapiens (man)
 C>Date: 21-Aug-1998 #sequence_revision 21-Aug-1998 #ext_change 09-Jul-2004
 C/Accession: S68960; S65926; S49149; S40150; I53516
 R:Richard, A.; Al-Imara, L.; Pope, F.M.
 Eur. J. Biochem. 238, 813-821, 1996
 A>Title: The complete cDNA sequence of laminin alpha-4 and its relationship to the other
 A:Reference number: S68960; PMID:96300249; PMID:8706685
 A:Accession: S68960
 A:Molecule type: mRNA
 A:Residues: 1-1816 <RIC>
 A:Cross-references: UNIPROT:Q16363; UNIPROT:Q14731; EMBL:X91171; NID:G1212962; PIDN:CAAG
 A:Experimental source: tissue type heart
 R:Jivanathan, A.; Salino, K.; Satiola, H.; Tryggvason, K.
 FEBS Lett. 365, 183-188, 1995
 A>Title: Primary structure and expression of a novel human laminin alpha-4 chain.
 A:Reference number: I53516; PMID:95300971; PMID:7781776
 A:Accession: S65926
 A:Molecule type: mRNA
 A:Residues: 1142, 'P', 144-177, 'P', 179-490, 'Y', 492-1056, 'P', 1058-1816 <IIV>
 A:Cross-references: EMBL:S78569; NID:G1042081; PIDN:AMB34635.1; PID:G1042082
 R:Richard, A.J.; Al-Imara, L.; Carter, N.; Levertha, M.; Lloyd, J.C.; Pope, F.M.
 submitted to the EMBL Data Library, December 1993
 A>Description: Localisation of the gene (LAMM4) to chromosome 6q21 and isolation of a pA
 A:Reference number: S49149
 A:Accession: S49149
 A:Molecule type: mRNA
 A:Residues: 236-1816 <RI2>
 A:Cross-references: EMBL:X76939; NID:G509805; PIDN:CAAS4258.1; PID:G509806
 R:Richard, A.J.; Al-Imara, L.; Carter, N.; Lloyd, J.C.; Pope, F.M.
 submitted to the EMBL Data Library, February 1993
 A>Description: Isolation of a partial cDNA encoding a protein homologous to laminin A. A
 A:Reference number: S40150
 A:Accession: S40150
 A:Molecule type: mRNA
 A:Residues: 1403-1541, 'S', 1543-1816 <RI3>
 A:Cross-references: EMBL:X70904; NID:G437804; PIDN:CAAS0261.1; PID:G437805
 C:Genetics:
 A:Gene: GDB:LAMA4; LAMA3
 A:Cross-references: GDB:203904; OMIM:600133
 A:Map position: 6q21-6q21
 C:Complex: Laminins are trimers of an alpha-type, a beta-type, and a gamma-type laminin
 C:Function:
 A>Description: Interact with cells and with other basement membrane proteins to promote
 C:Superfamily: laminin alpha-4 chain; laminin G repeat homology; laminin-type EGF-like h
 C:Keywords: basement membrane; cell binding; coiled coil; extracellular matrix; glycopro
 F:1-24/Domain: signal sequence #status predicted <SIG>
 F:25-1816/Product: laminin alpha-4 chain #status predicted <MAT>
 F:82-129/Domain: laminin-type EGF-like homology <LE1>
 F:132-184/Domain: laminin-type EGF-like homology <LE2>
 F:187-238/Domain: laminin-type EGF-like homology <LE3>
 F:241-265/Domain: laminin-type EGF-like homology <LE3>
 F:717-719/Region: cell attachment (R-G-D) motif
 F:662-1031/Domain: laminin G repeat homology <LG1>
 F:1068-1233/Domain: laminin G repeat homology <LG2>
 F:1252-1398/Domain: laminin G repeat homology <LG3>
 F:1488-1636/Domain: laminin G repeat homology <LG4>

F:1665-1816/Domain: laminin G repeat homology <LG5>
 F:104,215,308,458,524,550,571,574,631,639,735,751,754,780,803,1086,1281,1359,1411/Bindin
 F:266,269/Dileulide bonds: Interchain #status predicted
 Query Match 23.3%; Score 686; DB 1; Length 1816;
 Best Local Similarity 32.2%; Pred. No. 3,76-40;
 Matches 194; Conservative 101; Mismatches 245; Indels 62; Gaps 21;
 QY 1 KEFNKSGVEVRLPNDLDEKGYTSLSTFL-----QRPDLRENGGTEDMFVMTLGNKDDSK 56
 DB 829 MAFDQSAVHRSKSMDDLAFSLSLYMKPVPVPELTET---TADGFIYLGSKNAKK 885
 QY 57 DYIGNAVVDGQLTCYNNLGDREAVQIDQVLTSESOBAVNDYKFORIYQPAKILNTKE 116
 DB 886 EYMGALIKNDNLVYYNLTGTDVEIPLDS--KPVSSWPAYSVIYKIEVGHKGVLTLP 943
 QY 117 ATSNKPKAPAVDLEGGSSNTLNLDPEDAVPYVGYPPDELPRLAPPPKGLIEDD 176
 DB 944 SLSSYAEKFKIKGFGSDSLDLDPBDYVYGVGVSNFGLPTSLMLPGFVGLELAT 1003
 QY 177 LNEVTLSTYNTFTNTLNTTEVEPCRRK-----EESDKNYEGGYA--RIPTQPN--A 227
 DB 1004 LAMNDVSLYNTFTNTLNTTEVEPCRRK-----EESDKNYEGGYA--RIPTQPN--A 227
 QY 228 PPNPFYQITITQTVDRGLLFAENQDNFSLNIEDGNLMVRY-----KLNSEPPKKEI 280
 DB 1064 QVTRPDIEVRTPADNGLILAMVNGSMFRLERNGYLHVFDGFGSGRVHLEDTLKA- 1122
 QY 281 RRTINDGDHSLITITGLQKRMVNNVRSYRI---EGEIPDSYTYLGCP-----I 331
 DB 1123 --QINDAKYHEISL--IYNDKMTILVDRHAKSMNKNKIPFDIYIGAPPEILQSR 1179
 QY 332 AIRRFNISTPAFGCKMNL---KTSQVRLNDTVGYTKCSBDMKLVRTSPFRGGOM 388
 DB 1180 ALRAHLPDI-NFRCKMGFGQKQDFYLBETLTGYGCPBSLSRATYR--GQS 1236
 QY 389 SFTNLD-VPSTDRPLSFGFQTPQSPGTLNLHQRTSSILVLTEDGHIELSTRDSNIP 447
 DB 1237 FIASLOKISFPFGFGFRTIQNGNGLLFYASGSDFVSLDNGYIMDVK--GIKQV 1294
 QY 448 KSPGYTMGLLHVHVIDTSGLR--LLID-DQVLRNQRPLPSFNAOQSLR--LGG-- 499
 DB 1295 SVDKQYNGLSHF--VIVSSVPTREYLLVDSRSVSKNPTKGIQDTASEKKFYFGSP 1352
 QY 500 -----GHPEGCSNLYVRFOSPEYLDLASKSTKDDSLGGCSINKPPFLMFKSPKRF 554
 DB 1353 ISAOYANFPGCISNAVPTRVDRDEVEDPQRTTEKVTHTSLIECPLESSEPLFLHKKGNL 1412
 QY 555 NK 556
 DB 1413 SK 1414
 RESULT 3
 T10053
 Laminin alpha 5 chain - mouse (fragment)
 C:Species: Mus musculus (house mouse)
 C>Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #ext_change 09-Jul-2004
 C/Accession: T10053
 R:Miner, J.H.; Lewis, R.M.; Sanez, J.R.
 submitted to the EMBL Data Library, November 1997
 A:Reference number: Z16923
 A:Accession: T10053
 A>Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-3635 <MIN>
 A:Cross-references: UNIPROT:Q61001; EMBL:U37501; NID:G2599231; PID:G2599232
 C:Genetics:
 A:Gene: Lamas
 C:Keywords: basement membrane; cell binding; extracellular matrix
 F:1888-1939/Domain: laminin-type EGF-like homology <LE6>
 F:1942-1970/Domain: EGF homology <EGF>

3733-330/Domain: lam1n1n-type EGF-like homology <LRB2>
3733-400/Domain: lam1n1n-type EGF-like homology <LRB2>
3734-584/Domain: lam1n1n-type EGF-like homology <LRB1>
F1776-2115/Domain: III <DOM3>
F1776-1806/Domain: lam1n1n-type EGF-like homology [status atypical <LR1>
F1809-1856/Domain: lam1n1n-type EGF-like homology <LR2>
F1859-1914/Domain: lam1n1n-type EGF-like homology <LR3>
F1917-1967/Domain: lam1n1n-type EGF-like homology <LR4>
F1970-2014/Domain: lam1n1n-type EGF-like homology <LR5>
F1970-2061/Domain: lam1n1n-type EGF-like homology <LR6>
F2064-2109/Domain: lam1n1n-type EGF-like homology <LR7>
F2166-2697/Domain: I/II, heptad repeats <DOM2>
F2698-3712/Domain: G <DOM5>
F2698-2863/Domain: repeat G1 <RG1>
F2864-3048/Domain: repeat G2 <RG2>
F3049-3223/Domain: repeat G3 <RG3>
F3079-3200/Domain: lam1n1n G repeat homology <LG3>
F3334-3528/Domain: repeat G4 <RG4>
F3359-3712/Domain: repeat G5 <RG5>
F1847,1850,1943,2024,2136,2215,2267,2301,2323,2482,2524,2538,2569,2699,2720,2850,2938

Query Match 13.4%; Score 395; DB 2; Length 3712;
Best Local Similarity 25.5%; Pred. No. 5,6e-19;
Matches 155; Conservative 105; Mismatches 236; Indels 110; Gaps 27;

QY 1 MRFNGSGVEYRLPNDELDKGYTSLFLQRPDLRNGGTEDMYMTYG--NKDASK-- 56
DB 2675 VNFPRSTLLEKTEPEKTKLMTRTVLSTYFR---TTEBSG---FLLYGNNKTKQKKN 2727
QY 57 DYIGMAVDGGLTCVNNIGDRAEAVQIDQVLTSSSQEAVMDRVKQRIYQPAKLNTYKE 116
DB 2728 DFVAWEIYNGPIILTTDIGNPERITSDKYADGEMVQAVVDMG----PNAKLTIRE 2782
QY 117 ATSNKPKAPAYVDEEG---SSNTLNLDPEDAVYVGYP--PDFELPSRLFFPYKGC 171
DB 2783 L-----PNCDDVBEHKSGLTSSQNLTHYDKNSRLF-VGGYPSIDSPNAPDPLTNSFSG 2837
QY 172 IELDNLNENVLSTYNF-KTFPNLNTTEVEPCRRKRBSDKNYFEQGTARLPTQPNAP 229
DB 2838 IEDLKIGDESGLMNFVYGDDNDQARERDVLLKKKPYTGRLPFKNGVQLNATSNLKS 2897
QY 230 PNFIQ---TIQTYDRGLFPAENQDNFSLNIEGNLMVVRKLNSEPPKKGIRPTIND 286
DB 2898 RSSIQFSFKADKDTSGNLFFPYGRDKHYMSLEMDGALFENISLBEGGVQSGSDRYND 2957
QY 287 GKDHISI-----LITIGLQKRMWVNERSVRIEGEIFDPSTYYLGSLPIALREBF 337
DB 2958 NQMKHVQAEKRNKGLAKVDIV----ISRTAPLEADELEKRLRLYCGHP----RL 3009
QY 338 NIS---TPAFQCGMKNLKKTSGVRLNDTV---GYTKKCSDEMKLVRTASFSRGGMSFT 391
DB 3010 NTSISLQGNFQGCIDNVINQGVVDLTRYVGGVEBGSAKSFVTSYAAPHYGLRMW 3069
QY 392 NLDVPSIDRFQLSGFGFTQFSQSTLL---NHQTRSSSLVLTEDGHIELSTDSNPIFK 448
DB 3070 N--VSSDNNHNVHLFFKTTQPNGVLFYAANDH-QSSTIGLSLQDGLLKLKNSMSQSLVI-- 3124
QY 449 SPGYTMGLLH---HVASVIDPSG-LRLILDQVLRNRQRLPSFSNAQOSRLGGG--- 500
DB 3125 -----DRIILNDEBDHVTVOHTQSELRLYVDDV---DKRLGS---PQLILBSGDI 3172
QY 501 -----HFEGCISNLYVQFSGSPVTLDAKSKTKDASLGGCSLNK 541
DB 3173 FAGLPDNYRTRRNALASLAFVFGCISDVTY-----NBIINPANSLEKKGNNINGC----- 3223
QY 542 PPFMLTK 549
DB 3224 PPHVLAAY 3231

RESULT 5
553868
lam1n1n alpha-2 chain precursor - mouse

N/Alternate names: laminin M chain; merosin heavy chain
C/Species: Mus musculus (house mouse)
C/Date: 21-Aug-1998 #sequence revision 21-Aug-1998 #ext_change 09-Jul-2004
C/Accession: I490777, S50829; I48655; S31576; S53868
R/Bernier, S.M.; Utsun, A.; Sugiyama, S.; Dol, T.; Polietine, C.; Yamada, Y.
Matrix Biol. 14, 447-455, 1995
A/Title: Cloning and expression of laminin alpha 2 chain (M-chain) in the mouse.
A/Reference number: I490777, NCID:95316259; PMID:7795883
A/Accession: I49077
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: mRNA
A/Residues: 1-3106 <RES>
A/Cross-references: UNIPROT:Q60675; EMBL:U12147; NCID:9699109; PID:AC52165.1; PID:96992
R/Xu, H.; Wu, X.R.; Wewer, U.M.; Engvall, E.
Nature Genet. 8, 297-302, 1994
A/Title: Murine muscular dystrophy caused by a mutation in the laminin alpha-2 (Lama2) g
A/Reference number: 650829; NCID:95179178; PMID:7674173
A/Accession: S50829
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 64-281 <XUN>
A/Cross-references: GB:S75315; NCID:9833929; PID:AA33573.1; PID:9833930
R/Chang, A.C.; Wadsworth, S.; Colligan, J.E.
J. Immunol. 151, 1789-1801, 1993
A/Title: Expression of merosin in the thymus and its interaction with thymocytes.
A/Reference number: I48655; NCID:93346725; PMID:8345183
A/Accession: I48655
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: mRNA
A/Residues: 2162-2204, 'D', 2206-2213, 'E', 2216-2279 <RE2>
A/Cross-references: EMBL:X69869; NCID:953055; PID:CAA9502.1; PID:953056
C/Complex: Laminins are trimers of an alpha-type, a beta-type, and a gamma-type laminin
C/Function:
A/Description: Interact with cells and with other basement membrane proteins to promote
C/Superfamily: laminin alpha-1 chain, laminin G repeat homology; laminin-type EGF-like h
C/Keyword: Basement membrane; calcium binding; coiled coil; extracellular matrix; glyco
F/1-22/Domain: signal sequence; #status predicted <SIG>
F/23-3106/Product: laminin alpha-2 chain #status predicted <MAT>
F/283-337/Domain: laminin-type EGF-like homology <LE01>
F/340-407/Domain: laminin-type EGF-like homology <LE02>
F/410-462/Domain: laminin-type EGF-like homology <LE03>
F/465-511/Domain: laminin-type EGF-like homology <LE04>
F/514-523/Domain: laminin-type EGF-like homology #status atypical <LE05>
F/720-750/Domain: laminin-type EGF-like homology <LE06>
F/753-800/Domain: laminin-type EGF-like homology <LE07>
F/803-858/Domain: laminin-type EGF-like homology <LE08>
F/861-911/Domain: laminin-type EGF-like homology <LE09>
F/914-960/Domain: laminin-type EGF-like homology <LE10>
F/963-1007/Domain: laminin-type EGF-like homology <LE11>
F/1010-1053/Domain: laminin-type EGF-like homology <LE12>
F/1056-1099/Domain: laminin-type EGF-like homology <LE13>
F/1102-1121/Domain: laminin-type EGF-like homology #status atypical <LE14>
F/1123-1159/Domain: laminin-type EGF-like homology #status atypical <LE15>
F/1162-1171/Domain: laminin-type EGF-like homology #status atypical <LE16>
F/1376-1413/Domain: laminin-type EGF-like homology #status atypical <LE17>
F/1416-1462/Domain: laminin-type EGF-like homology #status atypical <LE18>
F/1465-1500/Domain: laminin-type EGF-like homology <LE19>
F/1523-1567/Domain: laminin-type EGF-like homology <LE20>
F/2166-2237/Domain: laminin G repeat homology <LG1>
F/2360-2520/Domain: laminin G repeat homology <LG2>
F/2546-2709/Domain: laminin G repeat homology <LG3>
F/2785-2933/Domain: laminin G repeat homology <LG4>
F/2960-3106/Domain: laminin G repeat homology <LG5>
Query Match 10.3%; Score 302; DB 1; Length 3106;
Best Local Similarity 22.1%; Pred. No. 1.8e-12;
Matches 131; Conservative 116; Mismatches 227; Indels 120; Gaps 30;
QY 32 RPDLRENG-----GTEDMFVMTYGNKDKSK--DYTGMAVVGQGLCVYNLGRRA 79
DB 2155 RPIKKGSTNNYVHTYKTAADNLITFLG---SAKPTDFAIEKRGKSKSFLMTVSGVG 2211
QY 80 EVOIDVLTSESGQBAVMRVRKFORITYQPAKNTYKATSNKPKA--PAVVDLEGSSSN 136

DB 2212 RVGFEDLTID-----DSWYRIEASRTGRNGISV---RALDGPXASWVPSTHVSPPGY 2264
QY 137 TLLNIDPDADVAVGVGPPDPFELPSRLAPPPYKGIIEIDNENVLSTYNKTFNNMT 196
DB 2265 TLLDND-ANAMLPVGLTGKTKKADAVVITFTGGMGTTYDKNPITGLMNRRE---KEG 2319
QY 197 EYEPCKRRKREESDK---YFEGTYARIPTOAPNAPFPFIOTI---QTYDRLGLFPFA 249
DB 2320 DCKGCTVAPQVWDSGCTGFQFGEYALV-SRPRIKRYR-ISTWPKRPTPSSALMTLA 2377
QY 250 NOD--NPISLNIEDGNLWRYKLNSEPKKGIKIDTI-----NDGKHSIITGKLOKR 302
DB 2378 TFDLDPMFVSELSDHVKVSYDLGS-----GMTSVSNQNNHDKWKA--FTLSRIKO 2429
QY 303 MNINV-----NERSVRLEGHFPD-----STYLGIP-----IATREPNISTAPQ 345
DB 2430 ANISTVIDSNQRENVATSSGNNFGLDLKADDKTYFGGLPLNMLSKAPDEVAVKRY 2489
QY 346 GCMKUL---KTSGVRLNDTVGVTKKSEPMKLVRTASPSRG--QMSFTNLVPSYDR 400
DB 2490 GGLKDIKISRTPTNLSPPDYGVTKGS--LENNVTSFKPGVVELAAVSIDVT--- 2544
QY 401 FQLSFGPTPOPSTLL-----NHQRTSSLVLTLEDG---HIELSTRD-S 442
DB 2545 -RINLSFSTRNBSGILLGSGGTLTPPRKRKQTTQAYVALFNLKGRLEVLHSGGRTMR 2603
QY 443 NPIPKSGTWDGLHHVSVISDTSGLRLIDQVLRNRQLRPFNSAQ-QSLRLDGG- 500
DB 2604 KVIKPEBPLFLFDGHEHVVH-ERTRGIFTVOIDDRHIOVLTEBPDIKVKLFVGGAP 2662
QY 501 -----HFGCISNVLVGRFSQSPVELDLASKTKDASIGGCSLNKP 542
DB 2663 PEFQSPPLRNIPAFQGCVMNLVINIP-----MPPAQIARKNMDIGCTYQKP 2711
RESULT 6
T23433
Hypothetical protein K08C7.3 - Caenorhabditis elegans
C/Species: Caenorhabditis elegans
C/Date: 15-Oct-1999 #sequence revision 15-Oct-1999 #ext_change 09-Jul-2004
C/Accession: T23433
R/Berks, M.
Submitted to the EMBL Data Library, March 1996
A/Reference number: Z19740
A/Accession: T23433
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: DNA
A/Residues: 1-3672 <WTL>
A/Cross-references: UNIPROT:Q21313; EMBL:Z70286; PID:CAA94293.1; GSPDB:GN00022; CESP:K0
A/Experimental source: clone K08C7
C/Genetics:
A/Genes: CESP:K08C7.3
A/Map position: 4
A/Intons: 66/1; 244/3; 563/4; 1187/3; 1248/3; 1300/1; 1460/1; 1623/3; 2361/3; 2968/3; 3
C/Superfamily: laminin alpha-1 chain; laminin G repeat homology; laminin-type EGF-like h
Query Match 10.2%; Score 298.5; DB 2; Length 3672;
Best Local Similarity 23.5%; Pred. No. 4.1e-12;
Matches 141; Conservative 106; Mismatches 233; Indels 121; Gaps 27;
QY 3 FNGKGVBRLLPNDLEDLKGYSLSLPLQRPDLRENGGTEDMFVMTYGNKDA----- 54
DB 2696 FEKSSLDLNTIPQRTYRSLAAHLDIFYRTR--QHG-----IPLFNGEERAVASRAVP 2748
QY 55 SDYIGMAVVDQGLTVYNLGRRAEVOIDVLTSESGQBAVMRVRKFORITYQPAKNT 114
DB 2749 TADYVAARIEYGRPTVYDLGAPAVVKD-----TPVNDGLMRILNTERI-----GKT 2797
QY 115 KEATSNKPKAPAVYDLE---GSSNTLNDPDEDAVFPVVGCPPPPELPSRLAPPPYKGC 171
DB 2798 VSVTLSPKNSVETAAETKSSVAGNKSVINLNOQISRLTFVGVGVPFARSISKDLVNDPFGD 2857


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QY 172 IELDDINENVLSYFNKFTFNLTATEVBPCKRRKESDKNY--FEGNGYA-----R 220
DB 2858 IESLKLHGEPILGLMNSREKNTNVNGAQKKPKITDADLVSLDGEYTSYKPSHMNDR 2917
QY 221 IPTQNPAPPNPFIQTITQTVDRGLLFFAENQDNFISLNTEDGMLMYRYKLNSPPPKKGI 280
DB 2918 KATKISLSFLTF-----SPHGLLFFVGKDKDFMLLEISDGVKLSVDLGS-----GV 2964
QY 281 RDTI-----NDGKHSILITIGLQKRMVNNERSVRIEGI----FDFT---YYLG 327
DB 2965 GQWITSSSYNDQKWH--VSIVREKHVYKIMIDGTEVLEGDVPKDSMSYTERFLYIG 3022
QY 328 GPIAIRERFNISTPAFQGMKRLKKTSGVRLND---TVGYTKCSBPKLVRTASFS 383
DB 3023 GTPSGLSVTRTI--VPLRGCTISVKLGSDNVDLSSHASKVGRSGC--PLHSVRYTSFIS 3078
QY 384 RGGQMSFTNLDPSTDRFQLSFGFQF---FQPSGTLINQRTSSLLVTL-EGGHLELST 439
DB 3079 DRTTASFNNAATERSED--VSATFEKFKRSTRQPSLSFTVNDDEDSVLSVINEGILTVIS 3137
QY 440 RD--SNIPFKSPGTMDGLLHVSVISDTSGRLIIDQVLRNRQLPSPSNAQGSRL 497
DB 3138 GEDIAITLELAASP-----DEKMHVYSIRKTYIIRIDADD-----SFSNEVARKIA 3183
QY 498 GGGH-----FEGCISNVLVQRFQSPREVLDLASKSTKQDASLGCSL 539
DB 3184 DSNPDASFLSAFSGKSGTSPFGCIGDVTL-----NGLDLPAN-SRIKESISLNGCSL 3237
QY 540 N 540
DB 3238 S 3238

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RESULT 7

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T37316
probable laminin alpha chain - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C>Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
C:Accession: T37316
R:Joh, K.; Zhu, K.; Hedgecock, E.M.; Inoue, T.; Horii, K.
submitted to the EMBL Data Library, August 1998
A:Description: laminin alpha chain gene in the nematode C. elegans.
A:Reference number: Z21681
A:Accession: T37316
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-3704 <JOB>
A:Cross-references: UNIPROT:P91904; EMBL:AB016806; PDB:BAJ2347.1
A:Experimental source: strain N2
C:Genetics:
A:Gene: epi-1
A:Map position: IV
A:Intons: 66/1; 284/3; 563/1; 1187/3; 1248/3; 1300/1; 1460/1; 1623/3; 2361/3; 2988/3; 3
C:Superfamily: laminin alpha-1 chain; laminin G repeat homology; laminin-type BGF-like h

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Query Match 10.2%; Score 298.5; DB 2; Length 3704;
Best Local Similarity 23.5%; Pred. No. 4.1e-12;
Matches 141; Conservative 106; Mismatches 233; Indels 121; Gaps 27;
QY 3 FNKSGVEVRLPNDLBDIKYTSLSLELQRPDLRENGCTEDMVTMGKDA-----54
DB 2696 FEKSSLDLNIPIRVTSSAAAHADISFYFRTB--QEHG-----IPLFPGNETAVGSRAPV 2748
QY 55 SKDYIGMAVVDGQLTCVYNLGDREAEVQDVLTVTESQCAVMDRVFQRIYOPAKIMYT 114
DB 2749 TADYVAABIEYGRPKITVDGDAPAVYKD-----TPVNDGMRRLNIERT-----GKT 2797
QY 115 KKAITSKPKRPAVYDLE---GSSNTLANIDPDNAVYVGGYPPDELPRKLAFPPPKGC 171
DB 2798 VSVTLKRPNSVETAEKSSVAGNKSVALNMQISRLFVGQVPTSARISIDLYNRDFVGD 2857
QY 172 IELDDINENVLSYFNKFTFNLTATEVBPCKRRKESDKNY--FEGNGYA-----R 220

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DB 2858 IESLKLHGEPILGLMNSREKNTNVNGAQKKPKITDADLVSLDGEYTSYKPSHMNDR 2917
QY 221 IPTQNPAPPNPFIQTITQTVDRGLLFFAENQDNFISLNTEDGMLMYRYKLNSPPPKKGI 280
DB 2918 KATKISLSFLTF-----SPHGLLFFVGKDKDFMLLEISDGVKLSVDLGS-----GV 2964
QY 281 RDTI-----NDGKHSILITIGLQKRMVNNERSVRIEGI----FDFT---YYLG 327
DB 2965 GQWITSSSYNDQKWH--VSIVREKHVYKIMIDGTEVLEGDVPKDSMSYTERFLYIG 3022
QY 328 GPIAIRERFNISTPAFQGMKRLKKTSGVRLND---TVGYTKCSBPKLVRTASFS 383
DB 3023 GTPSGLSVTRTI--VPLRGCTISVKLGSDNVDLSSHASKVGRSGC--PLHSVRYTSFIS 3078
QY 384 RGGQMSFTNLDPSTDRFQLSFGFQF---FQPSGTLINQRTSSLLVTL-EGGHLELST 439
DB 3079 DRTTASFNNAATERSED--VSATFEKFKRSTRQPSLSFTVNDDEDSVLSVINEGILTVIS 3137
QY 440 RD--SNIPFKSPGTMDGLLHVSVISDTSGRLIIDQVLRNRQLPSPSNAQGSRL 497
DB 3138 GEDIAITLELAASP-----DEKMHVYSIRKTYIIRIDADD-----SFSNEVARKIA 3183
QY 498 GGGH-----FEGCISNVLVQRFQSPREVLDLASKSTKQDASLGCSL 539
DB 3184 DSNPDASFLSAFSGKSGTSPFGCIGDVTL-----NGLDLPAN-SRIKESISLNGCSL 3237
QY 540 N 540
DB 3238 S 3238

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RESULT 8

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MEMPHIS
laminin alpha-2 chain - human (fragment)
N:Alternate names: laminin M chain; merosin heavy chain
C:Species: Homo sapiens (man)
C>Date: 30-Sep-1991 #sequence_revision 21-Aug-1998 #text_change 09-Jul-2004
C:Accession: P30082; A35899; A38970; S14461
R:Horii, H.; Kanamori, T.; Mizuta, T.; Yamaguchi, N.; Liu, Y.; Nagai, Y.
J. Biochem. 116, 1212-1219, 1994
A:Title: Human laminin M chain: Biotrope analysis of its monoclonal antibodies by immuno
A:Reference number: P30082; MUID:95221315; PMID:7535762
A:Accession: P30082
A:Molecule type: mRNA
A:Residues: 1-1751 <HOR>
A:Cross-references: UNIPROT:P24043
A:Experimental source: Placenta
R:Dirig, K.; Lelivo, I.; Argaves, W.S.; Ruoslahti, E.; Engvall, E.
Proc. Natl. Acad. Sci. U.S.A. 87, 3264-3268, 1990
A:Title: Merosin, a tissue-specific basement membrane protein, is a laminin-like protei
A:Reference number: A35899; MUID:90238994; PMID:2185464
A:Accession: A35899
A:Status: nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 'V', 623-1751 <EHR1>
A:Cross-references: EMBL:M59832
A:Accession: A38970
A:Molecule type: protein
A:Residues: 1368-1384; 1389-1406; 1593-1607 <EHR2>
A:Note: the sequence from Fig. 1 is inconsistent with that from Fig. 2 in lacking 1599-'
submitted to the EMBL Data Library, December 1990
A:Description: The tissue-specific basement membrane protein merosin is a laminin-like
A:Reference number: S14461
A:Molecule type: mRNA
A:Residues: 'V', 623-1264; 'R', 1266-1751 <LEI>
A:Cross-references: EMBL:M59832; NID:g187520; PDB:AAA63215.1; PID:g187521
C:Comment: This protein is a prominent component of the basement membrane that mediate
C:Genetics:
A:Gene: GDB:LAMA2; LAMM
A:Cross-references: GDB:132362; OMIM:156225
A:Map position: 6q22-6q23

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C:Complex: Laminins are trimers of an alpha-type, a beta-type, and a gamma-type laminin A;Description: Interact with cells and with other basement membrane proteins to promote C;Superfamily: laminin alpha-1 chain; laminin G repeat homology; laminin-type EGF-like R;C;Keywords: basement membrane; calcium binding; coiled coil; extracellular matrix; glycosyl F;R21-58/Domain: laminin-type EGF-like homology #stratus atypical <LE01> F;R61-107/Domain: laminin-type EGF-like homology <LE02> F;R110-165/Domain: laminin-type EGF-like homology <LE03> F;R168-212/Domain: laminin-type EGF-like homology <LE04> F;S527-567,1071-1300/Region: 3DM and 2DP binding F;R811-972/Domain: laminin G repeat homology <LG1> F;R1005-1165/Domain: laminin G repeat homology <LG2> F;R1191-1354/Domain: laminin G repeat homology <LG3> F;R1430-1578/Domain: laminin G repeat homology <LG4> F;R1605-1751/Domain: laminin G repeat homology <LG5> F;R1120,238,255,341,451,542,557,561,558,669,686,767,861,1001,1076,1119,1192,1199,1289,1505

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Query Match Summary      10.0% Score 294; DB 1; Length 1751;
Best Local Similarity   23.6%; Pred. No.2.8e-12;
Matches    135; Conservative 105; Mismatches 221; Indels 112; Gaps 28;

QY      DMFWVYLGNKDKASK--DYIGMAVVDGQLTCVYNLGDREAEVQI-DQVLTESESOGAEAVDR 99
       |||::||::||::||::||::||::||::||::||::||::||::||::||::||::||
DB      DNLLPYLG---SAKRIDFLTAIEMRKGVSFLMDVGSGVRVEYPLDLTIDDSYWRIVASR 877
QY      100 VKFQRITVPALANTYKEATSNKPRA---PAYTDLEGGSSNTILNLPEDDAVFYTGCIPPD 156
       |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
DB      878 TGRNGTISVRAL-----DGPKASIVSTHSHTSIPRGYTTLVD-ANMALFVGLGTGX 928
QY      157 FELPRLRFPPVKYCIEDDLLENVLSLYNFETFTFNLTWTEVEPCRRRKESDNK---YF 213
       |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
DB      929 LKKADAVAVITFTGCMGETPDYDNKFIGLMNPREE---XEGDCKGTGSPOVEDSEGTIQF 984
QY      214 EGTGYARIPTQPNAPFENFIOTI---QTVDRLGLEFAENOD-NFTSLNIEDGNLMVR 267
       |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
DB      985 DGEIGALVAL-SRPRIWYPN-I-STVMKEFRFTFSASSALIMLATIRLDLDFMSVELTGHIKYS 1042
QY      268 YKLNEEPPKEKGIRTI-----NDGKHSLITIGLOKRMWINNESVAIEGIPIPS 322
       |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
DB      1043 YDLGS-----GMASVSNONHNDDKMKS--FTLSRIKOANISTIVDTIOENEIATSS 1094
QY      323 T-----YYLGAIIP-----IAIERFINISTPAFOCGMKNL---KKTSGVRLND 362
       |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
DB      1095 SGNNGFLDLKADDKTYFGGLPTLRNLSMKAKAPEVNALKKYSGCLNDIELSRFPYNILSPD 1154
QY      363 TVGVTKKCSSEDMKLVRTLASFSRGG-QMSFTMLDVPSFDTRQOLSFGFTPOPSCGTL--- 417
       |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
DB      1155 YGVVTGKGS--LENNYTVTFSPKPGFEVLESVPVIDVGT---EINLSFSTKNESGITLLGS 1208
QY      418 -----NHQRTSSLVTLIEDGHIE--LST---RDSNIPFKSGTYMDGLLHHVS 462
       |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
DB      1209 GGTPAPPARRKRQICQAYYVILIINRGRLFEHLSTARAKKIIVIRPEPNLPHDGRHSVH 1268
QY      463 VISDTSGRLRLIDDQVLRNRQRLPSFSNAQ-OSSLRLGGG-----HFEGCISN 508
       |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
DB      1269 V-EERTGIFITQVQDENRRMYQMVLTEQPILEVAKLFVGCAPPEPQSPPLRNIPREGCIWN 1327
QY      509 VLVGRFSGSPRYLIDLASKTKKDASLGGCSLNK 541
       |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
DB      1328 LVINSVP-----MDPARPVSFKNADIGRCALOK 1355

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RESULT 9
MEMSA
 Laminin alpha-1 chain precursor - mouse
 N:Alternate names: laminin chain A1
 C:Species: Mus musculus (house mouse)
 C>Date: 30-Jun-1991 #sequence_revision 30-Jun-1991 #text_change 09-Jul-2004
 C:Accession: A31771; A30449; S00624; A30450; S08895; S02678; S01790; A30451; S14670
 R:Saeki, M.; Kleitman, H.K.; Huber, H.; Deutmann, R.; Yamada, Y.
 J. Biol. Chem. 263, 16536-16544, 1988
 A:Title: Laminin, a multidomain protein. The A chain has a unique globular domain and he
 A:Reference number: A31771; MUID:89034134; PMID:3182802

A:Accession: A31771
A:Molecule type: mRNA
A:Residues: 1-3084 <SAS>
A:Cross-references: UNIPROT:P19137; EMBL:J04064; NID:G309419; PIDDN:AAA39410.1; PID:G30949
A:Accession: A30449
A:Molecule type: protein
A:Residues: 183-195;570-571, 'A', 573-586;596-612, 'X', 614-617, 'EMK', 630-646;1217-1222, 'YFF'
2486;2624-2639;2818-2843;3009-3033, 'V', 3035 <SA2>
R:Hartl, L., Oberbaumer, I., Deutzmann, R.
R:J. Blochem. 173, 629-635, 1988
A:Title: The N terminus of laminin A chain is homologous to the B chains.
A:Reference number: S00624; MUID:8825080; PMID:3267223
A:Accession: S00624
A:Molecule type: mRNA
A:Residues: 1-208, 'T', 210-334 <HAR>
A:Cross-references: EMBL:X07737; NID:G52857; PIDDN:CAA30561.1; PID:G52858
A:Accession: A30450
A:Molecule type: protein
A:Residues: 311-335, 'N', 337-339;630-642, 'D', 644;692-724;737-748, 'X', 750-760, 'G', 762-763; 3-1389;1449-1459 <HA2>
A>Note: the sequence from Fig. 7 is inconsistent with that from Fig. 5 in having 209-116
R:Mann, K.; Deutzmann, R.; Timpl, R.
R:J. Blochem. 178, 71-80, 1988
A:Title: Characterization of proteolytic fragments of the laminin-110 complex and the
A:Reference number: S08895; MUID:89078415; PMID:2462498
A:Accession: S08895
A:Molecule type: protein
A:Residues: 153-169 <MAN>
R:Fujitawa, S.; Shinkai, H.; Deutzmann, R.; Paulsen, M.; Timpl, R.
Biochem. J. 252, 453-461, 1988
A:Title: Structure and distribution of N-linked oligosaccharide chains on various domain
A:Reference number: S02678; MUID:8832625; PMID:2458101
A:Accession: S02678
A:Molecule type: protein
A:Residues: 630-642, 'D', 644;2690-2704 <FUJ>
R:Deutzmann, R.; Huber, J.; Schmetz, K.A.; Oberbaumer, I.; Hartl, L.
Eur. J. Biochem. 177, 35-45, 1988
A:Title: Structural study of long arm fragments of laminin. Evidence for repetitive C-termin
A:Reference number: S01790; MUID:89030693; PMID:3181157
A:Accession: S01790
A:Molecule type: mRNA
A:Residues: 2538-3084 <DEU>
A:Cross-references: EMBL:X13459; NID:G55499; PIDDN:CAA1807.1; PID:G818014
A:Accession: A30451
A:Molecule type: protein
A:Residues: 1911-1929;1997-2006;2033-2045, 'X', 2047-2054, 'X', 2056-2066, 'X', 2068-2105;2120
470;2487-2498;2502-2525;2538-2557;2561-2591, 'X', 2593-2594;2600-2610;2616-2645;2648-2655
93;2898-3005, 'A', 3007-3033, 'V', 3035;3068-3083 <DE2>
A>Note: 2256-Val was also found
R:Olsen, D.; Nagayoshi, T.; Fazio, M.; Peltonen, J.; Jaakkola, S.; Sanborn, D.; Sasaki,
Lab. Invest. 60, 772-782, 1989
A:Title: Human laminin: cloning and sequence analysis of cDNAs encoding A, B1 and B2 cha
A:Reference number: A34961; MUID:8928063; PMID:2733383
A:Accession: S14670
A:Molecule type: protein
A:Residues: 2424-2433;2440-2451;2461-2467;2487-2525;2550-2557;2561-2593;2600-2610;2616-2
-2942, 'V', 2944-2964;2969-2976;2980-2993;2998-3000, 'I', 3002-3018, 'V', 3020-3034;3068-3083
C:Complex: laminins are trimers of an alpha-type, a beta-type, and a gamma-type laminin
A:Function:
A:Description: Interact with cells and with other basement membrane proteins to promote
A:Superfamily: laminin alpha-1 chain; laminin G repeat homology; laminin-type EGF-like h
A:Keywords: basement membrane; calcium binding; cell binding; coiled coil; extracellular
F:1-24/Domain: signal sequence #status predicted <SIG>
F:25-3084/Product: laminin alpha-1 chain #status predicted <MAT>
F:25-277/Domain: VI <DOM6>
F:277-331/Domain: laminin-type EGF-like homology <LE01>
F:331-401/Domain: V <DOM5>
F:401-458/Domain: laminin-type EGF-like homology <LE02>
F:458-507/Domain: laminin-type EGF-like homology <LE03>
F:507-519/Domain: laminin-type EGF-like homology <LE04>
F:519-715/Domain: laminin-type EGF-like homology #status atypical <LE05>
F:715-1166/Domain: IVD <DO4B>
F:1166-1166/Domain: IIVB <DO3B>

F:1403-1449/Domain: laminin-type EGF-like homology <LE18>
F:1452-1506/Domain: laminin-type EGF-like homology <LE19>
F:1509-1553/Domain: laminin-type EGF-like homology <LE20>
F:1554-2125/Domain: I/I, heptad repeats <DOM2>
F:2116-2120/Region: cell adhesion #status predicted
F:2126-3075/Domain: G <DOM>
F:2142-2300/Domain: laminin G repeat homology <LG1>
F:2329-2484/Domain: laminin G repeat homology <LG2>
F:2510-2676/Domain: laminin G repeat homology <LG3>
F:2534-2536/Region: cell attachment (R-G-D) motif
F:2739-2888/Domain: laminin G repeat homology <LG4>
F:2916-3073/Domain: laminin G repeat homology <LG5>
F:38,164,555,665,763,801,838,926,952,1045,1407,1579,1596,1678,1689,1717,1804,1894,1
rate (Asn) (covalent) #status predicted
F:297-305/Disulfide bonds: #status predicted

Query Match 9.2%; Score 270; DB 2; Length 3075;
Best Local Similarity 20.8%; Pred. No. 3.3e-10; Indels 116; Gaps 26;
Matches 130; Conservative 116; Mismatches 262;

7 SGVEVRLPDLLEDKY-----TSLSLFLQRPDLRENGGTEDMFVMTLGNKDS 55
2114 ASIKVASADRDICIRAYQPISTNTNLTILNKTEP-----DNLFLGSSSTS 2164
56 KQYIGAAVVDGQLTCYVNIADREAVQIDQVLTSESQEAAMDVKFQRIYQAKLN--Y 113
2165 -DELAEMERGRVAFIMDLGSGSTRLEFPDPFIDNRWHSI-----HYAREGNIGSL 2216
114 TKKATSNKPKAPAVYDLEGGSSNTL-LNLDPEDAVFYGGYPPDFELPSLRPPKGC 172
2217 VEMSSNQ-KSPFKTSKSPCTANAVLDN--NSTLMFVGLGQIKSPAVKATTHKGC 2272
173 ELDDLINENYLSLVNFKTTFNLNTEVE-PCR---RKESBDKNVEFGTGYARIPTOPNA 227
2273 GEAFNGKSGIGLWNY-----IERGKCRGCGSSQNDPSPFHDDGSGYSVKSLPA 2324
228 PEPNFIQTITQTYDRLGILFF--AENQDNFISLNIENQMLVRYKLNSEPKKGIQDTN 285
2325 TVTQIIMLFNTPSPNGILLYLGSYGRKDFLSIFLFRGRVYKMTDLGSGPTLLTDR-RYN 2383
286 DGDHSLITLIGLQKRMV---NYNERSVRIEGLI-----FDPSTVYLGGIPIA 332
2384 NGWYKIAQQRNKQGYLAVIDYVNSNKKTK-QGSETPGASSDLNLDKQPIYVGGILPSS 2442
333 IREBNFISTPAFGQCMKLNK-KTSGVRLNDIVGVTKKSEBWKLVRTASFRSGQMSPT 391
2443 RYVRBGVTTKSFVGIKMLEISRSTFDLNSYGVRKGC--LEPIRSVFLKGYIELP 2500
392 NLDVPESTRFQLSFGFQTFQPSGTL-----NHQRTSSLVLTLEDHIELST 439
2501 PKSLSPSESEWLVTFP--TTNSSGIIILALGQDVEKRGDRREAHVPFSSVWLIGNIEVHY 2558
440 RDSN-----IPIKSP-GTYMDGLHHVSVISDTSGRLILIDQ--VLRBQRRLSPFN 490
2559 NPQDGGKRLKALHAPGTGDSQANSISLVNRNRITTVQLDNNPVMKGLTVLVESKRT 2618
491 AQCGLRLG-----GHFEGCISNVLVORFSSQPEVLDLASKSTKKDASLGCC 537
Db 2619 NVSNLVVGGIPBEGGSLILTMRSFHGCIKNLIF-----NLIELDNRNSVGHQVYLDLC 2673
QY 538 SLNKKPPPL-----MLFKSPKPK 554
Db 2674 WLSERPKLAPDADSDKILREPRAF 2697

RESULT 11

T43291
laminin alpha chain - Caenorhabditis elegans
C/Species: Caenorhabditis elegans
C/Date: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 09-Jul-2004
C/Accession: T43291
R/Zhu, X.; Kuo, G.; Joh, K.; Hall, D.H.; Wadsworth, V.K.; Hutter, H.; Vogel, B.E.; Huang
submitted to the EMBL Data Library, June 1998

A/Description: Expression, function and evolution of laminin alpha chains.
A/Reference number: 222397
A/Accession: T43291
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: mRNA
A/Residues: 1-3102 <ZHU>
A/cross-references: UNIPROT:O45614; EMBL:AF074902; PIDN:AAC26793.1
A/Map position: 1
A/Note: lama1/2
C/Superfamily: laminin alpha-1 chain, laminin G repeat homology; laminin-type EGF-like h

Query Match 8.4%; Score 247; DB 2; Length 3102;
Best Local Similarity 22.1%; Pred. No. 1.5e-08;
Matches 128; Conservative 108; Mismatches 210; Indels 134; Gaps 30;

50 GNKDAKQYIGAAVVDGQLTCYVNIADREAVQIDQVLTSESQEA--MDRVKQRIYQ 107
2308 GRRTPSEHLAVEIKDKRVVHMDIGSK-----KMTNSHPINYPVSNDRVWYTHIDV 2361
108 FA---KLYNT--KEATSN--KPKAPAYDLEGG--SNTLNLDPEDAVFYGGYPPDF 157
2362 LRIGAAVVLTKAKSYDGFPRGAPVSVFVNSKXDNISFNITRGSTTIDV---TDE 2418
QY 158 ELPSRLRPPPYK-----GCIELDLINENYLSLVNFKTTFNLNTEVEPCRRKESDQY 212
Db 2419 TVASDIDGLTTHKFSIGVGLRIDEV---PLPLMSFST---TGECGATSPPKTSQRGH 2471
QY 213 FEGCTYARIPTOPNAFPNFIQTITQTYD-RGLIFF--AENQDNFISLNIENQMLVRYK 269
Db 2472 LFRDPFANVSNVSERTMSALTIVFNAPSNGLLFRGSEASGDVAIYLDGKVMFKIN 2531
QY 270 LNSEPKKGIQDTINDKQHSI-LITIGLQKRMVYNERSV---IRGE---IFD 320
Db 2532 LGGSVAELTSGNVYNDKQEHVKAIRTG---SEMYLVQVSDADFNVTIIGENTALME 2588
QY 321 PSTYLLGIPPAI-RERF-NISTPAFGQCMKLNK-----KTSGVRLN 361
Db 2589 NENHYVAGPMTLNKEVFGDINMNGFICITLVKPSQVGEILDLPHEHSGQTDSCSQVS 2648
QY 362 DRVGVTKKSEBWKLVRTASFRSGQMSPTNLDVPESTRFQLSFGFQTFQPSGTLNQT 421
Db 2649 ---GVTDK-----IIGFPGYLITTKGISDINSSTF--ASFRTRENGTILVYQS 2694
QY 422 RTSSLLVLTLED-----GHI-----ELSTRDSNIPIFSPTYMDGLLH 460
Db 2695 KIQK--VGRQSEDDGKGIAYFLRGYLVLHFGDASR--KEVTFRSHHPYNDQYHA 2751
QY 461 VSVISDTSGRLILIDQVLRNRQL--PSFNAQCSRLG-----GHF 502
Db 2752 VMEERNGKILSVKVDKEIGSQSISDETSVGTTSGRILLGFPDDLKPPNNEIPTSF 2811
QY 503 EGCISNVLV--VORFSSQPEVLDLASKSTKKDASLGCCSLN 540
Db 2812 IGCISDVFLMKRVSLEP-----KHNAQIGCMSD 2842

RESULT 12

F87908
protein T22A3.8 [imported] - Caenorhabditis elegans
C/Species: Caenorhabditis elegans
C/Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004
C/Accession: F87908; F87908
R:anonymous, The C. elegans Sequencing Consortium.
A/Title: Genome sequence of the nematode C. elegans: a platform for investigating biolog
A/Reference number: A75000; MUID:J9069613; PMID:9851916
A/Note: see websites genome.wustl.edu/gsc/C.elegans/ and www.sanger.ac.uk/Projects/C.ele
A/Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999; and
A/Accession: F87908
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-2823 <STO>

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A:Accession: E87908  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-2623 <ST2>  
C:Gene-references: GB:chr_1; PIDN:CAB03385.1; PIG:g3924881; GSPDB:GN00019; CESP:T22A3.B  
C:Genetics:  
A:Map position: 1  
A:Superfamily: laminin alpha-1 chain; laminin G repeat homology; laminin-type EGF-like h
```

Query Match 7.6%; Score 222.5; DB 2; Length 2823;

Best Local Similarity 21.7%; Pred. No. 7e+07;

Matches 119; Conservative 102; Mismatches 205; Indels 123; Gaps 28;

```
OY         50 GNKDAKDVIYGAVDQGLTCVNLGDRAEAVIQDVLTSESQAAY--MDRYKFORIYO 107  
| : : : : | : : : : | : : : : | : : : : | : : : :  
Db         2308 GRTGPSEHLAVEIRDKRVAHVHWDIGSGK-----KMITSHPINVPENDRVTHIDV 2361  
  
OY         108 PA---KLNT---KEATSN--KKAPRAYLDLGGSS--SNTLLNDPEDAVFYGGYPDPF 157  
| : : : : | : : : : | : : : : | : : : : | : : : :  
Db         2362 LRIGNAVNLVALKESYDGGEFKRGAPEVFVGNSKDNISIPNI.PGETTIDVG--TD8 2418  
  
OY         158 ELPSRLRPPEYK----GCIEELDDLNENVLSLYNKKTPTFNLTTEVEPRRRRESDXKY 212  
| : : : : | : : : : | : : : : | : : : : | : : : :  
Db         2419 TVASDIGLTTHKSGIVGLRIDEV---PLPMSPEST---TGCEGATSPPKTSQRGH 2471  
  
OY         213 FPGTGVARLPQTGNAPPFPNFQITQTVD--RGLLFF--AEQNDFEISLIEDIENLVARYK 269  
-2472 LPRDGFANYSMSVSERTMSALTVIPNAFSPNGLYFRSGEASGDVAIYANDGKWAFKN 2531  
  
OY         270 LNSEPPEKGIRDTINDGKHSH-LITIGLKLRKMINVERSVR---ISEE---IFD 320  
2532 LGGSVAELTSGQVVNYNDGKEHTVAKIRFG---SEWYLQVDSPADRFNVITGENTALNIE 2588  
  
OY         321 PSTYYLGAIPIAL-RERF-NISTPAFCMTOLK-----XTSGVRLN 361  
2589 NENVHYAGVPMTLNKFEVGINMNGFTICILITVPSQVGBLDDLPHESHOGKTDGCSQVS 2648  
  
OY         362 DWTGVTKKCSEDWKLVYTASFPSRCGWSFTMLADVSTDRLFOLFQTFOPQSGLTLNHOT 421  
2649 ----GVTDK-----IIIGPKPCGYLTRKSIDNSTPF-AFSFTRTBEGCTLVYQSS 2694  
  
OY         422 RTSSLIVLTED-----GHI-----ELSTRSNSIDLFKSPGTVMGLLHH 460  
| : : : : | : : : : | : : : : | : : : : | : : : :  
Db         2695 KLOK--VSKRDESDDKGYIAFLFRGYLVLPFGDASSR-KNAVTPRSSHPYNDQVHA 2751  
  
OY         461 VGIYSTSGRLRLIDDQVARRNQRL---PSFSMAQSRLQG-----GHF 502  
| : : : : | : : : : | : : : : | : : : : | : : : :  
Db         2752 VFMRNRGKIISVKVDDKEIGDSQGLSDETSVCITTSGRLLILGFSDDLKPNNNEIPTSF 2811  
  
OY         503 EGCIASNVLV 511  
| : : : : | : : : : | : : : : | : : : : | : : : :  
Db         2812 IGCISDVFL 2820
```

RESULT 13

T23064

hypothetical protein T22A3.8 - Caenorhabditis elegans (fragment)

C:Species: Caenorhabditis elegans

C>Date: 15-Oct-1999 #sequence_revison 15-Oct-1999 #text_change 09-Jul-2004

C:Accession: T23064; T25096

R:Barlow, K.

submitted to the EMBL Data Library, October 1997

A:Reference number: Z19669

A:Accession: T23064

A>Status: preliminary; translated from GB/EMBL/DDBJ

A:Molecule type: DNA

A:Residues: 1-2823 <WIL>

A:Cross-references UNIPROT:O45614; EMBL:AL008585; PIDN:CAA15432.1; GSPDB:GN00019; CESP:

A:Experimental source: clone H10E24

R:McMurray, A.

Submitted to the EMBL Data Library, October 1996

A:Reference number: Z19980
 A:Accession: J25096
 A:Status: preliminary; translated from GB/EMBL/DBD
 A:Molecule type: DNA
 A:Residues: 1-2823 <M12>
 A:Cross-references: EMBL:Z81125; PIDN:CAB03385.1; GSPDB:GN00019; CESP:T22A3.8
 A:Experimental source: clone T22A3
 C:Genetic8:
 A:Gene: CESP:T22A3.8
 A:Map position: 1
 A:Introns: 45/; 282/2; 312/3; 416/2; 1255/3; 1329/3; 1418/3; 1776/2; 1988/2; 2760/2
 C:Superfamily: laminin alpha-1 chain; laminin G repeat homology; laminin-type EGF-like
 Query Match 7.6%; Score 222.5; DB 2; Length 2823;
 Best Local Similarity 21.7%; Pred. No. 7e-07;
 Matches 119; Conservative 102; Mismatches 205; Indels 123; Gaps 28;
 50 GNKASXDYIGMAVVDGQLTCVYNIAGREARVQIDQVTESESGEAV--MDRVKFORVYQ 107
 Db GNKASXDYIGMAVVDGQLTCVYNIAGREARVQIDQVTESESGEAV--MDRVKFORVYQ 107
 2308 GRFQPSSEHLAVLRDKRVVVMHMDIGSK-----KATISHPINTVPSNDKRVTMHIDV 2361
 Qy 108 PA---KLNTY---KEATSN--KPRAPVYDLEGSS--SNTLLNDPBDVAVYGYGPPDF 157
 Db 2362 LRIGNAVNLVTLAKESYDGGFKPRGAPYSVVGNSKDNISFNITLPGRTTIDVG---TDR 2418
 158 ELPSRLRPPPKY----GCIELDLNENYLSLYNFKTTFNLTTEVEPCRRKESDKNY 212
 Db 2419 TVASDIDGLTTHKFGIVGRLIDEV---PLPLMSFESF---TGCEGANTSPKTSQRGH 2471
 Qy 213 FEGGVYARIPQPNAPFPNPFIQTITQTVD--RGLLF--AENQDNFISINTSDGNLMVRYK 269
 Db 2472 LFRDGFANVNSVSERTMSALTVTIFNPFSPNGILYFRGSEASGDFVALYINDGKVMFKIN 2531
 Qy 270 LNSPPPEKGIKRDITNDGKDSI-LITIGKLOKEMWIMVNSVSR---IEGR---IFD 320
 Db 2532 LGGSVAELTSSQNYVNDGKHTVAKIRG---SEMYLOVSDADRNVTIVGTETALNIE 2588
 Qy 321 FSTYILGIGIPAI--REPP-NISTPAFOGCMENLK-----KTSGVRLN 361
 Db 2589 NENHYVAGVPMTLNKEVFGDINMANGFICILITVXPQVGLDLDHPEHSQKTDGCSQVS 2648
 Qy 362 DTQVTVTKKCSMDKLVLTAFSPRGQMSFTMLDVPSIDRFDLSGFGQFQFSGTLLNQT 421
 Db 2649 ---EVTJK-----IIGPKFGYLTIGKISIDNSTF--AFSPFRRENGTLVYQSS 2694
 Qy 422 RTSLLVTLVD-----GHI-----ELSTRDSNIPIFKSPGYMDGLLH 460
 Db 2695 KLGK--VSKDSEDDGKGYLNFYLRGVLVHPKDASSR--KEVVTFRSSHNPYNDGQVHA 2751
 Qy 461 VSVISDTSGLRLIIDQVLRNQLR---PSFSNAQQSILRG-----GHP 502
 Db 2752 VFMERNGKLTISVKYDDKEIGDSQSLSDETSIGTSGRLILGGSFDDLPKPNNRKIPITSFF 2811
 Qy 503 EGCISNLY 511
 Db 2812 IGCISDVFL 2820
 RESULT 14
 A48216
 neurexin III-alpha secreted type 1 precursor - rat
 C:Species: Rattus norvegicus (Norway rat)
 C:Date: 26-May-1994 #sequence_revision 26-May-1994 #text_change 09-Dec-2002
 C:Accession: A48216; B48216
 R:ushkaryov, V.A.; Suedhof, T.C.
 Proc. Natl. Acad. Sci. U.S.A. 90, 6410-6414, 1993
 A>Title: Neurexin IIIalpha: extensive alternative splicing generates membrane-bound and
 A:Accession: A48216
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-1438 <USH>
 A:Cross-references: GB:LI4851

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: February 22, 2005, 08:07:29 ; Search time 95.5943 Seconds
(without alignments)
3026.590 Million cell updates/sec

Title: US-10-817-423-4

Perfect score: 2940

Sequence: 1 MRFNGKSGVRLPNDLEDL.....MLFKSPKRRFKRIENVNQL 565

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

UniProt 03:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	2940	100.0	1725	2	P70570	P70570 ratu
2	2704	92.0	3333	2	LM43_MOUSE	Q61789 mus musculu
3	2441	83.0	1668	2	Q6VU69	Q6VU69 homo sapien
4	2441	83.0	3277	2	Q6VU67	Q6VU67 homo sapien
5	2439	83.0	3333	2	Q6VU68	Q6VU68 homo sapien
6	2439	83.0	1713	1	LM43_HUMAN	Q16787 homo sapien
7	2439	83.0	1806	2	Q96TG0	Q96TG0 homo sapien
8	2439	83.0	3333	2	Q76B14	Q76B14 homo sapien
9	2224.5	75.7	1725	2	Q867A1	Q867A1 canis fami
10	712	24.2	3695	1	LM45_HUMAN	O15230 homo sapien
11	712	24.2	3695	2	Q8TD8	Q8TD8 homo sapien
12	685	23.3	1816	1	LM44_HUMAN	O15363 homo sapien
13	685	23.3	1254	2	Q91V70	Q91V70 mus musculu
14	685	23.3	1816	1	LM44_MOUSE	P97927 mus musculu
15	681	23.2	1524	2	Q6ZQX1	Q6ZQX1 mus musculu
16	681	23.2	3718	1	LM45_MOUSE	Q61001 mus musculu
17	492.5	16.8	670	2	Q9BT3	Q9BT3 homo sapien
18	395	13.4	3712	1	LM4 DROME	O00174 drosophila
19	395	13.4	3712	2	Q9VW0	Q9VW0 drosophila
20	359	12.2	3616	2	Q7PP9	Q7PP9 anopheles g
21	326	10.1	794	2	Q8R377	Q8R377 mus musculu
22	302	10.3	3106	1	LM42_MOUSE	Q60675 mus musculu
23	298.5	10.2	1518	2	Q21442	Q21442 caenorhabdi
24	298.5	10.2	3672	1	LM42_CAEEL	Q21313 caenorhabdi
25	298.5	10.2	3704	2	P919F4	P919F4 caenorhabdi
26	294	10.0	3110	1	LM42_HUMAN	P24043 homo sapien
27	285.5	9.7	858	2	Q8R145	Q8R145 mus musculu
28	280	9.5	3084	1	LM41_MOUSE	P19137 mus musculu
29	270	9.2	3075	1	LM41_HUMAN	P25391 homo sapien
30	247	8.4	3102	2	Q45614	Q45614 caenorhabdi
31	219.5	7.5	1247	2	Q7PT06	Q7PT06 anopheles g

32	216	7.3	1392	2	Q81UE3	Q81UE3 homo sapien
33	213.5	7.3	1541	1	NX3A_HUMAN	Q94C00 homo sapien
34	213	7.2	3375	2	Q81P51	Q81P51 drosophila
35	212.5	7.2	1203	2	Q6Z056	Q6Z056 mus musculu
36	212.5	7.2	1587	2	Q6P9K9	Q6P9K9 mus musculu
37	207.5	7.1	1363	1	NX1A_CHICK	Q9DD00 gallus gall
38	204.5	7.0	1514	2	NX1A_RAT	Q63372 ratu
39	200	6.8	1530	1	Q8CHE6	Q8CHE6 mus musculu
40	199.5	6.8	1530	2	NX1A_BOVIN	Q8146 bos taurus
41	198	6.7	1176	2	Q80Y87	Q80Y87 mus musculu
42	197	6.7	1560	2	Q18291	Q18291 caenorhabdi
43	196	6.7	1477	1	NX1A_HUMAN	Q9UBI1 homo sapien
44	196	6.7	3367	2	Q9XZC9	Q9XZC9 drosophila
45	195.5	6.6	747	2	Q7Z5W6	Q7Z5W6 homo sapien

ALIGNMENTS

RESULT 1	ID	PRELIMINARY	PRT	1725 AA.
P70570	P70570			
AC	P70570			
DT	01-FEB-1997 (TREMBLrel. 02, Created)			
DT	01-FEB-1997 (TREMBLrel. 02, Last sequence update)			
DT	01-MAR-2004 (TREMBLrel. 26, Last annotation update)			
DE	Laminin-5 alpha 3 chain.			
OS	Rattus norvegicus (Rat).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.			
OX	NCBI_Taxid=10116;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=97081969; PubMed=8923212;			
RA	Baker S.E., Hopkinson S.B., Fitchman M., Andreason G.L., Frasier F.,			
RA	Plopper G., Quaranta V., Jones J.C.R.,			
RT	"Laminin-5 and hemidesmosomes: role of the alpha 3 chain subunit in			
RT	hemidesmosome stability and assembly."			
RL	U. Cell Sci. 109:2509-2520 (1996).			
DR	EMBL; U61261; AAB17053.1; -.			
DR	HSP; P35070; 11P0.			
DR	GO; GO:0005606; C:laminin-1; IEA.			
DR	GO; GO:0005102; F:receptor binding; IEA.			
DR	GO; GO:0005198; F:structural molecule activity; IEA.			
DR	GO; GO:0030155; P:regulation of cell adhesion; IEA.			
DR	GO; GO:0030334; P:regulation of cell migration; IEA.			
DR	GO; GO:0045995; P:regulation of embryonic development; IEA.			
DR	InterPro: IPR008985; Cona 1 like_1ec_g1.			
DR	InterPro: IPR006209; EGF like.			
DR	InterPro: IPR002049; Laminin_EGF.			
DR	InterPro: IPR001791; Laminin_G.			
DR	InterPro: IPR009254; Laminin_I.			
DR	InterPro: IPR010307; Laminin_II.			
DR	InterPro: IPR003129; TSP N.			
DR	Pfam; PF00053; Laminin_EGF; 2.			
DR	Pfam; PF02210; Laminin_G_2; 4.			
DR	Pfam; PF06008; Laminin_I; 1.			
DR	Pfam; PF06009; Laminin_II; 1.			
DR	SMART; SM00180; EGF Lam; 2.			
DR	SMART; SM00282; LamG; 5.			
DR	PROSITE; PS00022; EGF 1; 1.			
DR	PROSITE; PS01186; EGF 2; 1.			
DR	PROSITE; PS01248; LAMININ_TYPE_EGF; 2.			
DR	PROSITE; PS50025; LAM_G_DOMAIN; 5.			
KW	Laminin EGF-like domain.			
SO	SEQUENCE 1725 AA; 190392 MW; 02BE43B3E72B0FB CRC64;			
Query Match	100.0%;	Score 2940;	DB 2;	Length 1725;
Best Local Similarity	100.0%;	Pred. No. 2.7e-191;		
Matches	565;	Conservative 0;	Mismatches 0;	Indels 0;
		Gaps 0;		
QY	1 MRFNGKSGVRLPNDLEDLKGYTSLFLPQRLRENGSTEDMFVYTLGNKQASXDYIG 60			

Db 782 MRFNGSGVEVRLLPNDLEDKGYTSLSLFLQRPDLBENGSTEDMPVWYIGNKDASRDYIG 841
 Qy 61 MAVVDQQLTCVYNIADGREAREVQIDQVLTSESESOEAVMDRVKFORIYQFAKNTYKKAETS 120
 Db 842 MAVVDQQLTCVYNIADGREAREVQIDQVLTSESESOEAVMDRVKFORIYQFAKNTYKKAETS 901
 Qy 121 KPRAPAVYDLEGSSNTLNLDPEDAVFYVGYGYPDPPELPSRLRFPYKGCITLIDLINEN 180
 Db 902 KPRAPAVYDLEGSSNTLNLDPEDAVFYVGYGYPDPPELPSRLRFPYKGCITLIDLINEN 961
 Qy 181 VLSLVNFKTPTNLTVEVPCRRKESDKNVEFGTYARIPTQPNAPFPNFQITQTV 240
 Db 962 VLSLVNFKTPTNLTVEVPCRRKESDKNVEFGTYARIPTQPNAPFPNFQITQTV 1021
 Qy 241 DRGLTFPFAENQDNFISLNTEDGNLMVRYKLNSEPKKGRDPTINGKHSILITIGKQ 300
 Db 1022 DRGLTFPFAENQDNFISLNTEDGNLMVRYKLNSEPKKGRDPTINGKHSILITIGKQ 1081
 Qy 301 KRWIVNNEKSVRIEGEIPFSTYYIAGTPIAIRERPNISTPAFQCGMKXLTGTVRL 360
 Db 1082 KRWIVNNEKSVRIEGEIPFSTYYIAGTPIAIRERPNISTPAFQCGMKXLTGTVRL 1141
 Qy 361 NDTVGYTKCSBEMKLVRTASPSRGGMSFTNLDVSTDRPOLSPRGQTFPQSGTLLNQ 420
 Db 1142 NDTVGYTKCSBEMKLVRTASPSRGGMSFTNLDVSTDRPOLSPRGQTFPQSGTLLNQ 1201
 Qy 421 TRTSSLVLTLEDGHIESTDSNIPIFKSPGYMDGLMHSVYSIPSGRLTIDQVLR 480
 Db 1202 TRTSSLVLTLEDGHIESTDSNIPIFKSPGYMDGLMHSVYSIPSGRLTIDQVLR 1261
 Qy 481 RNORLPSFNAQOSLRIGGHEGCTISNVLVORPSQSEVLDIASSTKXKASLGCCSIN 540
 Db 1262 RNORLPSFNAQOSLRIGGHEGCTISNVLVORPSQSEVLDIASSTKXKASLGCCSIN 1321
 Qy 541 KPPLMLFKSPKRFNGRIFNVOQL 565
 Db 1322 KPPLMLFKSPKRFNGRIFNVOQL 1346
 Qy 565 KPPLMLFKSPKRFNGRIFNVOQL 565
 Db 1346 KPPLMLFKSPKRFNGRIFNVOQL 1346
 RESULT 2
 LMA3 MOUSE STANDARD; PRT; 3333 AA.
 ID LMA3 MOUSE STANDARD; PRT; 3333 AA.
 AC 061789; 008751; Q61788; Q61966; Q9JHQ7;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DB Laminin alpha-3 chain precursor (Nicotin alpha subunit).
 GN Name=Lama3;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxId=10090;
 RN [1]
 RP SEQUENCE OF 1-58 FROM N.A., AND SEQUENCE OF 32-38.
 RX MEDLINE=97296337; PubMed=9151674; DOI=10.1083/jcb.137.3.685;
 RA Miner J.H., Paton B.L., Lentz S.I., Gilbert D.J., Snider W.D.,
 RA Jenkins N.A., Copeland N.G., Sane J.R.,
 RT "The laminin alpha chains: expression, developmental transitions, and
 RT chromosomal locations of alpha1-5, identification of heterotrimeric
 RT laminin 8-11, and cloning of a novel alpha3 isoform.",
 RL J. Cell Biol. 137:685-701(1997).
 RN [3]
 RP SEQUENCE FROM N.A. (ISOFORM A), AND SEQUENCE OF 716-3284 FROM N.A.
 RP (ISOFORM B).

RC STRAIN=BALE/c; TISSUE=Lung;
 RX MEDLINE=95394948; PubMed=7665604; DOI=10.1074/jbc.270.37.21820;
 RA Galliano M.-F., Aberdam D., Aguzzi A., Ortome J.-P., Meneguzzi G.,
 RT "Cloning and complete primary structure of the mouse laminin alpha 3
 RT chain. Distinct expression pattern of the laminin alpha 3A and alpha
 RT 3B chain isoforms.",
 RL J. Biol. Chem. 270:21820-21826(1995).
 RN [4]
 RP REVISIONS.
 RA Aberdam D.;
 RL Submitted (Apr-1997) to the EMBL/Genbank/DBJ databases.
 RN [5]
 RP SEQUENCE OF 1767-2485 FROM N.A.
 RX TISSUE=Lung;
 RC MEDLINE=94281750; PubMed=8012114;
 RA Aberdam D., Galliano M.-F., Mattei M.-G., Pisani-Spadefora A.,
 RA Ortome J.-P., Meneguzzi G.,
 RT "Assignment of mouse niclein genes to chromosomes 1 and 18",
 RL Mamm. Genome 5:229-233(1994).
 RN [6]
 RP SEQUENCE OF 1767-2485 FROM N.A.
 RC TISSUE=Lung;
 RX MEDLINE=94363405; PubMed=8081886;
 RA Aberdam D., Aguzzi A., Baudoin C., Galliano M.-F., Ortome J.-P.,
 RA Meneguzzi G.,
 RT "Developmental expression of niclein adhesion protein (laminin-5)
 RT subunits suggests multiple morphogenic roles",
 RL Cell Adhes. Commun. 2:115-129(1994).
 CC -1- FUNCTION: Binding to cells via a high affinity receptor, laminin
 CC is thought to mediate the attachment, migration and organization
 CC of cells into tissues during embryonic development by interacting
 CC with other extracellular matrix components.
 CC -1- FUNCTION: Laminin-5 is thought to be involved in (1) cell adhesion
 CC via integrin alpha-3/beta-1 in focal adhesion and integrin alpha-
 CC 6/beta-4 in hemidesmosomes, (2) signal transduction via tyrosine
 CC phosphorylation of p125-FAK and p80, (3) differentiation of
 CC keratinocytes (by similarity).
 CC -1- SUBUNIT: Laminin is a complex glycoprotein, consisting of three
 CC different polypeptide chains (alpha, beta, gamma), which are bound
 CC to each other by disulfide bonds into a cross-shaped molecule
 CC comprising one long and three short arms with globules at each
 CC end. The alpha-3 chain is a subunit of laminin-5
 CC (epiligrin/kalinin/niclein), and possibly also a component of
 CC laminin-6 (K-laminin) and laminin-7 (KS-laminin).
 CC -1- SUBCELLULAR LOCATION: Extracellular; found in the basement
 CC membranes (major component).
 CC -1- ALTERNATIVE PRODUCTS:
 CC Name=A;
 CC Name=B;
 CC Name=C;
 CC IsoId=Q61789-1; Sequence=Displayed;
 CC Name=A;
 CC IsoId=Q61789-2; Sequence=VSP_003038, VSP_003039;
 CC -1- TISSUE SPECIFICITY: Basal membrane of the upper alimentary tract
 CC and urinary and nasal epithelia, salivary glands and teeth (both
 CC variants). Isoform A is predominantly expressed in skin, hair
 CC follicles and developing neurons of the trigeminal ganglion.
 CC Isoform B was found in bronchi, alveoli, stomach, intestinal
 CC crypts, whisker pads, CNS, telencephalic neuroectoderm, thalamus,
 CC Rathke's pouch and periventricular subependymal germinal layer.
 CC -1- DOMAIN: The alpha-helical domains I and II are thought to interact
 CC with other laminin chains to form a coiled coil structure.
 CC -1- DOMAIN: Domains IV and G are globular.
 CC -1- SIMILARITY: Contains 15 laminin BGP-like domains.
 CC -1- SIMILARITY: Contains 5 laminin G-like domains.
 CC -1- SIMILARITY: Contains 1 laminin IV domain.
 CC -1- SIMILARITY: Contains 1 laminin N-terminal domain.
 CC This SWISS-PROT entry is copyrighted. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>)

CC or send an email to license@lsb-sib.ch).

CC EMBL: AJ293592; CAB9254.2; -
DR EMBL: U86353; AAC5179.1; -
DR EMBL: X84014; CAAS6837.1; -
DR EMBL: X84013; CAAS6836.1; ALT_FRAME.
DR EMBL: L20478; AAAS68091.1; -
DR HSSP: P02468; INPE.
DR MGD; MGT.99909; Lama3.
DR GO; GO:0005604; C:basement membrane; IDA.
DR InterPro; IPR008985; Cona_like_1ec_g1.
DR InterPro; IPR006209; EGF_like.
DR InterPro; IPR008979; Gal_bind_like.
DR InterPro; IPR009030; Grow_fac_recept.
DR InterPro; IPR008212; Lam_N2.
DR InterPro; IPR000034; Laminin_B.
DR InterPro; IPR002049; Laminin_EGF.
DR InterPro; IPR01791; Laminin_G.
DR InterPro; IPR009254; Laminin_I.
DR InterPro; IPR010307; Laminin_II.
DR InterPro; IPR008211; Laminin_N.
DR InterPro; IPR003129; TSP_N.
DR Pfam; PF00052; Laminin_B; 1.
DR Pfam; PF00053; Laminin_G; 3.
DR Pfam; PF00054; Laminin_I; 1.
DR Pfam; PF06008; Laminin_II; 1.
DR Pfam; PF06009; Laminin_III; 1.
DR Pfam; PF00055; Laminin_N; 1.
DR PRINTS; PR00011; EGF_LAMININ.
DR ProDom; PD003031; Laminin_B; 1.
DR PROSITE; PS00023; EGF_1; 10.
DR PROSITE; PS01186; EGF_2; 1.
DR PROSITE; PS00025; LAM_G_DOMAIN; 5.
DR PROSITE; PS01248; LAMININ_TYPE_EGF; 10.
DR Alternative Splicing; Basement membrane; Cell adhesion; Coiled coil;
KM Direct protein sequencing; Extracellular matrix; Glycoprotein;
Laminin EGF-like domain; Repeat; Signal.
PT SIGNAL 1 31
FT CHAIN 32 3333 Laminin alpha-3 chain.
FT DOMAIN 32 294 Laminin N-terminal (domain VI).
FT DOMAIN 295 725 Domain V.
FT DOMAIN 296 350 Laminin EGF-like 1.
FT DOMAIN 353 420 Laminin EGF-like 2.
FT DOMAIN 423 464 Laminin EGF-like 3.
FT DOMAIN 488 530 Laminin EGF-like 4.
FT DOMAIN 533 576 Laminin EGF-like 5.
FT DOMAIN 582 625 Laminin EGF-like 6.
FT DOMAIN 628 678 Laminin EGF-like 7.
FT DOMAIN 681 725 Laminin EGF-like 8.
FT DOMAIN 793 1262 Laminin domain IV 1 (domain IV B).
FT DOMAIN 1263 1464 Domain III B.
FT DOMAIN 1310 1353 Laminin EGF-like 9.
FT DOMAIN 1354 1403 Laminin EGF-like 10.
FT DOMAIN 1404 1454 Laminin EGF-like 11.
FT DOMAIN 1455 1464 Laminin EGF-like 12 (N-terminal).
FT DOMAIN 1465 1653 Laminin domain IV (domain IV A).
FT DOMAIN 1654 1821 Domain III A.
FT DOMAIN 1654 1821 Laminin EGF-like 12 (C-terminal).
FT DOMAIN 1687 1733 Laminin EGF-like 13.
FT DOMAIN 1734 1786 Laminin EGF-like 14.
FT DOMAIN 1787 1821 Laminin EGF-like 15 (incomplete).
FT DOMAIN 1822 2388 Domain II and I.
FT DOMAIN 2389 2590 Laminin G-like 1.
FT DOMAIN 2597 2759 Laminin G-like 2.
FT DOMAIN 2766 2926 Laminin G-like 3.
FT DOMAIN 2986 3150 Laminin G-like 4.
FT DOMAIN 3157 3330 Laminin G-like 5.
FT DOMAIN 1854 1983 Coiled coil (Potential).
FT DOMAIN 2015 2060 Coiled coil (Potential).
FT DOMAIN 2091 2168 Coiled coil (Potential).
FT DOMAIN 2214 2241 Coiled coil (Potential).
FT DOMAIN 2321 2386 Coiled coil (Potential).
PT SITE 2277 2279 Cell attachment site (Potential).

PT DISULFID 1310 1317 By similarity.
PT DISULFID 1312 1324 By similarity.
PT DISULFID 1326 1335 By similarity.
PT DISULFID 1338 1351 By similarity.
PT DISULFID 1354 1369 By similarity.
PT DISULFID 1356 1376 By similarity.
PT DISULFID 1378 1387 By similarity.
PT DISULFID 1390 1401 By similarity.
PT DISULFID 1404 1416 By similarity.
PT DISULFID 1406 1423 By similarity.
PT DISULFID 1425 1434 By similarity.
PT DISULFID 1437 1452 By similarity.
PT DISULFID 1687 1696 By similarity.
PT DISULFID 1689 1703 By similarity.
PT DISULFID 1706 1715 By similarity.
PT DISULFID 1718 1731 By similarity.
PT DISULFID 1734 1746 By similarity.
PT DISULFID 1736 1755 By similarity.
PT DISULFID 1757 1766 By similarity.
PT DISULFID 1769 1784 By similarity.
PT DISULFID 1822 1822 Interchain (Probable).
PT DISULFID 1825 1825 Interchain (Probable).

Query Match 92.0%; Score 2704; DB 1; Length 3333;
Best local Similarity 92.2%; Pred. No. 8.3e-175;
Matches 521; Conservative 15; Mismatches 29; Indels 0; Gaps 0;

QY 1 MRFNGSGVVRRLPNLDLKDGYTSLSLFQRPDLRENGTDMFYNYLGNKASXDYIG 60
DB 2390 MRFNGSGVVRRLPNLDLKDGYTSLSLFQRPDLRENGTDMFYNYLGNKASXDYIG 2449

QY 61 MAVVDQGLTCVNLGSRBAVQIDVLTSESGEAVMDRKPQRIYQAFALNTKRTSN 120
DB 2450 MAVVDQGLTCVNLGSRBAVQIDVLTSESGEAVMDRKSQRIYQAFALNTKRTST 2509

QY 121 KPRAPAVYDLGGSSNTLNLDPEDAVFYVGGYPPDFELPSRLRFPYKGCIELDLNEN 180
DB 2510 KPRAPAVYDLGGSSNTLNLDPEDAVFYVGGYPPDFELPSRLRFPYKGCIELDLNEN 2569

QY 181 VLSLYNFKTTFNLTTEVEPCRRKKESDKNVEGTGYARIPIQPNAPFNFYIQTQTV 240
DB 2570 VLSLYNFKTTFNLTTEVEPCRRKKESDKNVEGTGYARIPIQPNAPFNFYIQTQTV 2629

QY 241 DRGLTFPABNDPFIANTEDGMLRYKLNSEPPKRGIRDTINGKHSILITGKQ 300
DB 2630 DRGLTFPABNDPFIANTEDGMLRYKLNSEPPKRGIRDTINGKHSILITGKQ 2689

QY 301 KRWMINVNSRVLEGGIPDPSTYYLGGPIAIRERFNIPTPAFGCMKUKTSGVRL 360
DB 2690 KRWMINVNSRVLEGGIPDPSTYYLGGPIAIRERFNIPTPAFGCMKUKTSGVRL 2749

QY 361 NDTVGYTKKCSSEDMKLVRTASFSRGGMSFTNLDPVSTDRFQSLFGFTQPSGTLNHQ 420
DB 2750 NDTVGYTKKCSSEDMKLVRTASFSRGGMSFTNLDPVSTDRFQSLFGFTQPSGTLNHQ 2809

QY 421 TRTSSLLVYTEDGHISTDSNIPYFKSGGTMGILHNVYSISTSGRLIIDQVLR 480
DB 2810 TRTSSLLVYTEDGHISTDSNIPYFKSGGTMGILHNVYSISTSGRLIIDQVLR 2869

QY 481 RNRLRPSFNAQOSSLRGGHFEGCISNVYVORFSOSPEVLDLASKSTKQDASIGGCSLN 540
DB 2870 RNRLRPSFNAQOSSLRGGHFEGCISNVYVORFSOSPEVLDLASKSTKQDASIGGCSLN 2929

QY 541 KPPEFLMFKSPKRFNKRIFNVQL 565
DB 2930 KPPEFLMFKSPKRFNKRIFNVQL 2954

RESULT 3
Q6VU69 PRELIMINARY; PRT; 1668 AA.
AC Q6VU69;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)

```

DT 05-JUL-2004 (TrEMBLrel. 27, last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, last annotation update)
DE Laminin alpha 3 splice variant a.
GN Name=LAMA3;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22833568; PubMed=12915477; DOI=10.1093/hmg/ddg234;
RA McLean W.H., Irvine A.D., Hamill K.J., Whitlock N.V.,
RA Coleman-Campbell C.M., Mellerio J.B., Ashton G.S.,
RA Dopping-Hepenstal P.J., Bady R.A., Jamil T., Phillips R.J.,
RA Shabbir S.G., Haroon T.S., Khurehd K., Moore J.B., Page B.,
RA Darling J., Atherton D.J., Van Steensel M.A., Munro C.S., Smith F.J.,
RA McGrath J.A.;
RT "An unusual N-terminal deletion of the laminin (alpha)3a isoform leads
RT to the chronic granululation tissue disorder laryngo-oncho-cutaneous
RT syndrome.";
RL Hum. Mol. Genet. 12:2395-2409(2003).
RN [2]
RP SEQUENCE FROM N.A.
RA McLean W.H.I.;
RL Submitted (JUN-2003) to the EMBL/Genbank/DBJ databases.
DR EMBL; AY327114; AAQ72569.1; -.
DR GO; GO:0005606; C:lamlnin-1; IEA.
DR GO; GO:0005102; F:receptor binding; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR GO; GO:0030155; F:regulation of cell adhesion; IEA.
DR GO; GO:0030334; P:regulation of cell migration; IEA.
DR GO; GO:0045995; P:regulation of embryonic development; IEA.
DR InterPro; IPR001844; Chapman Cpn60.
DR InterPro; IPR008985; Cona_1like_1ec_g1.
DR InterPro; IPR006209; EGF_like.
DR InterPro; IPR002049; Laminin_EGF.
DR InterPro; IPR001791; Laminin_G.
DR InterPro; IPR009254; Laminin_I.
DR InterPro; IPR010307; Laminin_II.
DR InterPro; IPR003129; TSP_N.
DR Pfam; PF00053; Laminin_EGF; 1.
DR Pfam; PF02210; Laminin_G_2; 4.
DR Pfam; PF06008; Laminin_I; 1.
DR Pfam; PF06009; Laminin_II; 1.
DR SMART; SM00180; EGF_Lam; 2.
DR SMART; SM00282; LamG; 5.
DR PROSITE; PS00226; CHAPERONINS_CPN60; UNKNOWN_1.
DR PROSITE; PS01022; EGF_1; 1.
DR PROSITE; PS01186; EGF_2; 1.
DR PROSITE; PS01248; LAMININ_TYPE_EGF; 2.
DR PROSITE; PS50025; LAM_G_DOMAIN; 5.
KW Laminin EGF-like domain.
SQ
SEQUENCE 1668 AA; 184053 MW; 9EBFF5C45637645C CRC64;

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Query Match 83.0%; Score 2441; DB 2; Length 1668;
Best Local Similarity 81.9%; Pred. No. 2,7e-157;
Matches 463; Conservative 47; Mismatches 55; Indels 0; Gaps 0;

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QY 1 MRNNGSGVVRRLPNLEDEIKGTYSLSLFLQRPDLKENGTEIMFVMTLGNKASADYIG 60
DB 726 MRNNGSGVVRRLPNLEDEIKGTYSLSLFLQRPDSRENGCTEMMFVMTLGNKASADYIG 785
QY 61 MAVVDGQLTCVNMAGDREAEVQIDQVLTSSRSQBAWDRYKFORIYOPAKLNTYTKATSN 120
DB 786 MAVVDGQLTCVNMAGDREAEVQIDQVLTSSREAEVMDRVKFORIYOPAKLNTYTKATSN 845
QY 121 KPRAPAVYDLEGGSSNTLNTLDPEDAVFYVGYGPPPELPSRLRFPYKGCIELDLNEN 180
DB 846 KPETPGVYDMDGNSNTLNLDPENVYFYVGYGPPPEKLPKLSRSLSPFYKGCIELDLNEN 905
QY 181 VLSLNYFKTTFNLTTEVEECRRRKESDKNYFEGTGYARIPTQPNAPFPNFIQTITTV 240
DB 906 VLSLNYFKTTFNLTTEVEECRRRKESDKNYFEGTGYARVPTQPNAPFPNFIQTITTV 965

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QY 241 DRGLFPAENODNFISLNIIBDGNLWRYKLSNBPPEKGIKRTINDGKHSILITIGLQ 300
DB 966 DRGLFPAENODNFISLNIIBDGNLWRYKLSNBPPEKGIKRTINDGKHSILITIGLQ 1025
QY 301 KRMWNNVRSVRIBGELFDFSTYLLGGIPAIARERFNIISPAPGCKNLKKTSGVRL 360
DB 1026 KRMWNNVRSVRIBGELFDFSTYLLGGIPAIARERFNIISPAPGCKNLKKTSGVRL 1085
QY 361 NDTGVVTKKSGEDWTLVTTASPSRGGQMSFTNLDPVSTDRPOLSTGRPTPQSGTLNHQ 420
DB 1086 NDTGVVTKKSGEDWTLVTTASPSRGGQMSFTNLDPVSTDRPOLSTGRPTPQSGTLNHQ 1145
QY 421 TTSLSLVTLEBGEHIELSTRDSNTEIPFKSPGYMDGLAHVYSISDTSGRLTIDQVLR 480
DB 1146 TTSLSLVTLEBGEHIELSTRDSNTEIPFKSPGYMDGLAHVYSISDTSGRLTIDQVLR 1205
QY 481 RNQRLPSFSMAQGSRLRGHFEQGISNVLVQRPSPQSPFVLDLASKSTPKDASLGGCSLN 540
DB 1206 NSKRLKHISRSQSLRLGSGNPEGCSINVFQRLSLSPVLDLTSNLSKRVSLGGCSLN 1265
QY 541 KPPFLMLFKSPRRKGRIFNVNOL 565
DB 1266 KPPFLMLFKSTFRNKTFRINOL 1290

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RESULT 4

PRELIMINARY; PRT; 3277 AA.

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ID 06VU67
AC 06VU67,
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, last annotation update)
DE Laminin alpha 3 splice variant b2.
GN Name=LAMA3;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22833568; PubMed=12915477; DOI=10.1093/hmg/ddg234;
RA McLean W.H., Irvine A.D., Hamill K.J., Whitlock N.V.,
RA Coleman-Campbell C.M., Mellerio J.B., Ashton G.S.,
RA Dopping-Hepenstal P.J., Bady R.A., Jamil T., Phillips R.J.,
RA Shabbir S.G., Haroon T.S., Khurehd K., Moore J.B., Page B.,
RA Darling J., Atherton D.J., Van Steensel M.A., Munro C.S., Smith F.J.,
RA McGrath J.A.;
RT "An unusual N-terminal deletion of the laminin (alpha)3a isoform leads
RT to the chronic granululation tissue disorder laryngo-oncho-cutaneous
RT syndrome.";
RL Hum. Mol. Genet. 12:2395-2409(2003).
RN [2]
RP SEQUENCE FROM N.A.
RA McLean W.H.I.;
RL Submitted (JUN-2003) to the EMBL/Genbank/DBJ databases.
DR EMBL; AY327116; AAQ72571.1; -.
DR GO; GO:0005578; C:extracellular matrix (sensu Metazoa); IEA.
DR GO; GO:0005606; C:lamlnin-1; IEA.
DR GO; GO:0005198; F:receptor binding; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR GO; GO:0030155; F:regulation of cell adhesion; IEA.
DR GO; GO:0030334; P:regulation of cell migration; IEA.
DR GO; GO:0045995; P:regulation of embryonic development; IEA.
DR InterPro; IPR001844; Chapman Cpn60.
DR InterPro; IPR008985; Cona_1like_1ec_g1.
DR InterPro; IPR006209; EGF_like.
DR InterPro; IPR008979; EGF_bind_1like.
DR InterPro; IPR006210; IKGf.
DR InterPro; IPR000034; Laminin_B.
DR InterPro; IPR002049; Laminin_EGF.
DR InterPro; IPR001791; Laminin_G.
DR InterPro; IPR009254; Laminin_I.

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DR InterPro: IPR010307; Laminin II.
 DR InterPro: IPR008211; Laminin N.
 DR InterPro: IPR003129; TSP_N.
 DR Pfam: PF00052; Laminin_B; 1.
 DR Pfam: PF00053; Laminin_EGF; 8.
 DR Pfam: PF02210; Laminin_G_2; 4.
 DR Pfam: PF06008; Laminin_I_1.
 DR Pfam: PF06009; Laminin_I_1.
 DR Pfam: PF00055; Laminin_N; 1.
 DR PRINTS: PR00011; EGF_LAMININ.
 DR PRODOM: PD003031; Laminin_B; 1.
 DR SMART: SM00181; EGF; 8.
 DR SMART: SM00180; EGF; 14.
 DR SMART: SM00281; Lamb; 1.
 DR SMART: SM00282; Lamb; 5.
 DR SMART: SM00136; Lamnt; 1.
 DR PROSITE: PS00296; CHAPERONINS_CPN60; UNKNOWN_1.
 DR PROSITE: PS00022; EGF_1; 12.
 DR PROSITE: PS01166; EGF_2; 1.
 DR PROSITE: PS01248; LAMININ_TYPE_EGF; 13.
 DR PROSITE: PS50025; LAM_G_DOMAIN; 5.
 DR Laminin EGF-like domain.
 SQ SEQUENCE 3277 AA; 360209 MW; 3ACFE9983571228 CRC64;

Query Match 83.0%; Score 2441; DB 2; Length 3277;
 Best Local Similarity 81.9%; Pred. No. 6.9e-157;
 Matches 463; Conservative 47; Mismatches 55; Indels 0; Gaps 0;

QY 1 MRFNGSGVVRPLPNDLEDKGYTSLFLQRPDLRNGGTEDMFVYILGNKQASKDYIG 60
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 QY 61 MAVVDGQLTGVYVNGDEAREAVQIDVLTSESGEAVNDKRYKFORIYQPAKANTYKATSN 120
 DB 2395 MAVVDGQLTGVYVNGDEAREAVQIDVLTSESGEAVNDKRYKFORIYQPAKANTYKATSN 2454
 QY 121 KPRKAPVYDLEGSSNTLNLNDPEDAVFYGGYPPDELSRLRFPYKCIHELDDLEN 180
 DB 2455 KPRKAPVYDLEGSSNTLNLNDPEDAVFYGGYPPDELSRLRFPYKCIHELDDLEN 2514
 QY 181 VLSLYNFKTFLNLTTEVEPCRRKESDKNYFEGTGYARLPQPNAPFPNFIQTIQTV 240
 DB 2515 VLSLYNFKTFLNLTTEVEPCRRKESDKNYFEGTGYARLPQPNAPFPNFIQTIQTV 2574
 QY 241 DRGLLFAENQDNFISLNIEDGNLWVYKLNSEBPKEKGRDITNDKSHIITIGKQ 300
 DB 2575 DRGLLFAENQDNFISLNIEDGNLWVYKLNSEBPKEKGRDITNDKSHIITIGKQ 2634
 QY 301 KRWMINNERSVRIKGIIPDPSTYLLGIPAIIRERNISTPAPQGMKULKXTSGVRL 360
 DB 2635 KRWMINNERSVRIKGIIPDPSTYLLGIPAIIRERNISTPAPQGMKULKXTSGVRL 2694
 QY 361 NDVTVGTVKKSEDMKLVRTASFSRQGMSTPNDVPSTDRFQSLRFGQTFQPSGTLNHQ 420
 DB 2695 NDVTVGTVKKSEDMKLVRTASFSRQGMSTPNDVPSTDRFQSLRFGQTFQPSGTLNHQ 2754
 QY 421 TRTSLSLVLTEDGHIELSTDSNIPFKSPGTWMDGLHHVSVISDTSGLRLIDDPVLR 480
 DB 2755 TRTSLSLVLTEDGHIELSTDSNIPFKSPGTWMDGLHHVSVISDTSGLRLIDDPVLR 2814
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 DB 2815 RNQRLPFSNAQSLRIGGHPFGCCINVLVQFSGSPETVLDAKSTKQDASIGGCSLN 2874
 QY 541 KPEPLMLFKSPKREKRIFFNVQL 565
 DB 2875 KPEPLMLFKSPKREKRIFFNVQL 2899

IT 05-JUL-2004 (T-EMBLrel. 27, Created)
 IT 05-JUL-2004 (T-EMBLrel. 27, Last sequence update)
 IT 05-JUL-2004 (T-EMBLrel. 27, Last annotation update)
 DE Laminin alpha 3 splice variant b1.
 SN Name=IAMA3;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OC NCBI_TaxId=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=2833568; PubMed=12915477; DOI=10.1093/hmg/ddg234;
 RA McLean W.H., Irvine A.D., Hamill K.J., Whitlock N.V.,
 RA Coleman-Campbell C.M., Mellerio J.B., Ashton G.S.,
 RA Dopping-Hepenstal P.V., Bady R.A., Jamali T., Phillips R.J.,
 RA Shabbir S.G., Haroon T.S., Khurshid K., Moore J.B., Page B.,
 RA Darling J., Atherton D.J., Van Steensel M.A., Munro C.S., Smith F.J.,
 RA McGrath J.A.;
 RT "An unusual N-terminal deletion of the laminin (alpha)3a isoform leads
 to the chronic granulation tissue disorder laryngo-oncho-cutaneous
 RT syndrome";
 RT Hum. Mol. Genet. 12:2395-2409(2003).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA McLean W.H.I.;
 RA Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.
 RL EMBL: A1327115; AAQ72570.1; -
 DR GO: GO:0005578; C:extracellular matrix (sensu Metazoa); IEA.
 DR GO: GO:0005606; C:laminin-1; IEA.
 DR GO: GO:0005102; F:receptor binding; IEA.
 DR GO: GO:0005198; F:structural molecule activity; IEA.
 DR GO: GO:0030155; P:regulation of cell adhesion; IEA.
 DR GO: GO:0030334; P:regulation of cell migration; IEA.
 DR GO: GO:0045995; P:regulation of embryonic development; IEA.
 DR InterPro: IPR001844; Chaprinin Cpn60.
 DR InterPro: IPR008985; Cona like_1ec_g1.
 DR InterPro: IPR006209; EGF like.
 DR InterPro: IPR008979; Gal_bind_like.
 DR InterPro: IPR006210; IEGF.
 DR InterPro: IPR000034; Laminin_B.
 DR InterPro: IPR002049; Laminin_EGF.
 DR InterPro: IPR001791; Laminin_G.
 DR InterPro: IPR009254; Laminin_I.
 DR InterPro: IPR010307; Laminin_I1.
 DR InterPro: IPR010311; Laminin_I1.
 DR InterPro: IPR008211; Laminin_N.
 DR InterPro: IPR003129; TSP_N.
 DR Pfam: PF00052; Laminin_B; 1.
 DR Pfam: PF00053; Laminin_EGF; 8.
 DR Pfam: PF02210; Laminin_G_2; 4.
 DR Pfam: PF06008; Laminin_I_1.
 DR Pfam: PF06009; Laminin_I1.
 DR Pfam: PF00055; Laminin_N; 1.
 DR PRINTS: PR00011; EGF_LAMININ.
 DR PRODOM: PD003031; Laminin_B; 1.
 DR SMART: SM00181; EGF; 8.
 DR SMART: SM00180; EGF; 14.
 DR SMART: SM00281; Lamb; 1.
 DR SMART: SM00282; Lamb; 5.
 DR SMART: SM00136; Lamnt; 1.
 DR PROSITE: PS00296; CHAPERONINS_CPN60; UNKNOWN_1.
 DR PROSITE: PS00022; EGF_1; 12.
 DR PROSITE: PS01166; EGF_2; 1.
 DR PROSITE: PS01248; LAMININ_TYPE_EGF; 13.
 DR PROSITE: PS50025; LAM_G_DOMAIN; 5.
 DR Laminin EGF-like domain.
 SQ SEQUENCE 3333 AA; 366646 MW; 9F99A4988BF27D0 CRC64;

Query Match 83.0%; Score 2441; DB 2; Length 3333;
 Best Local Similarity 81.9%; Pred. No. 7.1e-157;
 Matches 463; Conservative 47; Mismatches 55; Indels 0; Gaps 0;

QY 1 MRFNGSGVVRPLPNDLEDKGYTSLFLQRPDLRNGGTEDMFVYILGNKQASKDYIG 60
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Db      2391 MRPNGSGVBYRLNDLEDKTSLSLFLQRPNSRNGTENTMFMITGKNDASRDYIG 2450
Qy      61 MAAVVDQGLTCVYNIAGDREARVQIDQVLTSESGEAVMDVKFORIYQFAMNTYKATSN 120
Db      2451 MAAVVDQGLTCVYNIAGDREARVQIDQVLTSESGEAVMDVKFORIYQFAMNTYKATSN 2510
Qy      121 KPRAPAVYDLEGSSNTLNLNDEPDVAVPYVGYGPPFELPSRLRFPFYKCIETLDLNN 180
Db      2511 KPEPVGVMDDGNSNTLNLNDEPDVAVPYVGYGPPFELPSRLRFPFYKCIETLDLNN 2570
Qy      181 VLSLVNFKTTPNLTNTEVEPCRRRKEESDKNYEGGVYARIPQAPAPNPFQITQTV 240
Db      2571 VLSLVNFKTTPNLTNTEVEPCRRRKEESDKNYEGGVYARIPQAPAPNPFQITQTV 2630
Qy      241 DRGLLFFAENODNFISLNTEDGNIMVRYKLNSEPPKRGKIRDTINDGKHSILITIGKQ 300
Db      2631 DRGLLFFAENODNFISLNTEDGNIMVRYKLNSEPPKRGKIRDTINDGKHSILITIGKQ 2690
Qy      301 KRMWIVNERSVRIEGBIIPFSTYYIGIPAIAREPNIISTPAFQCMKMLKKTSGVRL 360
Db      2691 KRMWIVNERSVRIEGBIIPFSTYYIGIPAIAREPNIISTPAFQCMKMLKKTSGVRL 2750
Qy      361 NDVGVTKKCSBDMKLVRTASFSRGGOMFTNLDPVSTDRFOLSPFGPOTPOPSGTLNHO 420
Db      2751 NDVGVTKKCSBDMKLVRTASFSRGGOMFTNLDPVSTDRFOLSPFGPOTPOPSGTLNHO 2810
Qy      421 TRTSSLVLTLEDGHIESTRDSNIPFKSPGYMDGLLHVSYISDTSGLRLIDDOVLR 480
Db      2811 TWTRNLQVLTLEDGHIESTRDSNIPFKSPGYMDGLLHVSYISDTSGLRLIDDOVLR 2870
Qy      481 RNORLPSFSNAQSLNLGGCHFGCCISNVLVQFSGSPVYLDAISYTKXKSLGGCSIN 540
Db      2871 NSRRLKHSSRSRSLGSGNFGCISNVFVQRLSLSPVLDLTSNLSLRDVSIGCSIN 2930
Qy      541 KPEFLMLFKSPKPKNGRIFFNVQL 565
Db      2931 KPEFLMLFKSPKPKNGRIFFNVQL 2955

Db      2931 KPEFLMLFKSPKPKNGRIFFNVQL 2955

RESULT 6
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ID      LMA3_HUMAN          STANDARD;          PRT;          1713 AA.
AC      Q16787; Q13679; Q13680;
DT      01-NOV-1997 (Rel. 35, Created)
DT      01-NOV-1997 (Rel. 35, Last sequence update)
DT      25-OCT-2004 (Rel. 45, Last annotation update)
DE      laminin alpha-3 chain precursor (Epiligrin 170 kDa subunit) (E170)
GN      (Nuclein alpha subunit).
OS      Homo sapiens (Human).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX      NCBI_TaxID=9606;
RN      [1]
RP      SEQUENCE FROM N.A.
RC      TISSUE=Keratinocytes;
RX      MEDLINE=94357926; PubMed=8077230;
RA      Ryan M.C., Tizard R., Vandevanter D.R., Carter W.G.;
RT      "Cloning of the lam3 gene encoding the alpha 3 chain of the adhesive
RT      ligand epiligrin. Expression in wound repair.";
RL      J. Biol. Chem. 269:22779-22787 (1994).
RN      [2]
RP      SEQUENCE OF 1-1331 FROM N.A. (ISOPFORMS A AND B).
RX      MEDLINE=96163880; PubMed=8586427;
RA      Vidal F., Baudouin C., Miguel C., Galliano M.-F., Christiano A.M.,
RA      Uitto J., Ottomeo J.-P., Meneguzzi G.;
RT      "Cloning of the laminin alpha 3 chain gene (LAMA3) and identification
RT      of a homozygous deletion in a patient with Herlitz junctional
RT      epidermolysis bullosa.";
RL      Genomics 30:273-280 (1995).
RN      [3]
RP      DISEASE.
RX      PubMed=12915477; DOI=10.1093/hmg/ddg234;

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RA      Irwin McLean W.H., Irvine A.D., Hamill K.J., Whitlock N.V.,
RA      Coleman-Campbell C.M., Melleiro J.E., Ashton G.S.,
RA      Dopling-Hependell P.J.H., Bady R.A.J., Jamil T., Phillips R.J.,
RA      Shabir S.G., Haxton T.S., Khurshid K., Moore J.R., Page B.,
RA      Darling J., Acheron D.J., Van Steensel M.A.M., Munro C.S.,
RA      Smith F.J.D., McGrath J.A.;
RT      "An unusual N-terminal deletion of the laminin alpha3a isoform leads
RT      to the chronic granulation tissue disorder laryngo-onycho-cutaneous
RT      syndrome.";
RL      Hum. Mol. Genet. 12:2395-2409 (2003).
CC      -1- FUNCTION: Binding to cells via a high affinity receptor, laminin
CC      is thought to mediate the attachment, migration and organization
CC      of cells into tissues during embryonic development by interacting
CC      with other extracellular matrix components.
CC      -1- FUNCTION: Laminin-5 is thought to be involved in (1) cell adhesion
CC      via integrin alpha-3/beta-1 in focal adhesion and integrin alpha-
CC      6/beta-4 in hemidesmosomes, (2) signal transduction via tyrosine
CC      phosphorylation of p125-FAK and p80, (3) differentiation of
CC      keratinocytes.
CC      -1- SUBUNIT: Laminin is a complex glycoprotein, consisting of three
CC      different polypeptide chains (alpha, beta, gamma), which are bound
CC      to each other by disulfide bonds into a cross-shaped molecule
CC      comprising one long and three short arms with globules at each
CC      end. The alpha-3 chain is a subunit of laminin-5
CC      (epiligrin/kalinin/nicein), and possibly also a component of
CC      laminin-6 (K-laminin) and laminin-7 (KS-laminin).
CC      -1- SUBCELLULAR LOCATION: Extracellular; found in the basement
CC      membranes (major component).
CC      -1- ALTERNATIVE PRODUCTS:
CC      Bient-Alternative splicing; Named isoforms=2;
CC      Name=A;
CC      IsoId=Q16787-1; Sequence=Displayed;
CC      Name=B;
CC      IsoId=Q16787-2; Sequence=VSP_003037;
CC      Note-incomplete sequence;
CC      -1- TISSUE SPECIFICITY: Skin; respiratory, urinary, and digestive
CC      epithelia and in other specialized tissues with prominent
CC      secretory or protective functions. Epithelial basement membrane,
CC      and epithelial cell tongue that migrates into a wound bed. A
CC      differential and focal expression of the alpha-3 chain is observed
CC      in the CNS.
CC      -1- INDUCTION: Laminin-5 is up-regulated in wound sites of human skin.
CC      -1- DOMAIN: The alpha-helical domains I and II are thought to interact
CC      with other laminin chains to form a coiled coil structure.
CC      -1- DOMAIN: Domain G is globular.
CC      -1- DISEASE: Defects in LAMA3 are a cause of junctional epidermolysis
CC      bullosa gravis (JEB) [MIM:226700]; also known as junctional
CC      epidermolysis bullosa Herlitz-Pearson type. JEB is a blistering
CC      disorder in skin that is characterized by a separation of basal
CC      cells from the basement membrane due to a decreased number of
CC      hemidesmosomes. Laminin-5 is missing from the basement membrane of
CC      patients with the gravis form of epidermolysis bullosa.
CC      -1- DISEASE: Defects in LAMA3 are the cause of laryngoonycho-cutaneous
CC      syndrome (LOCS) [MIM:245660]. LOCS is an autosomal recessive
CC      epithelial disorder confined to the Punjab Muslim population. The
CC      condition is characterized by cutaneous erosions, nail dystrophy
CC      and exuberant vascular granulation tissue in certain epithelia,
CC      especially conjunctiva and larynx.
CC      -1- SIMILARITY: Contains 3 laminin EGF-like domains.
CC      -1- SIMILARITY: Contains 5 laminin G-like domains.
CC      -1- This SWISS-PROT entry is copyright. It is produced through a collaboration
CC      between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC      the European Bioinformatics Institute. There are no restrictions on its
CC      use by non-profit institutions as long as its content is in no way
CC      modified and this statement is not removed. Usage by and for commercial
CC      entities requires a license agreement (see http://www.isb-sib.ch/announce/
CC      or send an email to license@sib-sib.ch).
CC      -----
CC      EMBL: L34155; AAA59483.1; -
CC      EMBL: X85107; CAA59428.1; -
CC      EMBL: X85108; CAA59429.1; -
CC      PIR: A55347; A55347.

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DR HSSP; P02468; INPR.
 DR Genew; HGNC:6483; LAMA3.
 DR MIM; 608005; -.
 DR MIM; 226700; -.
 DR MIM; 245660; -.
 DR GO; GO:0005604; C:basement membrane; TAS.
 DR GO; GO:0008544; P:epidermal differentiation; TAS.
 DR InterPro; IPR008985; Cona like_1ec_g1.
 DR InterPro; IPR006209; EGF_like_recept.
 DR InterPro; IPR009030; Grow_fac_recept.
 DR InterPro; IPR002049; Laminin_EGF.
 DR InterPro; IPR001791; Laminin_G.
 DR InterPro; IPR009254; Laminin_I.
 DR InterPro; IPR003129; TSP_N.
 DR Pfam; PF00053; Laminin_EGF; 2.
 DR Pfam; PF00054; Laminin_G; 2.
 DR Pfam; PF06008; Laminin_I; 1.
 DR Pfam; PF06009; Laminin_II; 1.
 DR PROSITE; PS00023; EGF_1; 1.
 DR PROSITE; PS01186; EGF_2; 1.
 DR PROSITE; PS01248; LAMININ_TYR_EGF; 2.
 DR PROSITE; PS50025; LAM_G_DOMAIN; 5.
 KM Alternative splicing; Basement membrane; Cell adhesion; Coiled coil;
 KM Epidermolysis bullosa; Extracellular matrix; Glycoprotein;
 KM Laminin EGF-like domain; Repeat; Signal.
 FT SIGNAL 1 20
 FT CHAIN 21 1713
 FT DOMAIN 46 201
 FT DOMAIN 67 113
 FT DOMAIN 114 166
 FT DOMAIN 167 185
 FT DOMAIN 186 769
 FT DOMAIN 770 971
 FT DOMAIN 978 1140
 FT DOMAIN 1147 1307
 FT DOMAIN 1366 1530
 FT DOMAIN 1537 1710
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 FT DOMAIN 702 765
 FT DOMAIN 1686 1713
 FT DISULFID 67 76
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 FT CARBOHYD 964 964
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 FT CARBOHYD 1131 1131
 FT CARBOHYD 1325 1325
 FT CARBOHYD 1477 1477
 FT CARBOHYD 1667 1667
 FT VARSPLIC 1 45
 FT CONFLICT 5 5
 FT CONFLICT 123 125
 FT CONFLICT 481 481

IT CONFLICT 754 754 R -> L (in Ref. 2).
 IT CONFLICT 969 969 E -> Q (in Ref. 2).
 IT CONFLICT 1052 1052 D -> A (in Ref. 2).
 IT CONFLICT 1184 1184 G -> A (in Ref. 2).
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 Query Match 83.0%; Score 2439; DB 1; Length 1713;
 Best Local Similarity 81.9%; Pred. No. 3,8e-157;
 Matches 463; Conservative 47; Mismatches 55; Indels 0; Gaps 0;
 QY 1 MRENGSGVVRLLPNLDELKGYTSLSLFLQRLDENGGEDMFWYTLGNKASDYIG 60
 DB 771 MRENGSGVVRLLPNLDELKGYTSLSLFLQRLDENGGEDMFWYTLGNKASDYIG 830
 QY 61 MAVVDGLTCVYMLGREAQVQIDVLTSESGEAMDRPKRRIQAPALNTKATSN 120
 DB 831 MAVVDGLTCVYMLGREAQVQIDVLTSESGEAMDRPKRRIQAPALNTKATSN 890
 QY 121 KPRAPAVYDLEGSSNTLNLDPEDAVFYGYGPPDFELPSRLRFPYKGCIELDLNEN 180
 DB 891 KPRTPGVYDMDGNNSNTLNLDPENAVFYGYGPPDFELPSRLRFPYKGCIELDLNEN 950
 QY 181 VLSLYNFKTFLNLTTEVEPCRRKESDKNVEGTGYARIPQNPAPFNFIQTITV 240
 DB 951 VLSLYNFKTFLNLTTEVEPCRRKESDKNVEGTGYARIPQNPAPFNFIQTITV 1010
 QY 241 DRGLLTPAENQDNFISLNIHDKMLNRYKLSNPPKRGIRDTINDGKHSILITGKQ 300
 DB 1011 DRGLLTPAENQDNFISLNIHDKMLNRYKLSNPPKRGIRDTINDGKHSILITGKQ 1070
 QY 301 KRMNINNVSVIBSGIFDFSTYYIGTPIAIRFPNISTPAFOGCMKULKXTSGVRL 360
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 QY 361 NDTVGYTKCKSEBDKLVRTASFSRQGMSEFTNLDPVSTDRFQSPGFQPSGTLNMQ 420
 DB 1131 NDTVGYTKCKSEBDKLVRTASFSRQGMSEFTNLDPVSTDRFQSPGFQPSGTLNMQ 1190
 QY 421 TRTSSLVLTEDGHILSTDSNIPFKSPGTMDGLHNVYSISTSGRLIDDOVLR 480
 DB 1191 TRTSSLVLTEDGHILSTDSNIPFKSPGTMDGLHNVYSISTSGRLIDDOVLR 1250
 QY 481 RNORLPFSNAOQSLGLGGFEGCISNLYVORFOSPEYLDLASXSTKQASIGGCSLN 540
 DB 1251 RNORLPFSNAOQSLGLGGFEGCISNLYVORFOSPEYLDLASXSTKQASIGGCSLN 1310
 QY 541 KPPEMLFKSPKRFNKRIFNVQL 565
 DB 1311 KPPEMLFKSPKRFNKRIFNVQL 1335
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 AC 096TGO;
 DT 01-DEC-2001 (Tremblrel. 19, Created)
 DT 01-DEC-2001 (Tremblrel. 19, Last sequence update)
 DT 01-MAR-2004 (Tremblrel. 26, Last annotation update)
 DE Alpha 3B chain of laminin-5 (Fragment).
 GN Name=LAMA3;
 OS Homo sapiens (human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OC NCBI_Taxid=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Aberdam D., Vidal, Baudoin, Miquel, Ottome, Meneguzzi;
 RL Submitted (FEB-1995) to the EMBL/GenBank/DBJ databases.
 DR EMBL; X84900; CA59325.1; -.
 DR HSSP; P02468; INPR.
 DR GO; GO:0005606; C:laminin-1; IBA.
 DR GO; GO:0005102; F:receptor binding; IBA.
 DR GO; GO:0005198; F:structural molecule activity; IBA.

DR GO; GO:0030155, P:regulation of cell adhesion; IEA.
DR GO; GO:0030334, P:regulation of cell migration; IEA.
DR GO; GO:0045995, P:regulation of embryonic development; IEA.
DR InterPro; IPR001844; Chaprinin Cpn60.
DR InterPro; IPR008985; ConA_like_1ec_g1.
DR InterPro; IPR006209; EGF_like.
DR InterPro; IPR000034; Laminin_B.
DR InterPro; IPR002049; Laminin_EGF.
DR InterPro; IPR001791; Laminin_G.
DR InterPro; IPR009254; Laminin_I.
DR InterPro; IPR010307; Laminin_II.
DR InterPro; IPR003129; TSP_N.
DR Pfam; PF00052; Laminin_B; 1.
DR Pfam; PF00053; Laminin_EGF; 2.
DR Pfam; PF02210; Laminin_G_2; 4.
DR Pfam; PF06008; Laminin_I; 1.
DR Pfam; PF06009; Laminin_II; 1.
DR ProDom; PD003031; Laminin_B; 1.
DR SMART; SM00180; EGF_Lam; 2.
DR SMART; SM00281; LamB; 1.
DR SMART; SM00282; LamG; 5.
DR PROSITE; PS00296; CHAPERONINS_CPN60; UNKNOWN_1.
DR PROSITE; PS00022; EGF_1; 2.
DR PROSITE; PS01186; EGF_2; 1.
DR PROSITE; PS01248; LAMININ_TYPE_EGF; 3.
DR PROSITE; PS50025; LAM_G_DOMAIN; 5.
KW Laminin EGF-like domain.
FT NON TER 1 1
SQ SEQUENCE 1806 AA; 199411 MW; EF94CDE2A52B93 CRC64;

Query Match 83.0%; Score 2439; DB 2; Length 1806;
Best Local Similarity 81.9%; Pred. No. 9.7e-157;
Matches 463; Conservative 47; Mismatches 55; Indels 0; Gaps 0;

QY 1 MRFNKGSGVEVRLPNLDELKGYTSLSLFLQRPDLRENGGTEDMFWYLGNDKASRDYIG 60
DB 864 MRFNKGSGVEVRLPNLDELKGYTSLSLFLQRPNSRNGGTEDMFWYLGNDKASRDYIG 923
QY 61 MAVVDQLTCVYNIADREAEVQIDVLTSESQEAVMDRVKFORIYQAFANTYTKATS 120
DB 924 MAVVDQLTCVYNIADREAEVQIDVLTSESQEAVMDRVKFORIYQAFANTYTKATS 983
QY 121 KPAAPAVYDIEGSSNTLNLDPEDAVFYVGYPPPELPSRLRPYPYKGCIELDLNEN 180
DB 984 KPAAPAVYDIEGSSNTLNLDPEDAVFYVGYPPPELPSRLRPYPYKGCIELDLNEN 1043
QY 181 VLSVYFKTFPNTTEVERCRRKESDKNYFEGGYARIPQNPAPPNFIQTIQTVV 240
DB 1044 VLSVYFKTFPNTTEVERCRRKESDKNYFEGGYARIPQNPAPPNFIQTIQTVV 1103
QY 241 DRGLLFFAENQDNFSLINIEDGNLMRYKLNSEPPYKGIKRTINDGKHSILITIGKIQ 300
DB 1104 DRGLLFFAENQDNFSLINIEDGNLMRYKLNSEPPYKGIKRTINDGKHSILITIGKIQ 1163
QY 301 KRMWIVNERSVRIEGEIPDFSTYYLGGIPAIAREPNIISTPAFGCMKMLKKTSGVRL 360
DB 1164 KRMWIVNERSVRIEGEIPDFSTYYLGGIPAIAREPNIISTPAFGCMKMLKKTSGVRL 1223
QY 361 NDVVGATKKCSBWKVRTASFSRQGMFTNIDVSTDRFQLSRFRQTFQSGTILANQ 420
DB 1224 NDVVGATKKCSBWKVRTASFSRQGMFTNIDVSTDRFQLSRFRQTFQSGTILANQ 1283
QY 421 TRTSLLVLTLEGGHIELSTRDSNIPIFKSPGYMDGLHHVSYISPTSGLRLLIDDOVR 480
DB 1284 TRTSLLVLTLEGGHIELSTRDSNIPIFKSPGYMDGLHHVSYISPTSGLRLLIDDOVR 1343
QY 481 RNORLPSFSAQSLRIGGHEGCIISNVLVQFSGSPVYLDLASKTKKDAISLGCSIN 540
DB 1344 RNORLPSFSAQSLRIGGHEGCIISNVLVQFSGSPVYLDLASKTKKDAISLGCSIN 1403
QY 541 KPEFLMLFKSPKPKFKGRIFFNVOL 565
DB 1404 KPEFLMLFKSPKPKFKGRIFFNVOL 1428

RESULT 8
ID 076E14 PRELIMINARY; PRT; 3333 AA.
AC 076E14;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Laminin alpha 3b chain.
GN Name=LAM3;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
OX NCBI_Taxid=9606;
RT [1]

RP SEQUENCE FROM N.A.
RA Kariya Y., Yasuda C., Nakashima Y., Ishida K., Tsubota Y.,
RA Miyazaki K.;
RT *Characterization of laminin 5B and NH2-terminal proteolytic fragment
RT of its alpha3b chain: promotion of cellular adhesion, migration, and
RT proliferation.";
RL J. Biol. Chem. 279:24774-24784(2004).

DR EMBL; AB107369; BADJ3428.1; -.
DR GO; GO:0005578; C:extracellular matrix (sensu Metazoa); IEA.
DR GO; GO:0005606; C:laminin-1; IEA.
DR GO; GO:0005102; F:receptor binding; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR GO; GO:0030155; P:regulation of cell adhesion; IEA.
DR GO; GO:0030334; P:regulation of cell migration; IEA.
DR GO; GO:0045995; P:regulation of embryonic development; IEA.
DR InterPro; IPR001844; Chaprinin Cpn60.
DR InterPro; IPR008985; ConA_like_1ec_g1.
DR InterPro; IPR006209; EGF_like.
DR InterPro; IPR008979; Gal_bind_like.
DR InterPro; IPR006210; IEGF.
DR InterPro; IPR000034; Laminin_B.
DR InterPro; IPR002049; Laminin_EGF.
DR InterPro; IPR001791; Laminin_G.
DR InterPro; IPR009254; Laminin_I.
DR InterPro; IPR010307; Laminin_II.
DR InterPro; IPR008211; Laminin_N.
DR InterPro; IPR003129; TSP_N.
DR Pfam; PF00052; Laminin_B; 1.
DR Pfam; PF00053; Laminin_EGF; 8.
DR Pfam; PF02210; Laminin_G_2; 4.
DR Pfam; PF06008; Laminin_I; 1.
DR Pfam; PF06009; Laminin_II; 1.
DR PRINTS; PR00051; EGF_LAMININ.
DR ProDom; PD003031; Laminin_B; 1.
DR SMART; SM00180; EGF; 8.
DR SMART; SM00181; EGF_Lam; 14.
DR SMART; SM00281; LamB; 1.
DR SMART; SM00282; LamG; 5.
DR SMART; SM00136; LamT; 1.
DR PROSITE; PS00296; CHAPERONINS_CPN60; UNKNOWN_1.
DR PROSITE; PS00022; EGF_1; 12.
DR PROSITE; PS01186; EGF_2; 1.
DR PROSITE; PS01248; LAMININ_TYPE_EGF; 13.
DR PROSITE; PS50025; LAM_G_DOMAIN; 5.
KW Laminin EGF-like domain.

QY 3333 AA; 366616 MW; 6F99AF4D4B99FCB0 CRC64;
SQ SEQUENCE 3333 AA; 366616 MW; 6F99AF4D4B99FCB0 CRC64;

Query Match 83.0%; Score 2439; DB 2; Length 3333;
Best Local Similarity 81.9%; Pred. No. 9.7e-157;
Matches 463; Conservative 47; Mismatches 55; Indels 0; Gaps 0;

QY 1 MRFNKGSGVEVRLPNLDELKGYTSLSLFLQRPDLRENGGTEDMFWYLGNDKASRDYIG 60
DB 2391 MRFNKGSGVEVRLPNLDELKGYTSLSLFLQRPNSRNGGTEDMFWYLGNDKASRDYIG 2450
QY 61 MAVVDQLTCVYNIADREAEVQIDVLTSESQEAVMDRVKFORIYQAFANTYTKATS 120

Db	2451	MAVVDGQLTCYNNLGDREBELQVDDILTKSEKXAMVRKFORLYQARANTYKATSS	2510
QY	121	KPKADAVYDLRGSSNTLLNTDPEDAVFYVGYPPEDFELPSRLRPPYKGCIELDLNNEN	180
Db	2511	KPEFPGVDMQGRNSNTLLNTDPEWNVVFYVGYPPEDFELPSRLSPPYKGCIELDLNNEN	2570
QY	181	VLSLNFKTTFNLTTEVPCRRRRESDKNYFESTGAALPIQONAPFPPIOTIOTTV	240
Db	2571	VLSLNFKTTFNLTTEVPCRRRRESDKNYFESTGAALPIQONAPFPPIOTIOTTV	2630
QY	241	DRGLLFFAENODNFISLNIEDGNLWVRKLNSEPPKRGKIDTINIDGDHSLITIGLQ	300
Db	2631	DRGLLFFAENODNFISLNIEDGNLWVRKLNSEPPKRGKIDTINIDGDHSLITIGLQ	2690
QY	301	KRMWINNERSVRIEGEIPDSSTYYLGGIPLAIRERFNISTRPAFGCKMNLKTTSGVRL	360
Db	2691	KRMWINNERSVRIEGEIPDSSTYYLGGIPLAIRERFNISTRPAFGCKMNLKTTSGVRL	2750
QY	361	NDTVGVTKKCSBDMCLVRTASPSRGGMSFNTLWVPSIDRQLASRGCPQPSGLTLNHQ	420
Db	2751	NDTVGVTKKCSBDMCLVRSASPSRGGMSFNTLWVPSIDRQLASRGCPQPSGLTLNHQ	2810
QY	421	TRTSSILVTLBEDGHIELSTRSDSNIPIFKSPGTMDGLLHHVSVISDTSGRLLLIDDPYLR	480
Db	2811	TWTRRLQYTLLEBGIYEIESTDSGCGIIFKSPGTMDGLLHHVSVISDMSGRLLLIDDPYLR	2870
QY	481	ENQRLPSFSNAQOSLRLGGHPEGCISNVLVQRFSSQSPFVLDLASKSTFKCDASLGGCSLN	540
Db	2871	NSKRLKHISRSRQSLRLGGSNPEGCISNVFQRLSLSPFVLDLTNSLKRDVUSLGGCSLN	2930
QY	541	KPPFLMLFKSPKRPYKGRIFNVNOL	555
Db	2931	KPPFLMLKGSSTRFKTKTFRNL	2935

RESULT 9	0867A1	PRELIMINARY;	PRT; 1725 AA.
ID	0867A1		
AC	0867A1;		
DT	01-JUN-2003 (TREMBl;rel. 24, Created)		
DT	01-JUN-2003 (TREMBl;rel. 24, Last sequence update)		
DT	01-MAR-2004 (TREMBl;rel. 26, Last annotation update)		
DE	Laminin alpha 3 (Fragment).		
OS	Caris familiaris (Dog).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi		
OC	Mammalia; Eutheria; Carnivora; Plisipedia; Canidae; Canis.		
OX	NCBI_Taxid=9615;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RA	Spirito F., Capri A., Guagnere E., Ortonne J.-P., Meneguzzi G.;		
RL	Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.		
DR	EMBL; AF236865; AAL54876.1; -		
DR	HSP; P11209; IG2C.		
DR	GO; GO:0005606; C:laminin-1, IEA.		
DR	GO; GO:0005102; F:receptor binding, IEA.		
DR	GO; GO:0005198; F:structural molecule activity, IEA.		
DR	GO; GO:0030155; P:regulation of cell adhesion, IEA.		
DR	GO; GO:0030334; P:regulation of cell migration, IEA.		
DR	GO; GO:0045935; P:regulation of embryonic development, IEA.		
DR	InterPro; IPR008985; ConL_1ike_1ec_gf.		
DR	InterPro; IPR006209; EGF_1ike.		
DR	InterPro; IPR002049; Laminin_EGF.		
DR	InterPro; IPR001791; Laminin_G.		
DR	InterPro; IPR009254; Laminin_I.		
DR	InterPro; IPR010307; Laminin_II.		
DR	InterPro; IPR003129; TSP_N.		
DR	Pfam; PF00053; Laminin_EGF; 2.		
DR	Pfam; PF02210; Laminin_G_2; 4.		
DR	Pfam; PF06008; Laminin_I_1.		
DR	Pfam; PF06009; Laminin_II_1.		
DR	SMART; SM00180; EGF_Lam; 2.		
DR	SMART; SM00282; LamG; 5.		

DR PROSITE; PS00023; EGF_1; 1.
 DR PROSITE; PS01166; EGF_2; 1.
 DR PROSITE; PS01248; LAMTININ_TYPE_EGF; 2.
 DR PROSITE; PS50025; LAM_G_DOMAIN; 5.
 DR LAMTININ_EGF-like domain.
 FT NOW_TIER 1725 1725
 SQ SEQUENCE 1725 AA; 191053 MW; DFT1EB0ELPBF5134C CRC64;

Query Match	75.7%	Score 2224.5	DB 2	Length 1725
Best Local Similarity	75.0%	Pred. No. 1.6e-142		
Matches 423	Conservative	60	Mismatches 80	Indels 1
				Gaps 1

Qy	MRFBKSGVYRLPNLDEJDKGYSLSLFPORPLRNGGGBDMFVWYLGKASXOYIG	60
Dd	782 MRFKSGVYRLPNLDEJDKGYSLSLFPORPSRSGSTENMFYMLGKDISRYIG	841
Qy	61 MAVVDGQLTCVYNLGDREAEVQIDQVLTJESSEQAEVMDRKFCORIYQPAKANTKATSN	120
Dd	842 MAVVDGRLTCVYNLGBGESELOVDQSVITKSETQBAIMDRVKFQRIYQFASANTYKATSN	901
Qy	121 KPKAPAVYDLGEGSSNTLLMLDPEPDVAFYQGYGPPEBELRSRLRFPFYKCIHELDTLNN	180
Dd	902 KPGSSQHEMDSGNSHTLLMLDEPNTYFYVGYGPSPDPTLPARLRFPEYKCIHELDTLNN	961
Qy	181 VLSLNYNFKTTPNLTNTTVEBCRRKKEESDKNYFEGSTAYRIPQOPNAPNPNFIQTIQTV	240
Dd	962 VLSLNYNFKTTPNLTNTTVEBCRRKKEESDKNYFEGSTAYRIPQOPNAPNPNFIQTIQTV	1021
Qy	241 DRGLLFAENQDNFISLNIEDGNLMVYKLNSEBPKCKGIDRTINDCKHSILITIGKQ	300
Dd	1022 DRGLLFAENQDNFISLNIEDGNLMVYKLNSEBPKCKGIDRTINDCKHSILITIGKQ	1081
Qy	301 KRMWINVNSVRIJEGEIPDPSTYYLGGIPLAIRERFNISTPAFQCKMKLKTSGVYRL	360
Dd	1082 NRISIAVSSONSQIDGIEPDPSTYYLGGIPLIRERFNISTPAFQCKMKLKTSGVYRL	1141
Qy	361 NDTYGVYKKKSEBMDKLVRTASFSNGQMSFTNLDVETDPEOJLSFGQTFOPSGETLLNHQ	420
Dd	1142 NDTYGVYKKKSEBMDKLVRTASFSNGQMSFTNLDVETDPEOJLSFGQTFOPSGETLLNHQ	1201
Qy	421 TRTSLSLLVTEDEGHIELSTRDSNPIPKFSFGTYMDGLLHVSVLSIDTSGRLRIDQVLR	480
Dd	1202 SPKHRYLQVTEDEGHIELSTRDSNPIPKFSFGTYMDGLLHVSVLSIDTSGRLRIDQVLR	1260
Qy	481 RNQRLPFSFNAQOSLRLGGGHFBCISLNVLYQFSQSEBYLDLASKSTKQDASLGCGSLN	540
Dd	1261 SNQRLQDLSQSOPLRYLGSGQFPECISNVFIQVRSKSPAVLDLASKSTKQDVSJGCGSLN	1320
Qy	541 KPPLPLMKFKSPKPKFNKGRIFNNW 564	
Dd	1321 KPPLPLMLRSGSTRLNKSHTFNNW 1344	

	RESULT 10		
LMAS	HUMAN		
ID	LMAS_HUMAN	STANDARD;	PRT; 3695 AA.
AC	O15230; OSWZ27; Q9H1P1;		
DT	16-OCT-2001 (Rel. 40, Created)		
DT	28-FEB-2003 (Rel. 41, Last sequence update)		
DT	05-JUL-2004 (Rel. 44, Last annotation update)		
DE	Laminin alpha-5 chain precursor.		
GN	Name=LMAS5; Synonyms=K1AA0533, K1AA1907;		
OS	Homo sapiens (Human).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.		
OX	NCBI_TaxId=9606;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RX	MEBLINB=1638749; PubMed=11780053; DOI=10.1038/414865a;		
RA	Deloukas P., Matthews L.H., Ashurst J.L., Burton J., Gilbert J.G.R.,		
RA	Jones M., Stavrides G., Almeida J.P., Babbage A.R., Bagguley C.L.,		
RA	Ballay J., Barlow R.F., Bates K.N., Beard L.M., Beare D.M.,		
RA	Beasley O.P., Bird C.P., Blakey S.E., Bridgeman A.M., Brown A.J.,		

RA Buck D., Burrill W.D., Butler A.P., Carder C., Carter N.P.,
 RA Chapman J.C., Ciamp M., Clark G., Clark L.N., Clark S.Y., Clee C.M.,
 RA Clegg S., Cobley V.E., Collier R.B., Connor R.E., Corby N.R.,
 RA Coulson A., Coville G.J., Deadman R., Dhani P.D., Dunn M.,
 RA Ellington A.G., Frankland J.A., Fraser A., French L., Garner P.,
 RA Grafton D.V., Griffiths C., Griffiths M.N.D., Gwilliam R., Hall R.E.,
 RA Hammond S., Harley J.L., Heath P.D., Ho S., Holden J.L., Howden P.J.,
 RA Huckle E., Hunt A.R., Hunt S.B., Jekosch K., Johnson C.M., Johnson D.,
 RA Kay M.P., Kimberley A.M., King A., Knights A., Laird G.K., Lawlor S.,
 RA Levesajohn M.H., Leverhulme M.A., Lloyd C., Lloyd D.M., Lovell J.D.,
 RA Marsh V.L., Martin S.L., McComachie L.J., McLeay K., McMurray A.A.,
 RA Milne S.A., Mistry D., Moore M.J.F., Mullikin J.C., Nickerson T.,
 RA Oliver K., Parker A., Patel R., Pearce T.A.V., Peck A.I.,
 RA Phillimore B.J.C.T., Prachalingam S.R., Plumb R.W., Ramsay H.,
 RA Race C.M., Ross M.T., Scott C.E., Sehra H.K., Showkseen R., Sims S.,
 RA Stuce C.D., Smith M.L., Soderlund C., Steward C.A., Sulston J.E.,
 RA Swann R.M., Sycamore N., Taylor R., Tee L., Thomas D.W., Thorpe A.,
 RA Tracey A., Tromans A.C., Vaudin M., Wall M., Wallis J.W.,
 RA Whitehead S.L., Whitaker P., Willey D.L., Williams L., Williams S.A.,
 RA Wilming L., Wray P.W., Hubbard T., Durbin R.M., Bentley D.R., Beck S.,
 RA Rogers J.,
 RT "The DNA sequence and comparative analysis of human chromosome 20.";
 RL Nature 414:865-871(2001).
 [2]
 RP SEQUENCE OF 197-1934 FROM N.A.
 RC TISSUE=Brain;
 RX MEDLINE=21456161; PubMed=11572484;
 RA Nagase T., Kikuno R., Ohara O.,
 RT "Prediction of the coding sequences of unidentified human genes. XXI.
 RT The complete sequences of 60 new cDNA clones from brain which code for
 RT large proteins.";
 RL DNA Res. 8:179-187(2001).
 [3]
 RP SEQUENCE OF 2051-3695 FROM N.A.
 RC TISSUE=Brain;
 RX MEDLINE=98280545; PubMed=9628581;
 RA Nagase T., Ishikawa K.-I., Miyajima N., Tanaka A., Kotani H.,
 RA Nomura N., Ohara O.,
 RT "Prediction of the coding sequences of unidentified human genes. IX.
 RT The complete sequences of 100 new cDNA clones from brain which can
 RT code for large proteins in vitro.";
 RL DNA Res. 5:31-39(1998).
 [4]
 RP SEQUENCE OF 2743-3695 FROM N.A.
 RC TISSUE=Placenta;
 RX MEDLINE=97415425; PubMed=9271224; DOI=10.1016/S0014-5793(97)00686-8;
 RA Durkin M.E., Loechel F., Mattei M.-G., Gilpin B.J., Albrechtsen R.,
 RA Newer U.M.,
 RT "Tissue-specific expression of the human laminin alpha5-chain, and
 RT mapping of the gene to human chromosome 20q13.2-13.3 and to distal
 RT mouse chromosome 2 near the locus for the ragged (Ra) mutation.";
 RL FBS Lett. 411:296-300(1997).
 [5]
 RP EXPRESSION IN RETINA.
 RX MEDLINE=20422761; PubMed=10964957;
 RA Libby R.T., Champilaud M.-F., Claudepierre T., Xu Y., Gibbons E.P.,
 RA Koch M., Burgeson R.B., Hunter D.D., Brunken W.J.,
 RT "Laminin expression in adult and developing retinae: evidence of two
 RT novel CNS laminins.";
 RL J. Neurosci. 20:6517-6528(2000).
 CC -1- FUNCTION: Binding to cells via a high affinity receptor, laminin
 CC is thought to mediate the attachment, migration and organization
 CC of cells into tissues during embryonic development by interacting
 CC with other extracellular matrix components.
 CC -1- SUBUNIT: Laminin-15 complex is an heterotrimer composed of three
 CC chains (alpha-5/beta-2/gamma-3) which are bound to each other by
 CC disulfide bonds into a cross-shaped molecule comprising one long
 CC and three short arms with globules at each end.
 CC -1- SUBCELLULAR LOCATION: Extracellular; found in the basement
 CC membrane (major component).
 CC -1- TISSUE SPECIFICITY: Expressed in heart, lung, kidney, skeletal
 CC muscle, pancreas, retina and placenta. Little or no expression in
 CC brain and liver.

CC -1- DOMAIN: Domain G is globular and is part of the major cell-binding
 CC site located in the long arm of the laminin heterotrimer.
 CC -1- SIMILARITY: Contains 22 laminin EGF-like domains.
 CC -1- SIMILARITY: Contains 5 laminin G-like domains.
 CC -1- SIMILARITY: Contains 2 laminin IV domains.
 CC -1- SIMILARITY: Contains 1 laminin N-terminal domain.
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 CC or send an email to license@ebi.ac.uk).
 CC -----
 DR EMBL, AL354836; CAC22310.1; AL7_SEQ.
 DR EMBL, AL354836; CAC22310.1; -.
 DR EMBL, AB067494; BAB67800.1; -.
 DR EMBL, AB011105; BAA25459.1; -.
 DR EMBL, Z595636; CAB09137.1; -.
 DR HSSP, P02468; INPE.
 DR Genew; HGNC:6485; LAMV5.
 DR MIM; 601033; -.
 DR InterPro; IPR008985; Cona-like_jec_g1.
 DR InterPro; IPR006209; EGF-like.
 DR InterPro; IPR008979; Gal_bind-like.
 DR InterPro; IPR009030; Grow_fac_recept.
 DR InterPro; IPR000034; Laminin_B.
 DR InterPro; IPR002049; Laminin_EG.
 DR InterPro; IPR001791; Laminin_G.
 DR InterPro; IPR009254; Laminin_I.
 DR InterPro; IPR010307; Laminin_II.
 DR InterPro; IPR008211; Laminin_N.
 DR InterPro; IPR008212; Lam_N2.
 DR InterPro; IPR003129; TGF_N.
 DR Pfam; PF000052; Laminin_B_1.
 DR Pfam; PF000053; Laminin_BGF_18.
 DR Pfam; PF000054; Laminin_G_2.
 DR Pfam; PF06008; Laminin_I_1.
 DR Pfam; PF06009; Laminin_II_1.
 DR Pfam; PF00055; Laminin_N_1.
 DR PRINTS; PR00011; EGF_LAMININ.
 DR ProDom; PD003031; Laminin_B_1.
 DR PROSITE; PS00022; EGF_1; 19.
 DR PROSITE; PS01186; EGF_2; 3.
 DR PROSITE; PS01248; LAMININ_TYPE_EGF; 19.
 DR PROSITE; PS50025; LAM_G_DOMAIN_5.
 DR Basemem membrane; Cell adhesion; Coiled coil; Extracellular matrix;
 KW Glycoprotein; Laminin EGF-like domain; Repeat; Signal.
 FT SIGNAL 1 35
 FT CHAIN 36 3695 Laminin alpha-5 chain.
 FT DOMAIN 36 299 Laminin N-terminal (domain VI).
 FT DOMAIN 300 358 Laminin EGF-like 1.
 FT DOMAIN 359 428 Laminin EGF-like 2.
 FT DOMAIN 429 474 Laminin EGF-like 3.
 FT DOMAIN 494 540 Laminin EGF-like 4.
 FT DOMAIN 541 586 Laminin EGF-like 5.
 FT DOMAIN 587 631 Laminin EGF-like 6.
 FT DOMAIN 632 676 Laminin EGF-like 7.
 FT DOMAIN 677 722 Laminin EGF-like 8.
 FT DOMAIN 723 775 Laminin EGF-like 9.
 FT DOMAIN 776 828 Laminin EGF-like 10.
 FT DOMAIN 829 850 Laminin EGF-like 11 (incomplete).
 FT DOMAIN 851 1437 Laminin domain IV 1 (domain IV B).
 FT DOMAIN 1438 1483 Laminin EGF-like 12.
 FT DOMAIN 1484 1527 Laminin EGF-like 13.
 FT DOMAIN 1528 1576 Laminin EGF-like 14.
 FT DOMAIN 1577 1627 Laminin EGF-like 15.
 FT DOMAIN 1628 1637 Laminin EGF-like 16 (N-terminal).
 FT DOMAIN 1638 1830 Laminin domain IV 2 (domain IV A).
 FT DOMAIN 1831 1863 Laminin EGF-like 16 (C-terminal).
 FT DOMAIN 1864 1912 Laminin EGF-like 17.
 FT DOMAIN 1913 1968 Laminin EGF-like 18.

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FT DOMAIN 1969 2022 laminin EGF-like 19.
FT DOMAIN 2023 2069 laminin EGF-like 20.
FT DOMAIN 2070 2116 laminin EGF-like 21.
FT DOMAIN 2117 2166 laminin EGF-like 22.
FT DOMAIN 2167 2235 laminin I and I.
FT DOMAIN 2236 2292 laminin G-like 1.
FT DOMAIN 2291 3115 laminin G-like 2.
FT DOMAIN 3124 3292 laminin G-like 3.
FT DOMAIN 3340 3513 laminin G-like 4.
FT DOMAIN 3520 3692 laminin G-like 5.
FT DOMAIN 3692 4221 Coiled coil (Potential).
FT DOMAIN 4221 2335 Coiled coil (Potential).
FT DOMAIN 2310 2670 Coiled coil (Potential).
FT SITE 1722 1724 Cell attachment site (Potential).
FT SITE 1838 1840 Cell attachment site (Potential).
FT DISULFID 300 309 By similarity.
FT DISULFID 302 322 By similarity.
FT DISULFID 324 333 By similarity.
FT DISULFID 336 356 By similarity.
FT DISULFID 359 368 By similarity.
FT DISULFID 361 393 By similarity.
FT DISULFID 396 405 By similarity.
FT DISULFID 408 426 By similarity.
FT DISULFID 429 440 By similarity.
FT DISULFID 431 447 By similarity.
FT DISULFID 449 458 By similarity.
FT DISULFID 461 471 By similarity.
FT DISULFID 494 506 By similarity.
FT DISULFID 496 515 By similarity.
FT DISULFID 517 526 By similarity.
FT DISULFID 529 538 By similarity.
FT DISULFID 541 553 By similarity.
FT DISULFID 543 560 By similarity.
FT DISULFID 562 571 By similarity.
FT DISULFID 574 584 By similarity.
FT DISULFID 587 599 By similarity.

```

Query Match 24.2%; Score 712; DB 1; Length 3695;

Best Local Similarity 33.1%; Pred. No. 6.4e-35; Matches 194; Conservative 96; Mismatches 214; Indels 82; Gaps 21;

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1 MRFGKSGEVRLEPNDELDKGYTSLFLORPLRENGGTEDEFWYVYLNKDKASKOYIG 60
2737 MKRGRSGVQRTLRDLADLAAYALAKFYLDGSPBEGQTEDEFWYVYVMSKRAKTYMG 2796
61 MAVVDGQLTCVYNGDR-EAEVQIDQVLTSESGEAVMDRVKFORIYQPAKANTYKE--- 116
2797 VSLRDKKVMHYVQGEAGPAVLISIDEDIGEQ-----FAAVSLDRTLQFGHMSVTVRKOM 2850
117 --ATSKPKAPAYVDLEGGSSNTLANTDPEDAVYVGGYPPDFELPSRLRPPYKGCIEL 174
2851 IQRTKQDTVAFGA---EG-----LANTRPDPFVYVGGYSTFPPLLRFPGYRGCIEM 2902
175 DDLENENTSLYNTKTEFNLTTEVEPCRRKE-----SDKNYEGTGVARIPTQPR-AP 228
2903 DTLNEEVAVSLYNTKRTQLDANDRPAKRSKSTGDPPLTDSYDGGFAKISDSOIST 2962
229 FPNFIQTITQTVDRGLLEPAENQDNFTSLNIEDGNLWVRYKANS-----EPP----- 275
2963 TKRPEGLRLVSVSGVLPFLKQSQPFLCLAVQBSLVLLVDPGAKKAVPLQPPPLTS 3022
276 KEKCIPTINDGKDHSLITITGKQKQKMWNVN---SVRISEITDFSTYYIGI--- 329
3023 ASKAIQ-----VFLIGSGRKRVLVVERATVYSVEQDDLEADAYVYGGVPPD 3071
330 --PLAIRERFNISTPAFGCKGNLK--KTSGVRLNDTVYVTKKSGDMVLVTASFSR 384
3072 QLPSPSLAKWLP-TGGSVRGCKYKALKAGKYVDLKRIN-TTGVSGAGCTADLLVGAMTFHG 3129
385 GG--QMSFTNLVDVSTDRPOLSPFGQTFQPSGTLNQTRTSLVLTLEDGHIELSTRDS 442
3130 HGFLRLALSNV-ADLTGVNVSGFHFSAQDSALLYRASPDGLCQVSLQGRVSLQTLRT 3188

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QY 443 NIDIFKSPGYMDGLLHNHVSVIDTSGRLRLIDDOV--LRNRQLPSFSAQOS---LR 496
DB 3189 EV---KIQAGFADGAPHYVAFYGNATGVMLYVDDQGLQMKPHGPPPELQPPGPPRL 3245
QY 497 LGG-----GHFEGCISNVLVQPSGSPFVLDLASKSTYKQDASLG 535
DB 3246 LGGLPESGRTYNSFGCSISNVFVRLGPRQVFPDLQONTAGSNVSTG 3291

RESULT 11
Q8TDF8 PRELIMINARY; PRT; 3695 AA.
ID O8TDF8
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Laminin alpha5 chain precursor.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21935381; Pubmed=11821406; DOI=10.1074/jbc.M11228200;
RA Dol M., Thyboll J., Kortsemaa J., Jansson K., Iivanainen A.,
RA Parvadeh M., Timpel R., Hedin U., Swedenborg J., Tryggvason K.;
RT "Recombinant human laminin-10 (alpha5beta3gamma1). Production,
RT purification, and migration-promoting activity on vascular endothelial
RT cells."
RT J. Biol. Chem. 277:12741-12748(2002).
RL EMBL; AF443072; AAM12527.1; -.
DR HSSP; P02468; INPR.
DR GO; GO:0005605; C:basal lamina; NAS.
DR GO; GO:0005178; F:integrin binding; IDA.
DR GO; GO:0005198; F:structural molecule activity; IC.
DR GO; GO:0001525; P:angiogenesis; NAS.
DR GO; GO:0016477; P:cell migration; IDA.
DR GO; GO:0008037; P:cell proliferation; NAS.
DR GO; GO:0008037; P:cell recognition; NAS.
DR GO; GO:0007010; P:cytoskeleton organization and biogenesis; NAS.
DR GO; GO:0004970; P:embryonic development; NAS.
DR GO; GO:0045446; P:endothelial cell differentiation; NAS.
DR GO; GO:0048041; P:focal adhesion formation; NAS.
DR GO; GO:0007229; P:integrin-mediated signaling pathway; IMP.
DR InterPro; IPR008985; ConA_like_1ec_91.
DR InterPro; IPR006209; EGF-like.
DR InterPro; IPR008979; Gal bind like.
DR InterPro; IPR009030; Grow_fac_recept.
DR InterPro; IPR000034; Laminin_B.
DR InterPro; IPR002049; Laminin_EGF.
DR InterPro; IPR001791; Laminin_G.
DR InterPro; IPR009254; Laminin_I.
DR InterPro; IPR010307; Laminin_II.
DR InterPro; IPR008211; Laminin_N.
DR InterPro; IPR001638; SBP_bac_3.
DR InterPro; IPR001368; TNFR_c6.
DR InterPro; IPR003129; TSP_N.
DR Pfam; PF00052; Laminin_EGF.1.
DR Pfam; PF00053; Laminin_EGF.20.
DR Pfam; PF02210; Laminin_G.2; 4.
DR Pfam; PF06008; Laminin_I.1.
DR Pfam; PF06009; Laminin_II.1.
DR Pfam; PF06010; Laminin_III.1.
DR Pfam; PF00055; Laminin_N.1.
DR PRINTS; PR00011; EGF_LAMININ.
DR PRODOM; PD003031; Laminin_B.1.
DR SMART; SM00180; EGF_Lam; 20.
DR SMART; SM00281; LamB.1.
DR SMART; SM00282; LamG.5.
DR SMART; SM00136; LamH.1.
DR PROSITE; PS00022; EGF_1; 19.
DR PROSITE; PS01186; EGF_2; 3.
DR PROSITE; PS01248; LAMININ TYPE EGF; 19.
DR PROSITE; PSS0025; LAM_G_DOMAIN; 5.

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DR PROSITE; PS01039; SBP_BACTERIAL_3; UNKNOWN_1.
 DR PROSITE; PS00652; TNFR_NGFR_1; UNKNOWN_1.
 DR PROSITE; PS00650; TNFR_NGFR_2; 1.
 KM Laminin EGF-like domain; Signal.
 FT SIGNAL 1 35 Potential.
 FT CHAIN 36 3695 laminin alpha5 chain.
 SQ SEQUENCE 3695 AA; 399645 MW; 697038525368E0A3 CRC64;
 Query Match 24.2%; Score 712; DB 2; Length 3695;
 Best Local Similarity 33.1%; Pred. No. 6,4e-39;
 Matches 194; Conservative 96; Mismatches 214; Indels 82; Gaps 21;
 QY 1 MRNNGSGVFRRLNDLEDKYTSLSLTPQRPDLNENGTEDMPVYLGAKDASDYIG 60
 DB 2737 MKENGSGVQLRTFPRDLADLAAYTALKFYLGPEPEPGQTEPRFVWYMGSRQATDYNG 2796
 QY 61 MAVVDDQLTCVNLGDR-EAEVQIDQVLTSESGEAMDRVQRRTYQPAKNTYGE--- 116
 DB 2797 VSLDKKVMWVYQLGEGPVALSIDEDIGQ-----FAAVSLDKRTLQFGHMSVTVEROM 2850
 QY 117 --ATSNKPKAPAVYDEGGSSNTLLNLPEDAVFYVGGYPPDELPRLPPEYKCIETL 174
 DB 2851 IQETKGDVYAPGA---EG-----LNLNRPDVIFYVGGYSTTTPPLARFPGRCIEM 2902
 QY 175 DDLENVSLYNEKTFPNTTEVEPCRRKEE---SDKNYEEGTGARIPTQEN-AP 228
 DB 2903 DTLNEEVSLYNEFERFQDLTAVDPRCARSKSTGDPWLTGSGYLDGTFARISFDSQIST 2962
 QY 229 FHPPIQITVTYVRLGLFPAENDNPISLNIEBGNLMVRKANS-----EPP----- 275
 DB 2963 TKRPEGLKRVSYSGVLFKQOSQFLCAVQSGSLVLVDFAGLKKAVLPQPPPLTS 3022
 QY 276 KKKGIDTINDKDHSLITIGLKQKMWNNVNER---SVRIEGLFDFSTYIIGI--- 329
 DB 3023 ASALIQ-----VELLGSRRKRVLYVERATYVSQBNDLEADAYILGSGVPP 3071
 QY 330 --PIAIRERFNISTPAFGQCMKULK---KTSGVRLNDVGTGKCSBDMKLVRTASFSR 384
 DB 3072 QLPPSLRLMFLP-TGSGVRGCVKGIKALGKYVLDKRLN-TTGVASGCTADLLVGRAMTFNG 3129
 QY 385 CG--QMSFTMLDVPSIDRQLSFGFQFQPSGSLNHQRTSSSLATYLEGHIELSTRDS 442
 DB 3130 HGLRLALSNV-APLTGNVYSGRGFSAQDSALLYRASDGLCYVELQGRVSLQLLRF 3188
 QY 443 NIPIFKSPGYMDGLLHVSVISDTSGRLIIDQV--LRRNRLPSFSNAQOS---LR 496
 DB 3189 EV---KTQAGFADGAPHYVAFYSNATGVMLYVDDQLQGMKPHGPPPELQPPGEPRLL 3245
 QY 497 LGG-----GHFEGCISNVLVQFSPSPFVLDLASKTYKQASLG 535
 DB 3246 LGGLPESGRTYNFSGCISNVFVRLGLPQKRVFPLQQWLAGSVNVSTG 3291
 RESULT 12
 LMA4_HUMAN STANDARD; PRT; 1816 AA.
 ID LMA4_HUMAN Q16363; Q14735; Q15335; Q9UE18; Q9UJN9;
 AC Q16363; Q14735; Q15335; Q9UE18; Q9UJN9;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Laminin alpha-4 chain precursor.
 DS Name=LMA4;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX TISSUE=Petal lung;
 RX MEDLINE=95300971; Pubmed=7781776; DOI=10.1016/0014-5793(95)00462-1;
 RA Iivanainen A., Sainio K., Satiola H., Tryggvason K.;
 RT "Primary structure and expression of a novel human laminin alpha 4
 chain.";

RL FEBS Lett. 365:183-188(1995).
 (2)
 RP SEQUENCE FROM N.A.
 RP TISSUE=Heart;
 RC MEDLINE=97454279; Pubmed=9310354;
 RX Richards A.J., Luccarini C., Pope F.M.;
 RT "The structural organisation of LMA4, the gene encoding laminin
 alpha4.";
 RT Eur. J. Biochem. 248:15-23(1997).
 RL [3]
 RP SEQUENCE OF 236-1816 FROM N.A.
 RC TISSUE=Heart;
 RX MEDLINE=95048381; Pubmed=7959779;
 RA Richards A.J., Al-Imara L., Carter N.P., Lloyd J.C., Leversha M.A.,
 RA Pope F.M.;
 RT "Localisation of the gene (LMA4) to chromosome 6q21 and isolation of
 a partial cDNA encoding a variant laminin A chain.";
 RL Genomics 22:237-239(1994).
 RN [4]
 RP SEQUENCE OF 66-1816 FROM N.A.
 RA Subby B.;
 RL Submitted (MAR-1998) to the EMBL/Genbank/DBJ databases.
 CC -1- FUNCTION: Binding to cells via a high affinity receptor, laminin
 is thought to mediate the attachment, migration and organization
 of cells into tissues during embryonic development by interacting
 with other extracellular matrix components.
 CC -1- SUBUNIT: Laminin is a complex glycoprotein, consisting of three
 different polypeptide chains (alpha, beta, gamma), which are bound
 to each other by disulfide bonds into a cross-shaped molecule
 comprising one long and three short arms with globules at each
 end.
 CC -1- SUBCELLULAR LOCATION: Extracellular; found in the basement
 membranes (major component).
 CC -1- TISSUE SPECIFICITY: In adult, strong expression in heart, lung,
 ovary small and large intestines, placenta, liver; weak or no
 expression in skeletal muscle, kidney, pancreas, testis, prostate,
 brain. High expression in fetal lung and kidney. Expression in
 fetal and newborn tissues is observed in certain mesenchymal cells
 in tissues such as smooth muscle and dermis.
 CC -1- DOMAIN: The alpha-helical domains I and II are thought to interact
 with other laminin chains to form a coiled coil structure.
 CC -1- DOMAIN: Domain G is globular.
 CC -1- SIMILARITY: Contains 4 laminin EGF-like domains.
 CC -1- SIMILARITY: Contains 5 laminin G-like domains.
 CC -1- CAUTION: Gene LMA4 was formerly called LMA3.
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 between the Swiss Institute of Bioinformatics and the EMBL outstation -
 the European Bioinformatics Institute. There are no restrictions on its
 use by non-profit institutions as long as its content is in no way
 modified and this statement is not removed. Usage by and for commercial
 entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 or send an email to license@isb-sib.ch).
 CC
 CC EMBL; 578569; AAB34635.1; -;
 CC EMBL; X91171; CAA62596.1; -;
 CC EMBL; Y14240; CAA74636.1; -;
 CC EMBL; X76939; CAA54258.1; -;
 CC EMBL; Z59289; -; NOT_ANNOTATED_CDS.
 CC PIR; S68960; S68960.
 CC HSSP; P02468; INPE.
 CC DR Genew; HGNC:6484; LMA4.
 CC MIM; 600133; -;
 CC DR GO; GO:0005605; C;basal lamina; TAS.
 CC GO; GO:0005201; F;extracellular matrix structural constituent; TAS.
 CC DR InterPro; IPR008985; Cona_1like_1ec_g1.
 CC DR InterPro; IPR006209; EGF_1like.
 CC DR InterPro; IPR002049; Laminin_EGF.
 CC DR InterPro; IPR001791; Laminin_G.
 CC DR InterPro; IPR009254; Laminin_I.
 CC DR InterPro; IPR010307; Laminin_II.
 CC DR InterPro; IPR003129; TSP_N.
 CC DR Pfam; PF00053; Laminin_EGF; 3.

DR Pfam; PF00054; Laminin G; 3.
 DR Pfam; PF06008; Laminin I; 1.
 DR Pfam; PF06009; Laminin II; 1.
 DR PROSITE; PS00022; EGF_1; UNKNOWN 1.
 DR PROSITE; PS50025; LAM G DOMAIN; 5.
 DR PROSITE; PS01248; LAMININ TYPE BGF; 3.
 KM Basement membrane; Cell adhesion; Coiled coil; Extracellular matrix;
 KM Glycoprotein; Laminin BGF-like domain; Repeat; Signal.
 PT SIGNAL 1
 PT CHAIN 24
 PT CHAIN 25
 PT CHAIN 82
 PT CHAIN 131
 PT CHAIN 132
 PT CHAIN 186
 PT CHAIN 187
 PT CHAIN 240
 PT CHAIN 241
 PT CHAIN 255
 PT CHAIN 825
 PT CHAIN 1028
 PT CHAIN 1040
 PT CHAIN 1227
 PT CHAIN 1227
 PT CHAIN 1395
 PT CHAIN 1462
 PT CHAIN 1633
 PT CHAIN 1640
 PT CHAIN 1813
 PT CHAIN 313
 PT CHAIN 396
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 PT CHAIN 178
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 PT CHAIN 265
 PT CHAIN 265
 PT CHAIN 276
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 PT CHAIN 491
 PT CHAIN 491
 PT CHAIN 1057
 PT CHAIN 1057
 PT CHAIN 1110
 PT CHAIN 1110
 PT CHAIN 1816
 PT CHAIN 1816

Query Match 23.3%; Score 686; DB 1; Length 1816;
 Best Local Similarity 32.2%; Pred. NO. 1.4e-37;
 Matches 194; Conservative 101; Mismatches 245; Indels 62; Gaps 21;

QY 1 MRNKGSGVEVRLPNDEJDKGYTSLFLP-----QRDLAENGSTETMPFMYLGNKDAK 56

DB 829 MFEDGSAVEVHRTSMDDLKATSLTYKKPEVKPELLE---TDQFLTYLGSNKK 885
 QY 57 DYIGMAVVDGQLTCVYNLGDREAEVQIDOVLTSESOEAVMDVKFQRIYQAKLNTYKE 116
 DB 886 EYVGLAIKIDNLYVYNLGLKQVEIPLDS--KPSWPAFVSIVKIERVGHKVFELTP 943
 QY 117 ATNKKRAVAVDLEGGSSNTLLNLPDAVFFVGVGPPDFELPSLRFPFYGCLELD 176
 DB 944 SLSTLBEKFKIKGEGSGDSDLLDPEDEVFVGVGVPSPFKPTSLNLPFGVCLELAT 1003
 QY 177 LNEVNLVNFKTPFNANTTEVEPCRRK-----EESDKNFGGTGYA--RIYQPN--A 227
 DB 1004 LNDVSLVNFKTIYMDSTSTVPCARDKLAFTQSPAASFTFGSGAVVARDTRCKFG 1063
 QY 228 PEPNPTQITQTVDRGLLPEAENQDNFISLNEGMLNARY-----KLNSEPPREKGI 280
 DB 1064 QVTRPFLVETPADNGILLVNGSMFPLEMNGVLYHYVDYDGFSSGRVHLEDTLKA- 1122
 QY 281 RDTINDGKHSLITGKQKRWIVNERSVRI---EGEIPFSTYLGITP-----I 331
 DB 1123 --QINDAKTHEISI--YHNDKMKILVDRHVKSMONKCKIPFTDIYIGAPPEILQSR 1179
 QY 332 AIRERFNISPPARQGMKUL---KKTSGVRLNDVGVTKKSGEDMKLVRTASRGQM 388
 DB 1180 ALPAHPLDI-NRQCKGQFQKQKPNLEQTEITGVGCEPDSILSHRAFV--GQS 1236
 QY 389 SFTNLD-VPSYDRFQSLFQFQPSGTLNMQRTSLVLTDEGHIELSTDSNIPF 447
 DB 1237 FMSIQKISFPDFEGFPNRTIQPNGLFYASGSDVFSISLNDGVINDV--GIKV 1294
 QY 448 KSPGTMDGLHVSIVSDTSGLR--LLID-DQVLRNQRLEPSNAQSLR--LGG-- 499
 DB 1295 SVDKQVNDGISHF--YISSVSPRYELIVDKSVGSKNPKKIEQTOSEKFEYGGSP 1352
 QY 500 -----GHPGCTSNLVQRPSPQSEVYLDLASKSTKQDASIGGSLKKPPLMKFKSPKR 554
 DB 1353 ISAQVYVNFCTISNAYFTRVDVEVDVFORYERKVTSLYECPISSPLFLHKKGK 1412
 QY 555 NK 556
 DB 1413 SK 1414

RESULT 13
 ID Q91VVO PRELIMINARY; PRT; 1254 AA.
 AC Q91VVO;
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
 DE 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 GN Lama4 protein (Fragment).
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OC NCBI TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=mx FVB/N; TISSUE=Mammary tumor;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heien F.,
 RA Datchenko L., Musunna K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Schetz T.E.,
 RA Brownstein M.J., Ueda T.B., Yoshizuki S., Carninci P., Prange C.,
 RA Rana S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fehey J., Helton E., Kettelman W., Madan A., Rodriguez S., Sanchez A.,

RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
 RA Krzyzinski M.I., Skaleja U., Smalins D.E., Schnerch A., Schein J.B.,
 RA Jones S.J., Marra M.A.,
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences.";
 RT Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=mlx FVB/N; TISSUE=Mammary tumor;
 RA Strausberg R.;
 RL Submitted (May-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC008533; AA008533.1; -.
 DR HSSP; Q60675; 1QD0.
 DR MGD; MG1:109321; Lama4.
 DR GO; GO:0005605; C:basal lamina; IDA.
 DR GO; GO:0005615; C:extracellular space; TMS.
 DR GO; GO:0001568; P:blood vessel development; IMP.
 DR Pfam; PF02210; Laminin_G_2; 5.
 DR Pfam; PF06009; Laminin_II; 1.
 DR SMART; SM00282; LamG; 5.
 DR PROSITE; PSS0025; LAM_G_DOMAIN; 5.
 DR NON TER
 SQ SEQUENCE 1254 AA; 139723 MW; 54D49EF763D37CD9 CRC64;
 Query Match 23.3%; Score 685; DB 2; Length 1254;
 Best Local Similarity 32.2%; Pred. No. 9,7e-38;
 Matches 193; Conservative 100; Mismatches 251; Indels 56; Gaps 20;
 QY 1 MRPNGSGVVRRLPNDLEDKGTSLSLFQ--RPDLBENGSTEDMFYVYLGAKQASD 57
 DB 267 MMEFGGSAVEHVKVAVVDLKAFTSLYKPPKPAEPGVAVAQFVLYLGSKNAKKE 326
 QY 58 YIGMAVVDGQLCVNYLGPBRAEVOVDQVLTESQEAAMDRCFQRIYQFAKLANTKXA 117
 DB 327 YMGIAIKNDLVVYVYVLMGKQVEILDS--KPVSSPAFSTYKIRVGKGVFLTPVS 384
 QY 118 TSNKPRAPAVYDLEGSSNTLLNLDPEDAVFYGVYPPFELPSRLRPPYKGCIELDL 177
 DB 385 LSTAEKFKIKGEFAGDSDSLDLTDEDTFYVYGVPANPKLPASLNLSSYSCLELATL 444
 QY 178 NENVSLVNFKTFNTTEVEPCRRK---EESDKVFEGTGYA--RIPTQPN--AP 228
 DB 445 NNDVLSLVNFKHYNDPSKSVPCARDKLAFTQSRASAYFFDSSYAVVDITRGGFQ 504
 QY 229 FPFVIGTIGTVYDRLFFAENDNFIINIEDGNLMVYKLN--SEPKKGRDT----- 283
 DB 505 VTRFDIEIRTPANGVLVLLMVNGSMFSLMRNGYLHVFDFGFSNGPVH--LEDTLKKA 562
 QY 284 -INDGKHSLITIGKLQKRMWVNVRSVRI---EGEIPDFSTYVIGIPIAIRERFNI 339
 DB 563 QINDAKYHEISI-IYNDKKMLVDRRHVKSVDNEKKIPFDIYIGAPQGVLOSRTL 621
 QY 340 STPA-----FQGMKQL--KKTGVVRLNDIVGTTKCKSEDKLVRTASFSRQGMSTP 391
 DB 622 RAHLPLDIIFRGCMKMFQFQKQFNLLEQETELGVGCEPESDLISRAAFN--GGSFLA 679
 QY 392 NLD-VSTDRFQSLSPQTFQPSGTLNHNQTRSSSLVLTLEDHIELSTRDSNIPFKXP 450
 DB 680 STICKIFPFGFEGFEPRLQPNGLFFYTSGSDFVSIISLNDTVMDVK--GIKWSMD 737
 QY 451 GTVMGGLLHH-VSVISDTSGRLILDDQVLRNQRPLPSFNAQOS-----LRLGG---- 499
 DB 738 KQYHDLPHFVVISIDTR-YELVVDKSLRGRGN--PTKKAQOTQTEKKPFPGGSPIS 794
 QY 500 ---GHFEGCISNVLVORFSGSPFVLDLASKSTKQDASLGCGSLNKPFLMLFKSPRRFK 556
 DB 795 PQYANFTGCISNAYFTRLDREVDEBDFQRYSEKWHSTLYECPIESSPLFLHKKGNSSK 854
 RESULT 14
 LMA4_MOUSE

ID LMA4_MOUSE STANDARD; PRT; 1816 AA.
 AC P97927; 088785; P70409;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Laminin alpha-4 chain precursor.
 GN Name=Lama4;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OK NCBI_Taxid=10090;
 RN [1]
 RP SEQUENCE FROM N.A., AND SEQUENCE OF 462-469, 478-483, 776-782 AND
 RP 940-945.
 RC STRAIN=BALB/c; TISSUE=Endothelial cells;
 RX MEDLINE=9736307; PubMed=9219532;
 RA Friessner M., Noeckel H., Pausch F., Roeder C., Hahn A., Deutzmann R.,
 RA Sorokin L.M.;
 RT "Cloning of the mouse laminin alpha 4 cDNA. Expression in a subset of
 RT endothelium.";
 RL Eur. J. Biochem. 246:727-735(1997).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Heart;
 RX MEDLINE=97202462; PubMed=9049981; DOI=10.1016/S0945-053X(96)90162-6;
 RA Liu J., Mayne R.;
 RT "The complete cDNA coding sequence and tissue-specific expression of
 RT the mouse laminin alpha 4 chain.";
 RL Matrix Biol. 15:433-437(1996).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BALB/c;
 RX MEDLINE=98010627; PubMed=9346933; DOI=10.1074/jbc.272.44.27862;
 RA Iivanainen A., Kortemaa J., Sahberg C., Morita T., Bergmann U.,
 RA Theisfeldt J., Tryggvason K.;
 RT "Primary structure, developmental expression, and immunolocalization
 RT of the murine laminin alpha4 chain.";
 RL J. Biol. Chem. 272:27862-27868(1997).
 RN [4]
 RP SEQUENCE OF 836-1106 FROM N.A.
 RC STRAIN=ICR; TISSUE=Placenta;
 RX MEDLINE=97296337; PubMed=9151674; DOI=10.1083/jcb.137.3.685;
 RA Miner J.H., Patton B.L., Lentz S.I., Gilbert D.J., Snider W.D.,
 RA Jenkins N.A., Copeland N.G., Sane J.R.;
 RT "The laminin alpha chains: expression, developmental transitions, and
 RT chromosomal locations of alpha-5, identification of heterotrimeric
 RT laminin 8-11, and cloning of a novel alpha3 isoform.";
 RL J. Cell Biol. 137:685-702(1997).
 RN [5]
 RP SEQUENCE OF 1467-1691 FROM N.A.
 RC TISSUE=Placenta;
 RX MEDLINE=97187457; PubMed=9034910;
 RX DOI=10.1002/(SICI)1096-9861(19970224)378:4<547::AID-CMB93>3.0.CO;2-2;
 RA Lentz S.I., Miner J.H., Sane J.R., Snider W.D.;
 RT "Distribution of the ten known laminin chains in the pathways and
 RT targets of developing sensory axons.";
 RL J. Comp. Neurol. 378:547-561(1997).
 CC -!- FUNCTION: Binding to cells via a high affinity receptor, laminin
 CC is thought to mediate the attachment, migration and organization
 CC of cells into tissues during embryonic development by interacting
 CC with other extracellular matrix components.
 CC -!- SUBUNIT: Laminin is a complex glycoprotein, consisting of three
 CC different polypeptide chains (alpha, beta, gamma), which are bound
 CC to each other by disulfide bonds into a cross-shaped molecule
 CC comprising one long and three short arms with globules at each
 CC end.
 CC -!- SUBCELLULAR LOCATION: Extracellular; found in the basement
 CC membranes (major component).
 CC -!- TISSUE SPECIFICITY: Strongly expressed in peripheral nerves,
 CC cardiac muscle, fat, dermis, lung stroma, aortic endothelium,
 CC endocardium and endothelium of blood vessels in skin and brain.
 CC -!- DOMAIN: The alpha-helical domains I and II are thought to interact
 CC with other laminin chains to form a coiled coil structure.

CC -1- DOMAIN: Domain G is globular.
 CC -1- SIMILARITY: Contains 4 laminin G-like domains.
 CC -1- SIMILARITY: Contains 5 laminin G-like domains.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL: U88950; AAB41840.1; -
 DR EMBL: Y09827; CA70970.1; -
 DR EMBL: U88865; AAC24725.1; -
 DR EMBL: U88352; AAC5178.1; -
 DR EMBL: U69176; AAC52982.1; -
 DR HSSP: P02468; INPE.
 DR MGD: MGI:109321; Lama4.
 DR GO: GO:0005604; C-basement membrane; IDA.
 DR InterPro: IPR008985; Cona_1like_1ec_g1.
 DR InterPro: IPR006209; EGF_1like.
 DR InterPro: IPR009030; Grow_fac_recept.
 DR InterPro: IPR002049; Laminin_EGF.
 DR InterPro: IPR001791; Laminin_G.
 DR InterPro: IPR009254; Laminin_I.
 DR InterPro: IPR010307; Laminin_II.
 DR InterPro: IPR003129; TSP_N.
 DR Pfam: PF00053; Laminin_EGF_3.
 DR Pfam: PF00054; Laminin_G_4.
 DR Pfam: PF06008; Laminin_I_1.
 DR Pfam: PF06009; Laminin_II_1.
 DR PROSITE: PS00022; EGF_1; UNKNOWN 1.
 DR PROSITE: PS01248; LAMININ TYPE EGF_3.
 DR PROSITE: PS0025; LAM G DOMAIN; 5.
 DR Basement membrane; Cell adhesion; Coiled coil;
 DR Direct protein sequencing; Extracellular matrix; Glycoprotein;
 KM Laminin EGF-like domain; Repeat; Signal.
 KM Laminin EGF-like domain; Repeat; Signal.
 FT CHAIN 1 1816 Laminin alpha-4 chain.
 FT DOMAIN 82 131 Laminin EGF-like 1.
 FT DOMAIN 132 186 Laminin EGF-like 2.
 FT DOMAIN 187 240 Laminin EGF-like 3.
 FT DOMAIN 241 255 Laminin EGF-like 4 (Incomplete).
 FT DOMAIN 256 825 Domain I and I.
 FT DOMAIN 826 1030 Laminin G-like 1.
 FT DOMAIN 1042 1222 Laminin G-like 2.
 FT DOMAIN 1229 1397 Laminin G-like 3.
 FT DOMAIN 1462 1633 Laminin G-like 4.
 FT DOMAIN 1640 1813 Laminin G-like 5.
 FT DOMAIN 431 523 Coiled coil (potential).
 FT DOMAIN 556 604 Coiled coil (potential).
 FT DOMAIN 655 717 Coiled coil (potential).
 FT DOMAIN 770 799 Coiled coil (potential).
 FT SITE 717 719 Cell attachment site (potential).
 FT DISULFID 82 91 By similarity.
 FT DISULFID 84 98 By similarity.
 FT DISULFID 101 110 By similarity.
 FT DISULFID 113 129 By similarity.
 FT DISULFID 132 146 By similarity.
 FT DISULFID 134 155 By similarity.
 FT DISULFID 157 166 By similarity.
 FT DISULFID 169 184 By similarity.
 FT DISULFID 187 202 By similarity.
 FT DISULFID 189 209 By similarity.
 FT DISULFID 212 221 By similarity.
 FT DISULFID 224 238 By similarity.
 FT DISULFID 266 265 Interchain (Probable).
 FT DISULFID 269 269 Interchain (Probable).
 FT CARBOHYD 104 104 N-linked (GlcNAc...)
 FT CARBOHYD 104 104 N-linked (GlcNAc...)
 FT CARBOHYD 115 115 N-linked (GlcNAc...)
 FT CARBOHYD 308 308 N-linked (GlcNAc...)
 FT CARBOHYD 333 333 N-linked (GlcNAc...)
 FT CARBOHYD 333 333 N-linked (GlcNAc...)

IT CARBOHYD 458 458 N-linked (GlcNAc...)
 IT CARBOHYD 550 550 N-linked (GlcNAc...)
 IT CARBOHYD 571 571 N-linked (GlcNAc...)
 IT CARBOHYD 574 574 N-linked (GlcNAc...)
 IT CARBOHYD 631 631 N-linked (GlcNAc...)
 IT CARBOHYD 639 639 N-linked (GlcNAc...)
 IT CARBOHYD 735 735 N-linked (GlcNAc...)
 IT CARBOHYD 751 751 N-linked (GlcNAc...)
 IT CARBOHYD 754 754 N-linked (GlcNAc...)
 IT CARBOHYD 780 780 N-linked (GlcNAc...)
 IT CARBOHYD 803 803 N-linked (GlcNAc...)
 IT CARBOHYD 1088 1088 N-linked (GlcNAc...)
 IT CARBOHYD 1283 1283 N-linked (GlcNAc...)
 IT CARBOHYD 1361 1361 N-linked (GlcNAc...)
 FT CARBOHYD 8 8 C -> S (in Ref. 2).
 FT CARBOHYD 18 18 C -> Y (in Ref. 2).
 FT CARBOHYD 248 248 C -> R (in Ref. 3).
 FT CARBOHYD 297 297 G -> A (in Ref. 3).
 FT CARBOHYD 431 433 THR -> HPS (in Ref. 2).
 FT CARBOHYD 679 679 S -> C (in Ref. 3).
 FT CARBOHYD 703 703 D -> G (in Ref. 2).
 FT CARBOHYD 706 706 N -> H (in Ref. 2).
 FT CARBOHYD 728 728 K -> R (in Ref. 2).
 FT CARBOHYD 730 730 F -> I (in Ref. 2).
 FT CARBOHYD 779 779 R -> G (in Ref. 1; AA sequence).
 FT CARBOHYD 810 810 R -> S (in Ref. 3).
 FT CARBOHYD 867 867 AEP -> QT (in Ref. 2).
 FT CARBOHYD 936 936 K -> E (in Ref. 3).
 FT CARBOHYD 970 970 L -> V (in Ref. 3).
 FT CARBOHYD 1132 1132 H -> R (in Ref. 2).
 FT CARBOHYD 1200 1200 F -> I (in Ref. 2).
 FT CARBOHYD 1382 1382 D -> A (in Ref. 2).
 FT CARBOHYD 1413 1414 NS -> EF (in Ref. 1).
 FT CARBOHYD 1489 1489 A -> S (in Ref. 2).
 SQ SEQUENCE 1816 AA; 201818 MM; B49C45F3A4599D8 CRC64;
 Query Match 23.3%; Score 685; DB 1; Length 1816;
 Best Local Similarity 32.2%; Pred. No. 1.6e-37;
 Matches 193; Conservative 100; Mismatches 251; Indels 56; Gaps 20;
 1 MRENGSGVVRRLPNLDELKGYTSLSPFQ---RPDLRENGSTEDMFVNYLGNKQASKD 57
 829 MMEFGSAYEVHVKVSDVDLKAFTSLVKKPPEKPAEPGAWAVDQFVLYISKNKKE 888
 58 YICGAVVDGQLCTVNLGDBEAVQIDVLTSESGEAVNDRYKFORIYPAKLNTYKKA 117
 889 YMGIAIKNDLVVYVNLGMQDVEILLDS--KPVSSMPAYPSIVKIERVGRGKVFITVPS 946
 118 TSNKPRAPAVYDLEGGSSNTLNLDPEDAVFYVGYPPDELSRLRFPYKCIETDDL 177
 947 LSTYARKEFLKGEFPAQDSDLDTPEBDVFFYVGVGPANKEPLASLNLPSYSGLELATL 1006
 178 NENVLISLVNPKTFNNTTEVERCRRK-----EESDKNFEGNGYA--RIPTQPN--AP 228
 1007 NNDVLSYFNKHIYNDPSKSVPCARDKALFQTSRAASYFFDSSYAVVADITRRGFGQ 1066
 229 FPNFIQTIQTVVDRGLLFFAENQDNFTSLNIEDNIMVRYKLN-SSEPKEKGIQRT---- 283
 1067 VTRFDIEIRPADNGVILMVNGSMFSLMRNGYLHVFDYFGSNGPVH--LEDTLKKA 1124
 284 -INDGDHSLITITGLQKRMVNNVRSVRI---EGEIFDEFTYITGIPIMAREFNI 339
 1125 QINDATYHELSI-IYNDKRMILVVRRAVKSITDNEKKKLPFTDIYIGAPQVLOSRTL 1183
 340 STPA-----FOGCMKUL---KTSGVRLNDIVGVTKKSGEDMKLVYTAASRGQMSFT 391
 1184 RAHLPLDINRGCMKGRQPKDQFNLEQRETIQVGVGCPEDSLISRATFN--QGSAFIA 1241
 392 NLD-VBSTDRFQSLSPQRTQPSGTLNMQTRISSLLVLTLEDGHIELSTDSNIPFKSP 450
 1242 SIQKISFDFEFGGFRTLPNGLLFFYYSGSADVPSISLNDQITVAVDVK--GIKWNSTD 1299
 451 GTYMDGLLHH-VSVISDTSGILRLIDQVLRNRQRLPSFSNAQOS-----LRLGG---- 499

DB 1300 KQYHDLPHFVVISIDTR-YELVVKSRIRGN--PTKGAKQOTTEKFFYGGSPIS 1356
QY 500 ---GHEGICISNVLVQRFSGSPYVLDLASKSTKKDASLGCSLANKPPFLMLFKSPRRFNK 556
DB 1357 PQVANTGCGISNAYFRLDRDVEVEDFQRYSEKVVHSLVYECPIESSPLFLHKKGNSSK 1416

RESULT 15
Q6ZQAL
ID Q6ZQAL PRELIMINARY; PRT; 1524 AA.
AC Q6ZQAL;
DT 05-JUL-2004 (TEMBLrel. 27, Created)
DT 05-JUL-2004 (TEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TEMBLrel. 27, Last annotation update)
DE MKIA0533 protein (Fragment).
GN Name=MKIA0533;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Embryonic tail;
RX PubMed=14621295;
RA Okazaki N., Kikuno R., Ohara R., Iamamoto S., Koseki H., Hiraoka S.,
RA Suga Y., Nagase T., Ohara O., Koga H.;
RT "Prediction of the coding sequences of mouse homologues of KIA gene:
RT II. the complete nucleotide sequences of 500 mouse KIA-homologous
RT cDNAs identified by screening of terminal sequences of cDNA clones
RT randomly sampled from size-fractionated libraries.",
RL DNA Res. 10:167-180(2003).
DR EMBL; AK129157; BAC97967.2; -
DR GO; GO:0005604; C:basement membrane; IDA.
DR GO; GO:0005615; C:extracellular space; TAS.
DR GO; GO:0005178; P:integrin binding; IDA.
DR GO; GO:000515; P:protein binding; IPT.
DR GO; GO:0001763; P:branching morphogenesis; IDA.
DR GO; GO:000324; P:lung development; IMP.
DR GO; GO:0007517; P:muscle development; IMP.
DR InterPro; IPR008965; Cona like_1ec_g1.
DR InterPro; IPR006209; EGF like.
DR InterPro; IPR009030; Grow_fac_recept.
DR InterPro; IPR002049; Laminin_EGF.
DR InterPro; IPR001791; Laminin_G.
DR InterPro; IPR009254; Laminin_I.
DR InterPro; IPR010307; Laminin_II.
DR InterPro; IPR001368; TNFR_c6.
DR InterPro; IPR003129; TSP_N.
DR Pfam; PF00053; Laminin_EGF; 2.
DR Pfam; PF02210; Laminin_G_2; 4.
DR Pfam; PF06008; Laminin_I; 1.
DR Pfam; PF06009; Laminin_II; 1.
DR PRINTS; PR00011; EGF/LAMININ.
DR SMART; SM00180; EGF_Lam; 2.
DR SMART; SM00282; LamG; 5.
DR PROSITE; PS00022; EGF_1; UNKNOWN_3.
DR PROSITE; PS01248; LAMININ TYPE EGF; UNKNOWN_1.
DR PROSITE; PS00025; LAM G DOMAIN; 5.
DR PROSITE; PS00652; TNFR_NGFR_1; UNKNOWN_1.
KW Laminin EGF-like domain.
FT NON_TER 1
FT NON_TER 1524
SQ SEQUENCE 1524 AA; 166516 MW; F43411828F8B691 CRC64;

Query Match 23.2%; Score 683; DB 2; length 1524;
Best Local Similarity 31.8%; Pred. No. 1.8e-37;
Matches 166; Conservative 111; Mismatches 210; Indels 78; Gaps 22;

QY 1 MRENGSGVVRPLPNLDELKGYTSLPLQRPDLRENGG--TEDMPVWYLGKDKASKDY 58
DB 572 MKRNGSGVRLRPLDLADLAAYTALKFHIQSFVPAPBPGKNTGDHFLVLMGSRQATGDY 631

QY 59 IGMNAVVGQLTGVNULGDR-EAEVQIDQVLTSESSQEAVMDRYKQRIYQPAKNIYTKEA 117
DB 632 MGVSLRNQKVMWVYRLGKAGPTTLISIDENIGQ-----PAVVSIDRTLQGFHMSVYVE- 684
QY 118 TSNKPKAPVAVDLEBGS-----SNTLNLDPEDAVYVGGYPPDPFLPSRLRPPYKGCIE 173
DB 685 -----KQVHEIKADTYAPSGSEGLNHHPPDPFVYVGGYISNFTPPPLRFRPGIGCIE 738
QY 174 IDOLINENVLSTLYNFKTTNLTTEVEPCRRKKE-----SDKNYEGTGVARIPYQPNAP 228
DB 739 METLINEBVSLYNFQGTMLDTAVDKPCARSKATGDPWLTQSGYLDGSGFARISPEKQ-- 796
QY 228 FPN---PIQITQTTVDKGLPFAENQDNFISLINEDGULMRYKLS-----EPK- 276
DB 797 FENTKRFPQDELVLVSNGIIFPLKQESQFLCLAVQEGTLVLYFDGSGIKKADPLQPPQA 856
QY 277 ----EKGIKDTINDKQHSILITIGKLQKRMVINNERSVNRBGIIPFSTYYLGGI--- 329
DB 857 LTAASKALQVFLAAGNRKRLV--KVERATVFSVDQNNML--EMAD--AYLGGVPE 908
QY 330 --PIAIRERFNISTPFAFGCKMNLK---KTSGVVNLNDTVGVTKKCSBDMKLVRTASFSR 384
DB 909 QLPPLRLQLFP-SGGSVAGCIKGIKALGKYVDLKRNL--TTGISFGCTADLVLGRMTFHG 966
QY 385 GGQMSFTMLDV-PTSDRFQLSFGFOTFQPSGTLNHNQRTSLVYTTLEDGHIELSTRSN 443
DB 967 HGFLLPALPDAPIITEVYSGFGFGTQDNMLLYRTSPDPGYQVSLREGHVTLAFPMQ 1026
QY 444 IIFKSPGYMDGLHHVSVISDTSGLRLTIDD--QVLRNRQRLPSFNAQ-----QSLRL 497
DB 1027 V--ETQRYFADGADPHYAFYSNVTGVMVYDDQLQVKSHERTTPTMLQLOPEBPSRLLL 1083
QY 498 GG-----GHEGICISNVLVQRFSGSPYVLDLASKSTKKDASLG 535
DB 1084 GGLPVSGTFHNSGCGISNVFQRLAGPQRYVFDLHQMGSVAVSVG 1128

Search completed: February 22, 2005, 08:24:23
Job time : 98.5943 secs

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OM protein - protein search, using sw model

Run on: February 22, 2005, 08:04:10 : Search time 104.16 Seconds
(without alignments)
2097.921 Million cell updates/sec

Title: US-10-817-423-4

Perfect score: 2940

Sequence: 1 MRNKGKSGVVRLPNDLEDL.....MLFKSPKRFKGRIFVNVQL 565

Scoring table:

BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

1: A_Geneseq_16Dec04:*
2: Geneseqp19808:*
3: Geneseqp19808:*
4: Geneseqp20018:*
5: Geneseqp20028:*
6: Geneseqp20038:*
7: Geneseqp20038:*
8: Geneseqp20048:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2940	100.0	1694	3 AAB48461	Aab48461 Rat lamin
2	2940	100.0	1725	3 AAB48460	Aab48460 Rat lamin
3	2439	83.0	1693	3 AAB48459	Aab48459 Human lam
4	2439	83.0	1693	3 AAB48457	Aab48457 Human lam
5	2439	83.0	1713	3 AAB48458	Aab48458 Human cer
6	2439	83.0	1713	6 ABR92102	Abrr92102 Human cer
7	2439	83.0	1713	7 ADD29904	Add29904 Human lam
8	2439	83.0	1713	7 ADG37225	Adg37225 Human lam
9	2439	83.0	1713	8 ABM81957	Abm81957 Tumour-as
10	2439	83.0	1713	8 ADR87606	Adr87606 Human lam
11	2439	83.0	1724	3 AAB48456	Aab48456 Human lam
12	2439	83.0	3332	7 ADB08094	Adb08094 Novel pro
13	2431	82.7	1713	2 AAR70148	Aar70148 Deduced s
14	1310	44.6	770	2 AAW26584	Aaw26584 Rat hemid
15	717.5	24.4	3597	5 ABB09503	Abb09503 Human lam
16	717.5	24.4	3600	5 ABB09501	Abb09501 Human lam
17	717	24.4	3690	8 ADM87254	Adm87254 Human pro
18	715	24.3	1677	8 ADM87708	Adm87708 Human EST
19	715	24.3	3695	8 ADI28030	Adi28030 ECMCAD pr
20	715	24.3	3695	8 ADN04478	Adn04478 Antipsoct
21	715	24.3	3696	5 AAE17310	Aae17310 Human lam
22	715	24.3	3705	5 AAE17309	Aae17309 Human lam
23	712	24.2	1601	4 AAM39009	Aam39009 Human pol
24	712	24.2	1640	5 ABB09504	Abb09504 Human lam
25	712	24.2	1640	8 ADO10049	Ado10049 Novel hum

26	712	24.2	1645	7 ADL15098	Adl15098 Human mal
27	712	24.2	1645	7 ADN95658	Adn95658 Human BEC
28	712	24.2	3695	5 ABB81588	Abb81588 Human lam
29	694	23.6	1792	3 AAB48443	Aab48443 Human lam
30	694	23.6	1800	3 AAB48445	Aab48445 Human lam
31	694	23.6	1816	3 AAB48442	Aab48442 Human lam
32	694	23.6	1816	8 ADR87600	Adr87600 Human lam
33	694	23.6	1824	3 AAB48444	Aab48444 Human lam
34	688	23.4	1823	5 ABP63020	Abp63020 Human pol
35	686.5	23.4	3597	8 ADO10047	Ado10047 Novel hum
36	686	23.3	1581	7 ADJ68348	Adj68348 Human hea
37	685	23.3	1816	8 ADP08401	Adp08401 Human lam
38	685	23.3	953	5 AAM50358	Aam50358 Human lam
39	683	23.2	984	5 ABB80819	Abb80819 Heparin b
40	683	23.2	1792	3 AAB48447	Aab48447 Mouse lam
41	683	23.2	1816	3 AAB48446	Aab48446 Mouse lam
42	683	23.2	1816	7 ADC01877	Adc01877 Human lam
43	681	23.2	1816	7 ADC01879	Adc01879 Human lam
44	681	23.2	3635	5 ABB81589	Abb81589 Mouse lam
45	681	23.2	3635	5 AAM50357	Aam50357 Mouse lam

ALIGNMENTS

RESULT 1
AAB48461
ID AAB48461 standard; protein; 1694 AA.
XX
AC AAB48461;
XX
DT 02-MAR-2001 (first entry)
XX
DE Rat laminin 5 polypeptide, SEQ ID NO: 12.
XX
KW Rat; laminin 5; vulnary; antitumor; antidiabetic;
KM cell adhesion promoter; wound healing; ulcers; burn; skin graft;
KV periodontitis; gingivitis; Type I diabetes; angiogenesis regulation.
XX
XS Rattus norvegicus.
OS
XX
PN WO200066731-A2.
XX
PD 09-NOV-2000.
XX
PP 28-APR-2000; 2000WO-US011459.
XX
PR 30-APR-1999; 99US-0131720P.
PR 21-AUG-1999; 99US-0149738P.
PR 24-SEP-1999; 99US-0155945P.
XX
PA (BIOG-) BIOSYSTEM INC.
XX
PI Boutaud A;
XX
DR WPI, 2000-687538/67.
DR N-PSDB; AAC83722.
XX
PT Laminin 5-expressing cells, used to accelerate wound healing associated
PT with diabetic foot ulcers, venous ulcers, pressure sores, skin surgery,
PT burns, acute wounds and skin grafts.
XX
XX
PS Claim 3; Page 117-122; 232pp; English.
XX
XX
The present sequence is a laminin 5 chain polypeptide. Recombinant
laminin 5-expressing cells are used to accelerate wound healing,
especially diabetic foot ulcers, venous ulcers, pressure sores, skin
surgery, burns, acute wounds, skin grafts, corneal ulcerations, gastro-
intestinal ulcers, periodontitis, and gingivitis. They are also used to
improve the biocompatibility of medical devices, and to promote cell
adhesion to a surface. They can be used for the ex vivo treatment of Type
I diabetes. Laminin can also be used to regulate angiogenesis. The cell
line produces and secretes recombinant heterotrimeric laminin, whereas

CC prior art cell lines have been created that produce but do not secrete
CC only one or two chain laminins
XX
XX
SQ Sequence 1694 AA;

Query Match 100.0%; Score 2940; DB 3; Length 1694;
Best Local Similarity 100.0%; Pred. No. 1.5e-261;
Matches 565; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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1 MRFNGSGVYRLPNLDELKGYTSLFLQRPDLRENGGTEDMFWMTLGNKDAKDYIG 60
DB 751 MRFNGSGVYRLPNLDELKGYTSLFLQRPDLRENGGTEDMFWMTLGNKDAKDYIG 810
QY 61 MAVVDGQLTCVYNLGDREAEVQIDQVLTSESQEAVMDRYKFORIYQPAKLNTYKATSN 120
DB 811 MAVVDGQLTCVYNLGDREAEVQIDQVLTSESQEAVMDRYKFORIYQPAKLNTYKATSN 870
QY 121 KKPAAVYDLEGGSSNTLLNLPEDAVFYVGGYPPDFELPSRLRPPYKGCIELDLNEN 180
DB 871 KKPAAVYDLEGGSSNTLLNLPEDAVFYVGGYPPDFELPSRLRPPYKGCIELDLNEN 930
QY 181 VLSLYNFKTTFNLNTTEVEPCRRRKBESDKNYFEGGYARIPYQNAAPPNFIOITQTV 240
DB 931 VLSLYNFKTTFNLNTTEVEPCRRRKBESDKNYFEGGYARIPYQNAAPPNFIOITQTV 990
QY 241 DRGLLFFAENQDNFISLNIEDGNLWRYKLNSEPPKEKGRDITNDKSHLITIGKQ 300
DB 991 DRGLLFFAENQDNFISLNIEDGNLWRYKLNSEPPKEKGRDITNDKSHLITIGKQ 1050
QY 301 KKMWINVRSVRIRIEGIFDFSTYYLGGIPAIRERFNISTPAFGCKMKLKKTSGVVRL 360
DB 1051 KKMWINVRSVRIRIEGIFDFSTYYLGGIPAIRERFNISTPAFGCKMKLKKTSGVVRL 1110
QY 361 NDTVGYTKKCSBDMKLVRTASFRGGQMSFTNLDPVSTRFQLSFGFOTFQPSGTLNHQ 420
DB 1111 NDTVGYTKKCSBDMKLVRTASFRGGQMSFTNLDPVSTRFQLSFGFOTFQPSGTLNHQ 1170
QY 421 TRTSSLVLTLEBDEGHIELSTRDSNIPIFKSPGYMDGLLHVSVISDTSGLRLIIDQVLR 480
DB 1171 TRTSSLVLTLEBDEGHIELSTRDSNIPIFKSPGYMDGLLHVSVISDTSGLRLIIDQVLR 1230
QY 481 RNQRLPSFSNAQOSLRLGGHFEBCISNVLVQRFQSPRYLDAKSTTKDASLGGCSLN 540
DB 1231 RNQRLPSFSNAQOSLRLGGHFEBCISNVLVQRFQSPRYLDAKSTTKDASLGGCSLN 1290
QY 541 KPPFLMLFKSPKRFNKGRIFNNQL 565
DB 1291 KPPFLMLFKSPKRFNKGRIFNNQL 1315
```

RESULT 2
AAB48460
ID AAB48460 standard; protein; 1725 AA.
XX
AC AAB48460;
XX
DT 02-MAR-2001 (first entry)
XX
DE Rat laminin 5 polypeptide, SEQ ID NO: 10.
XX
XX Rat; laminin 5; vulnerary; antiulcer; antiinflammatory; antidiabetic;
XX cell adhesion promoter; wound healing; ulcers; burn; skin graft;
XX periodontitis; gingivitis; Type I diabetes; angiogenesis regulation.
OS Rattus norvegicus.
XX
XX WO200066731-A2.
XX
XX 09-NOV-2000.
XX
XX 28-APR-2000; 2000WO-US011459.
XX
XX 30-APR-1999; 99US-0131720P.
XX
XX

PR 21-AUG-1999; 99US-0149738P.
PR 24-SEP-1999; 99US-0155945P.
XX
XX
PA (BIOS-) BIOSTATUM INC.
XX
XX Boutaud A/
XX
XX WPI; 2000-687538/67.
XX
XX N-PSDB; AAC83721.
XX

PT Laminin 5-expressing cells, used to accelerate wound healing associated
PT with diabetic foot ulcers, venous ulcers, pressure sores, skin surgery,
PT burns, acute wounds and skin grafts.
XX
XX
PS Claim 3; Page 104-109; 232pp; English.

CC The present sequence is a laminin 5 chain polypeptide. Recombinant
CC laminin 5-expressing cells are used to accelerate wound healing,
CC especially diabetic foot ulcers, venous ulcers, pressure sores, skin
CC surgery, burns, acute wounds, skin grafts, corneal ulcerations, gastro-
CC intestinal ulcers, periodontitis, and gingivitis. They are also used to
CC improve the biocompatibility of medical devices, and to promote cell
CC adhesion to a surface. They can be used for the ex vivo treatment of type
CC I diabetes. Laminin can also be used to regulate angiogenesis. The cell
CC line produces and secretes recombinant heterotimeric laminin, whereas
CC prior art cell lines have been created that produce but do not secrete
CC only one or two chain laminins
XX
XX

Sequence 1725 AA;

Query Match 100.0%; Score 2940; DB 3; Length 1725;
Best Local Similarity 100.0%; Pred. No. 1.5e-261;
Matches 565; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
1 MRFNGSGVYRLPNLDELKGYTSLFLQRPDLRENGGTEDMFWMTLGNKDAKDYIG 60
DB 782 MRFNGSGVYRLPNLDELKGYTSLFLQRPDLRENGGTEDMFWMTLGNKDAKDYIG 841
QY 61 MAVVDGQLTCVYNLGDREAEVQIDQVLTSESQEAVMDRYKFORIYQPAKLNTYKATSN 120
DB 842 MAVVDGQLTCVYNLGDREAEVQIDQVLTSESQEAVMDRYKFORIYQPAKLNTYKATSN 901
QY 121 KKPAAVYDLEGGSSNTLLNLPEDAVFYVGGYPPDFELPSRLRPPYKGCIELDLNEN 180
DB 902 KKPAAVYDLEGGSSNTLLNLPEDAVFYVGGYPPDFELPSRLRPPYKGCIELDLNEN 961
QY 181 VLSLYNFKTTFNLNTTEVEPCRRRKBESDKNYFEGGYARIPYQNAAPPNFIOITQTV 240
DB 962 VLSLYNFKTTFNLNTTEVEPCRRRKBESDKNYFEGGYARIPYQNAAPPNFIOITQTV 1021
QY 241 DRGLLFFAENQDNFISLNIEDGNLWRYKLNSEPPKEKGRDITNDKSHLITIGKQ 300
DB 1022 DRGLLFFAENQDNFISLNIEDGNLWRYKLNSEPPKEKGRDITNDKSHLITIGKQ 1081
QY 301 KKMWINVRSVRIRIEGIFDFSTYYLGGIPAIRERFNISTPAFGCKMKLKKTSGVVRL 360
DB 1082 KKMWINVRSVRIRIEGIFDFSTYYLGGIPAIRERFNISTPAFGCKMKLKKTSGVVRL 1141
QY 361 NDTVGYTKKCSBDMKLVRTASFRGGQMSFTNLDPVSTRFQLSFGFOTFQPSGTLNHQ 420
DB 1142 NDTVGYTKKCSBDMKLVRTASFRGGQMSFTNLDPVSTRFQLSFGFOTFQPSGTLNHQ 1201
QY 421 TRTSSLVLTLEBDEGHIELSTRDSNIPIFKSPGYMDGLLHVSVISDTSGLRLIIDQVLR 480
DB 1202 TRTSSLVLTLEBDEGHIELSTRDSNIPIFKSPGYMDGLLHVSVISDTSGLRLIIDQVLR 1261
QY 481 RNQRLPSFSNAQOSLRLGGHFEBCISNVLVQRFQSPRYLDAKSTTKDASLGGCSLN 540
DB 1262 RNQRLPSFSNAQOSLRLGGHFEBCISNVLVQRFQSPRYLDAKSTTKDASLGGCSLN 1321
QY 541 KPPFLMLFKSPKRFNKGRIFNNQL 565
DB 1322 KPPFLMLFKSPKRFNKGRIFNNQL 1346
```

RESULT 3
AAB48457
ID AAB48459 standard; protein; 1693 AA.
XX
AC AAB48459;
XX
DT 02-MAR-2001 (first entry)
XX
DE Human laminin 5 polypeptide, SEQ ID NO: 8.
XX
KW Human; laminin 5; vulnery; antiulcer; antiinflammatory; antidiabetic;
KM cell adhesion promoter; wound healing; ulcers; burn; skin graft;
KW periodontitis; gingivitis; Type I diabetes; angiogenesis regulation.
XX
OS Homo sapiens.
XX
PN MO20006731-A2.
XX
PD 09-NOV-2000.
XX
PF 28-APR-2000; 2000MO-US011459.
XX
PR 30-APR-1999; 99US-0131720P.
PR 21-AUG-1999; 99US-0149738P.
PR 24-SEP-1999; 99US-0155945P.
XX
PA (BIOS-) BIOSTATUM INC.
XX
PI Boutaud A;
XX
DR WPI; 2000-687538/67.
DR N-PSDB; AAC83720.
XX
PT Laminin 5-expressing cells, used to accelerate wound healing associated
PT with diabetic foot ulcers, venous ulcers, pressure sores, skin surgery,
PT burn, acute wounds and skin grafts.
XX
PS Claim 3; Page 91-97; 232pp; English.
XX
CC The present sequence is a laminin 5 chain polypeptide. Recombinant
CC laminin 5-expressing cells are used to accelerate wound healing,
CC especially diabetic foot ulcers, venous ulcers, pressure sores, skin
CC surgery, burns, acute wounds, skin grafts, corneal ulcerations, gastro-
CC intestinal ulcers, periodontitis, and gingivitis. They are also used to
CC improve the biocompatibility of medical devices, and to promote cell
CC adhesion to a surface. They can be used for the ex vivo treatment of Type
CC I diabetes. Laminin can also be used to regulate angiogenesis. The cell
CC line produces and secretes recombinant heterotrimeric laminin, whereas
CC prior art cell lines have been created that produce but do not secrete
CC only one or two chain laminins
XX
SQ Sequence 1693 AA;
XX
Query Match 83.0%; Score 2439; DB 3; Length 1693;
Best Local Similarity 81.9%; Pred. No. 3e-215;
Matches 463; Conservative 47; Mismatches 55; Indels 0; Gaps 0;

1 MRFRNGSGVEVRLLPNDELKGYTSLSLFLQRPDLRENGGTEDMFVYVYLGNKXASXQYIG 60
DB 751 MRFRNGSGVEVRLLPNDELKGYTSLSLFLQRPDLRENGGTEDMFVYVYLGNKXASXQYIG 810
QY 61 MAVVDGQLTCVYNLGDREAEVQIDQVLTSESQEAHVDRVYFORIYQPAKLNTYKATSN 120
DB 811 MAVVDGQLTCVYNLGDREAEVQIDQVLTSESQEAHVDRVYFORIYQPAKLNTYKATSN 870
QY 121 KPRAPAVYDLGGSSNTLLNDPDAVYVYGGYPPDELSRLRFPYKGCIEHDDNEN 180
DB 871 KPRAPAVYDLGGSSNTLLNDPDAVYVYGGYPPDELSRLRFPYKGCIEHDDNEN 930
QY 181 VLSLYNFKTFLNLTVEPCRRKESDKNYFEGTGYARIPQNPAPFPIQTITQTV 240
1171 TWTRNLQVLTLEDVYILSTSDSGPFRKPGQYMDGLHVSYSINSGRLTIDQQLR 1230
QY 481 RNRQLPFSNAQSLRIGGHEGCI SNVLVORFSSPEVLDASKSTKDAISLGGCSLN 540
DB 1231 NSKRLKHISSSKSLMLGSGNFEKCSNVFVQRLSPFVLDLTSNLRDVSIGGCSLN 1290
QY 541 KPPFLMLFKSPKRNKRIENVNL 565
DB 1291 KPPFLMLFKSGSTRFNKTFPRINQL 1315
RESULT 4
AAB48457
ID AAB48457 standard; protein; 1693 AA.
XX
AC AAB48457;
XX
DT 02-MAR-2001 (first entry)
XX
DE Human laminin 5 polypeptide, SEQ ID NO: 4.
XX
KW Human; laminin 5; vulnery; antiulcer; antiinflammatory; antidiabetic;
KM cell adhesion promoter; wound healing; ulcers; burn; skin graft;
KW periodontitis; gingivitis; Type I diabetes; angiogenesis regulation.
XX
OS Homo sapiens.
XX
PN MO20006731-A2.
XX
PD 09-NOV-2000.
XX
PF 28-APR-2000; 2000MO-US011459.
XX
PR 30-APR-1999; 99US-0131720P.
PR 21-AUG-1999; 99US-0149738P.
PR 24-SEP-1999; 99US-0155945P.
XX
PA (BIOS-) BIOSTATUM INC.
XX
PI Boutaud A;
XX
DR WPI; 2000-687538/67.
DR N-PSDB; AAC83718.
XX
PT Laminin 5-expressing cells, used to accelerate wound healing associated
PT with diabetic foot ulcers, venous ulcers, pressure sores, skin surgery,
PT burn, acute wounds and skin grafts.
XX
PS Claim 3; Page 66-71; 232pp; English.
XX
CC The present sequence is a laminin 5 chain polypeptide. Recombinant
CC laminin 5-expressing cells are used to accelerate wound healing,
CC especially diabetic foot ulcers, venous ulcers, pressure sores, skin
CC surgery, burns, acute wounds, skin grafts, corneal ulcerations, gastro-
CC intestinal ulcers, periodontitis, and gingivitis. They are also used to
CC improve the biocompatibility of medical devices, and to promote cell
CC adhesion to a surface. They can be used for the ex vivo treatment of Type

CC I diabetes. Laminin can also be used to regulate angiogenesis. The cell
CC line produces and secretes recombinant heterotrimeric laminin, whereas
CC prior art cell lines have been created that produce but do not secrete
CC only one or two chain laminins

XX Sequence 1693 AA;

Query Match 83.0%; Score 2439; DB 3; Length 1693;
Best Local Similarity 81.9%; Pred. No. 3e-215;
Matches 463; Conservative 47; Mismatches 55; Indels 0; Gaps 0;

QY 1 MRFNGSGVEVRLPNDLEDKGTSLSLFLQRPDLRENGTDMFVMTLGNKDAKDYIG 60
DB 751 MRFNGSGVEVRLPNDLEDKGTSLSLFLQRPDRSRENGTDMFVMTLGNKDAKDYIG 810
QY 61 MAVVDGQLTCVYNLGDREAVQIDVLTSESOEAVMDRKPFRITQPAKANTKATSN 120
DB 811 MAVVDGQLTCVYNLGDREAVQIDVLTSESOEAVMDRKPFRITQPAKANTKATSN 870
QY 121 KPRKAPVYDLDEGSSNTLLNLDPEDAVFYVGGYPPDFELPSRLRPPYKGCIELDLNEN 180
DB 871 KPRTPGVYDMDGNSNTLLNLDPEDAVFYVGGYPPDFELPSRLRPPYKGCIELDLNEN 930
QY 181 VLSLNFKTFNLNTTVEPCRRKESDKNYFEGTGARIPQPNAPPPNFITQITTV 240
DB 931 VLSLNFKTFNLNTTVEPCRRKESDKNYFEGTGARIPQPNAPPPNFITQITTV 990
QY 241 DRGLLFFAENODNFIISLNIEDGNLMRYKLNSEPPKEKGRDITNGKHSILITIGKQ 300
DB 991 DRGLLFFAENODNFIISLNIEDGNLMRYKLNSEPPKEKGRDITNGKHSILITIGKQ 1050
QY 301 KRMWNNVRSVRIEIEIPDSTYYLGGIPAIIRERFNISTPAFGCKMKLKKTSGVRL 360
DB 1051 KRMWNNVQNTIIDGVDFDSTYYLGGIPAIIRERFNISTPAFGCKMKLKKTSGVRL 1110
QY 361 NDVGVYTKKCSBDMKLVRSASFSRGQSLSTDLGLPPTDHLQASFGQTFQPSGILLHQ 420
DB 1111 NDVGVYTKKCSBDMKLVRSASFSRGQSLSTDLGLPPTDHLQASFGQTFQPSGILLHQ 1170
QY 421 TRTSLLVLTLEDGHIESTDSNIPFKSPCTMDGLHHVSVISSTSGRLIIDVOYR 480
DB 1171 TRTRNLQVLTLEDGHIESTDSNIPFKSPCTMDGLHHVSVISSTSGRLIIDVOYR 1230
QY 481 RNQRLPSFNAQOSRLRGGHFEGCISNVLVQRFSSPEVLDASKSTKDAKSLGGCSLN 540
DB 1231 NSKRLKHISRSRQSLRGGHFEGCISNVLVQRFSSPEVLDASKSTKDAKSLGGCSLN 1290
QY 541 KPPLMLFKSPKRFNKGRIFFNVQL 565
DB 1291 KPPLMLFKSGSTRFNKTKTFRINQL 1315

RESULT 5
AAB48458
ID AAB48458 standard; protein; 1713 AA.

AC AAB48458;

DT 02-MAR-2001 (first entry)

XX Human laminin 5 polypeptide, SEQ ID NO: 6.

XX Human; laminin 5; vulnary; antiulcer; antiinflammatory; antidiabetic;

XX cell adhesion promoter; wound healing; ulcers; burn; skin graft;

XX periodontitis; gingivitis; Type I diabetes; angiogenesis regulation.

XX Homo sapiens.

XX OS

XX PN WO200066731-A2.

XX PD 09-NOV-2000.

XX PF 28-APR-2000; 2000MO-US011459.

XX 30-APR-1999; 99US-0131720P.
PR 21-AUG-1999; 99US-0149738P.
PR 24-SEP-1999; 99US-0155945P.

XX (Bios-) BIOSSTATUM INC.

XX Boulaud A;

XX WPI, 2000-687538/67.

XX N-PSDB; AAC83719.

XX Laminin 5-expressing cells, used to accelerate wound healing associated
XX with diabetic foot ulcers, venous ulcers, pressure sores, skin surgery,
XX burns, acute wounds and skin grafts.

XX Claim 3; Page 79-84, 232pp; English.

XX The present sequence is a laminin 5 chain polypeptide. Recombinant
XX laminin 5-expressing cells are used to accelerate wound healing,
XX especially diabetic foot ulcers, venous ulcers, pressure sores, skin
XX surgery, burns, acute wounds, skin grafts, corneal ulcerations, gastro-
XX intestinal ulcers, periodontitis, and gingivitis. They are also used to
XX improve the biocompatibility of medical devices, and to promote cell
XX adhesion to a surface. They can be used for the ex vivo treatment of Type
XX I diabetes. Laminin can also be used to regulate angiogenesis. The cell
XX line produces and secretes recombinant heterotrimeric laminin, whereas
XX prior art cell lines have been created that produce but do not secrete
XX only one or two chain laminins

XX Sequence 1713 AA;

Query Match 83.0%; Score 2439; DB 3; Length 1713;
Best Local Similarity 81.9%; Pred. No. 3.1e-215;
Matches 463; Conservative 47; Mismatches 55; Indels 0; Gaps 0;

QY 1 MRFNGSGVEVRLPNDLEDKGTSLSLFLQRPDLRENGTDMFVMTLGNKDAKDYIG 60
DB 771 MRFNGSGVEVRLPNDLEDKGTSLSLFLQRPDRSRENGTDMFVMTLGNKDAKDYIG 830
QY 61 MAVVDGQLTCVYNLGDREAVQIDVLTSESOEAVMDRKPFRITQPAKANTKATSN 120
DB 831 MAVVDGQLTCVYNLGDREAVQIDVLTSESOEAVMDRKPFRITQPAKANTKATSN 890
QY 121 KPRKAPVYDLDEGSSNTLLNLDPEDAVFYVGGYPPDFELPSRLRPPYKGCIELDLNEN 180
DB 891 KPRTPGVYDMDGNSNTLLNLDPEDAVFYVGGYPPDFELPSRLRPPYKGCIELDLNEN 950
QY 181 VLSLNFKTFNLNTTVEPCRRKESDKNYFEGTGARIPQPNAPPPNFITQITTV 240
DB 951 VLSLNFKTFNLNTTVEPCRRKESDKNYFEGTGARIPQPNAPPPNFITQITTV 1010
QY 241 DRGLLFFAENODNFIISLNIEDGNLMRYKLNSEPPKEKGRDITNGKHSILITIGKQ 300
DB 1011 DRGLLFFAENODNFIISLNIEDGNLMRYKLNSEPPKEKGRDITNGKHSILITIGKQ 1070
QY 301 KRMWNNVRSVRIEIEIPDSTYYLGGIPAIIRERFNISTPAFGCKMKLKKTSGVRL 360
DB 1071 KRMWNNVQNTIIDGVDFDSTYYLGGIPAIIRERFNISTPAFGCKMKLKKTSGVRL 1130
QY 361 NDVGVYTKKCSBDMKLVRSASFSRGQSLSTDLGLPPTDHLQASFGQTFQPSGILLHQ 420
DB 1131 NDVGVYTKKCSBDMKLVRSASFSRGQSLSTDLGLPPTDHLQASFGQTFQPSGILLHQ 1190
QY 421 TRTSLLVLTLEDGHIESTDSNIPFKSPCTMDGLHHVSVISSTSGRLIIDVOYR 480
DB 1191 TRTRNLQVLTLEDGHIESTDSNIPFKSPCTMDGLHHVSVISSTSGRLIIDVOYR 1250
QY 481 RNQRLPSFNAQOSRLRGGHFEGCISNVLVQRFSSPEVLDASKSTKDAKSLGGCSLN 540
DB 1251 NSKRLKHISRSRQSLRGGHFEGCISNVLVQRFSSPEVLDASKSTKDAKSLGGCSLN 1310
QY 541 KPPLMLFKSPKRFNKGRIFFNVQL 565

Db 1311 KPPEFLMLKSGSTRFNTKTFRINQL 1335

RESULT 6
ABR92102
ID ABR92102 standard; protein; 1713 AA.

XX ABR92102;

DT 10-SEP-2003 (first entry)

DE Human cervical cancer cell marker encoding cDNA SEQ ID NO:113.

XX Human; cervical cancer; cervical cancer marker; cancer therapy;

KW detection; gene therapy; vaccine.

OS Homo sapiens.

XX MO2002101075-A2.

PD 19-DEC-2002.

PF 12-JUN-2002; 2002MO-US018638.

PR 13-JUN-2001; 2001US-0298155P.

PR 13-JUN-2001; 2001US-0298155P.

PR 14-NOV-2001; 2001US-0335936P.

PA (MILL-) MILLENNIUM PHARM INC.

PI Schlögel R, Chen Y, Zhao X, Monahan JB, Kamatkar S;

PI Gannavarapu M, Glatt K, Hoersch S;

DR N-PSDB; ACF12884.

XX WPI; 2003-156967/15.

XX N-PSDB; ACF12884.

XX WPI; 2003-156967/15.

XX N-PSDB; ACF12884.

XX WPI; 2003-156967/15.

XX N-PSDB; ACF12884.

XX WPI; 2003-156967/15.

XX N-PSDB; ACF12884.

XX WPI; 2003-156967/15.

XX N-PSDB; ACF12884.

XX WPI; 2003-156967/15.

XX N-PSDB; ACF12884.

XX WPI; 2003-156967/15.

XX N-PSDB; ACF12884.

XX WPI; 2003-156967/15.

XX N-PSDB; ACF12884.

XX WPI; 2003-156967/15.

XX N-PSDB; ACF12884.

XX WPI; 2003-156967/15.

QY 121 KPRAPAVYDLBGGSSNTLNLDPEDAVFYVGYPDPFELPSRLRPPRYKGLIELDNLNEN 180
Db 891 KPETPGVYDMGNSNTLNLDPENNVFYVGYPDPFELPSRLRPPRYKGLIELDNLNEN 950
QY 181 VLSVNFKTFNTNTEVEPCRRRKEESDNTFEGTGVARIPTQPNAPFPNPQTQITV 240
Db 951 VLSVNFKTFNTNTEVEPCRRRKEESDNTFEGTGVARIPTQPNAPFPNPQTQITV 1010

QY 241 DRGLFPAFNOQNFISLNTEDGLMRYKLNSEPRKGRDITNGKHSILITGKQ 300
Db 1011 DRGLFPAFNOQNFISLNTEDGLMRYKLNSEPRKGRDITNGKHSILITGKQ 1070

QY 301 KRMWIVNERSVAREGEIFDPSTYVGGIPAIAREFNISTPAFQCMKTKTSGVRL 360
Db 1071 KRMWIVNERSVAREGEIFDPSTYVGGIPAIAREFNISTPAFQCMKTKTSGVRL 1130

QY 361 NDTVGVTKKCSBDMKLVRSAPFSGQMSFTMLDVPSTDRFOLSPFGQTQPSGTLINQ 420
Db 1131 NDTVGVTKKCSBDMKLVRSAPFSGQMSFTMLDVPSTDRFOLSPFGQTQPSGTLINQ 1190

QY 421 TRTSSLLVLEDEGHIELSTRDSNIPFKSPGTYMDGLHVSYSITSGRLIIDQVLR 480
Db 1191 TRTSSLLVLEDEGHIELSTRDSNIPFKSPGTYMDGLHVSYSITSGRLIIDQVLR 1250

QY 481 RNORLPSFNAQOSLRLGGHFECSNVLVORFSQSPFVLDASSTYKKAASLGGCSLN 540
Db 1251 RNORLPSFNAQOSLRLGGHFECSNVLVORFSQSPFVLDASSTYKKAASLGGCSLN 1310

QY 541 KPPEFLMLKSGSTRFNTKTFRINQL 565
Db 1311 KPPEFLMLKSGSTRFNTKTFRINQL 1335

RESULT 7
ADD29904
ID ADD29904 standard; protein; 1713 AA.

XX ADD29904;

DT 15-JAN-2004 (first entry)

DE Human laminin alpha 3 seq id 2.

XX ophthalmological; dermatological; laminin alpha 3; G3 domain;

KW cell adhesion function; cell movement effect; epithelial tissue function;

XX retinal detachment; cosmetic surgery; skin graft; human.

OS Homo sapiens.

XX JP2003093064-A.

PD 02-APR-2003.

PF 20-SEP-2001; 2001JP-00287519.

PR 20-SEP-2001; 2001JP-00287519.

PA (KAGA-) KAGAKU GIYUTSU SHINKO JIGYODAN.

DR (KIHARA-) ZH KIHARA KINEN YOKOHAMA SHIMEI KAGAKU.

DR WPI; 2003-817304/77.

DR N-PSDB; ADD29903.

PT Novel modified G3 domain of laminin alpha 3 chain useful for controlling

XX cell adhesion and cell movement.

Claim 1; SEQ ID NO 2; 49pp; Japanese.

The invention describes a modified laminin alpha3 chain comprising one or

more amino acid deletions, substitutions or additions at region

corresponding to a region of G3 domain having amino acids 1214-1324 of

laminin alpha3 chain having a fully defined sequence of 1713 amino acids

as given in the specification. (II) can control cell adhesion function and

CC cell movement effect. A composition comprising laminin is useful for
CC maintaining or treating the function of epithelial tissue and
CC treatment or prevention of retinal detachment and in cosmetic surgery and
CC skin graft. The modified region of laminin alpha3 chain can control cell
CC adhesion function and cell movement effect. This is the amino acid
CC sequence of human laminin alpha 3.

XX Sequence 1713 AA;

Query Match 83.0%; Score 2439; DB 7; Length 1713;

Best Local Similarity 81.9%; Pred. No. 3,1e-215;

Matches 463; Conservative 47; Mismatches 55; Indels 0; Gaps 0;

```
QY 1 MFNFGSGVEVRLPNDLEDKGYTSLFLQRPDLRENGSTEDMFVMTLGNKDSKDYIG 60
DB 771 MFNFGSGVEVRLPNDLEDKGYTSLFLQRPDLRENGSTEDMFVMTLGNKDSKDYIG 830
QY 61 MAVVNGQLTCVYVNLGDRBAEVDQVLTSESQEAAMDVKYQRIYQPAKNTYKATSN 120
DB 831 MAVVNGQLTCVYVNLGDRBAEVDQVLTSESQEAAMDVKYQRIYQPAKNTYKATSN 890
QY 121 KKPAPAVYDLEGSSNTLNLDPEDAVFYVGGYPPDFELPSRLRPPPYKGCIELDLNN 180
DB 891 KKPAPAVYDLEGSSNTLNLDPEDAVFYVGGYPPDFELPSRLRPPPYKGCIELDLNN 950
QY 181 VLSLVNFKTFTNLTTEVEPCRRKESDKNYFEGTGYARIPTPQNPAPPPNFQTIQTV 240
DB 951 VLSLVNFKTFTNLTTEVEPCRRKESDKNYFEGTGYARIPTPQNPAPPPNFQTIQTV 1010
QY 241 DRGLLFFAENQDNFISLNIEDGMLMRYKLNSEPPKEKIRPTINDGHSILITIGKQ 300
DB 1011 DRGLLFFAENQDNFISLNIEDGMLMRYKLNSEPPKEKIRPTINDGHSILITIGKQ 1070
QY 301 KMMINNVRSVRIEGBIFDFSTYYLGGIPAIAREFNISTPAFOGCKNLKKTSGVRL 360
DB 1071 KMMINNVRSVRIEGBIFDFSTYYLGGIPAIAREFNISTPAFOGCKNLKKTSGVRL 1130
QY 361 NDVTGVTYKCCSEBDKLVRTASFSRGQMSFTNLDPVSTDRFQLSFGQTFQPSGTLNHQ 420
DB 1131 NDVTGVTYKCCSEBDKLVRTASFSRGQMSFTNLDPVSTDRFQLSFGQTFQPSGTLNHQ 1190
QY 421 TRTSSLVTLLEBQHIELSTRDSNIPFKSPGTMYDGLLHHVSVISDTSGLRLIDQVLR 480
DB 1191 TRTSSLVTLLEBQHIELSTRDSNIPFKSPGTMYDGLLHHVSVISDTSGLRLIDQVLR 1250
QY 481 RNQRLPSFSNAQOSRLGSGHPEGICISNVLVORFSGSPVYLDLASKSTKKDASLGCCSLN 540
DB 1251 RNQRLPSFSNAQOSRLGSGHPEGICISNVLVORFSGSPVYLDLASKSTKKDASLGCCSLN 1310
QY 541 KPPFLMLFKSPKRFNKGRIFNVNQI 565
DB 1311 KPPFLMLFKSGTRFNKTKTFRINQL 1335
```

RESULT 8

ADG37225 ID ADG37225 standard; protein; 1713 AA.

XX ADG37225;

XX 26-FEB-2004 (first entry)

XX Human laminin-6 alpha 3 subunit.

XX human; laminin-6; alpha 3; B1 subunit; B2 subunit; cell-movement;

XX cell-adhesion; dermatological; neuroprotective; muscular;

XX epithelial tissue; nervous tissue; varicella disease.

XX Homo sapiens.

XX JP2003212791-A.

XX 30-JUL-2003.

XX 17-JAN-2002; 2002JP-00009227.
XX 17-JAN-2002; 2002JP-00009227.
XX (KAGA-) KAGAKU GIJUTSU SHINKO JIGYODAN.
XX WPI; 2003-819867/77.
XX N-PSDB; ADG37224.

PT Composition comprising laminin-6 for regulation of cell-movement activity
PT and/or cell-adhesion activity, useful for treating or maintaining
PT function of epithelial tissue, nervous tissue and muscles.

PS Claim 2; SEQ ID NO 2; 55pp; Japanese.

CC This invention describes a novel composition comprising the human laminin
CC -6 alpha 3, B1 or B2 subunits for regulation of cell-movement activity
CC and/or cell-adhesion activity. The products of the invention have
CC dermatological, neuroprotective and muscular activity. The composition of
CC the invention is useful for treating or maintaining the function of the
CC epithelial tissue, the nervous tissue and muscles and is also useful for
CC treatment or prevention of varicella disease.

XX Sequence 1713 AA;

Query Match 83.0%; Score 2439; DB 7; Length 1713;

Best Local Similarity 81.9%; Pred. No. 3,1e-215;

Matches 463; Conservative 47; Mismatches 55; Indels 0; Gaps 0;

```
QY 1 MFNFGSGVEVRLPNDLEDKGYTSLFLQRPDLRENGSTEDMFVMTLGNKDSKDYIG 60
DB 771 MFNFGSGVEVRLPNDLEDKGYTSLFLQRPDLRENGSTEDMFVMTLGNKDSKDYIG 830
QY 61 MAVVNGQLTCVYVNLGDRBAEVDQVLTSESQEAAMDVKYQRIYQPAKNTYKATSN 120
DB 831 MAVVNGQLTCVYVNLGDRBAEVDQVLTSESQEAAMDVKYQRIYQPAKNTYKATSN 890
QY 121 KKPAPAVYDLEGSSNTLNLDPEDAVFYVGGYPPDFELPSRLRPPPYKGCIELDLNN 180
DB 891 KKPAPAVYDLEGSSNTLNLDPEDAVFYVGGYPPDFELPSRLRPPPYKGCIELDLNN 950
QY 181 VLSLVNFKTFTNLTTEVEPCRRKESDKNYFEGTGYARIPTPQNPAPPPNFQTIQTV 240
DB 951 VLSLVNFKTFTNLTTEVEPCRRKESDKNYFEGTGYARIPTPQNPAPPPNFQTIQTV 1010
QY 241 DRGLLFFAENQDNFISLNIEDGMLMRYKLNSEPPKEKIRPTINDGHSILITIGKQ 300
DB 1011 DRGLLFFAENQDNFISLNIEDGMLMRYKLNSEPPKEKIRPTINDGHSILITIGKQ 1070
QY 301 KMMINNVRSVRIEGBIFDFSTYYLGGIPAIAREFNISTPAFOGCKNLKKTSGVRL 360
DB 1071 KMMINNVRSVRIEGBIFDFSTYYLGGIPAIAREFNISTPAFOGCKNLKKTSGVRL 1130
QY 361 NDVTGVTYKCCSEBDKLVRTASFSRGQMSFTNLDPVSTDRFQLSFGQTFQPSGTLNHQ 420
DB 1131 NDVTGVTYKCCSEBDKLVRTASFSRGQMSFTNLDPVSTDRFQLSFGQTFQPSGTLNHQ 1190
QY 421 TRTSSLVTLLEBQHIELSTRDSNIPFKSPGTMYDGLLHHVSVISDTSGLRLIDQVLR 480
DB 1191 TRTSSLVTLLEBQHIELSTRDSNIPFKSPGTMYDGLLHHVSVISDTSGLRLIDQVLR 1250
QY 481 RNQRLPSFSNAQOSRLGSGHPEGICISNVLVORFSGSPVYLDLASKSTKKDASLGCCSLN 540
DB 1251 RNQRLPSFSNAQOSRLGSGHPEGICISNVLVORFSGSPVYLDLASKSTKKDASLGCCSLN 1310
QY 541 KPPFLMLFKSPKRFNKGRIFNVNQI 565
DB 1311 KPPFLMLFKSGTRFNKTKTFRINQL 1335
```

RESULT 9

ABM81957

ID ABM81957 standard; protein; 1713 AA.
 XX
 AC ABM81957;
 XX
 DT 18-NOV-2004. (first entry)
 XX
 DB Tumour-associated antigenic target (TAT) polypeptide PRO2799, SEQ:5041.
 XX
 KM Tumour-associated antigenic target; TAT; human; overexpression; cancer;
 KM tumour; diagnosis; cell proliferative disorder; breast cancer;
 KM colorectal cancer; lung cancer; ovarian cancer; liver cancer;
 KM central nervous system cancer; bladder cancer; pancreatic cancer;
 KM cervical cancer; melanoma; leukemia; hybridisation probe;
 KM chromosome identification; chromosome mapping; gene mapping;
 KM gene therapy; cytostatic.
 XX
 OS Homo sapiens.
 XX
 PN MO2004030615-A2.
 XX
 PD 15-APR-2004.
 XX
 PF 29-SEP-2003; 2003MO-US028547.
 XX
 PR 02-OCT-2002; 2002US-0414971P.
 XX
 (GETH) GENENTECH INC.
 XX
 PI Wu TD, Zhang Z, Zhou Y;
 XX
 DR MPI; 2004-347921/32.
 DR N-PSDB; ACN40327.
 XX
 PT New tumor-associated antigenic target polypeptides and nucleic acids,
 PT useful in preparing a medicament for treating or detecting a
 PT proliferative disorder, e.g. breast, lung, colorectal, ovarian or
 PT prostate cancer or tumor.
 XX
 PS Claim 12; SEQ ID NO 5041; 7273pp; English.
 XX
 CC The invention relates to human tumour-associated antigenic target (TAT)
 CC polypeptides, and their related nucleic acids. The TAT polypeptides are
 CC overexpressed in cancer tissues compared to normal tissues, and may thus
 CC serve as effective targets for the diagnosis and treatment of cancer in
 CC mammals. The invention also relates to nucleic acid and polypeptide
 CC sequences at least 80% identical to the TAT nucleic acids and
 CC polypeptides; expression vectors and host cells comprising a TAT nucleic
 CC acid; an antibody specific for a TAT polypeptide; a peptide or organic
 CC molecule which binds to a TAT polypeptide; fusion proteins comprising a
 CC TAT polypeptide; and methods and compositions for the treatment or
 CC diagnosis of cancer in mammals. TAT polypeptides, nucleic acids,
 CC antibodies, antagonists, binding molecules and compositions are useful
 CC for diagnosing or treating a cell proliferative disorder associated with
 CC increased TAT expression, particularly cancers such as breast cancer,
 CC colorectal cancer, lung cancer, ovarian cancer, liver cancer, bladder
 CC cancer, pancreatic cancer, cervical cancer, cancers of the central
 CC nervous system, melanoma and leukaemia. TAT nucleic acids may further be
 CC used as hybridisation probes, in chromosome and gene mapping, in
 CC chromosome identification and in gene therapy. The present sequence
 CC represents a TAT polypeptide of the invention
 XX
 SQ Sequence 1713 AA;
 Query Match 83.0%; Score 2439; DB 8; Length 1713;
 Best Local Similarity 81.9%; Pred. No. 3.1e-215;
 Matches 463; Conservative 47; Mismatches 55; Indels 0; Gaps 0;
 QY 1 MRNGSGVAVRPNLEDEKGYTSLFLQRPDLRNGGTEPMFWYLNKQASKDYIG 60
 DB 771 MRNGSGVAVRPNLEDEKGYTSLFLQRPDLRNGGTEPMFWYLNKQASRDIYIG 830
 QY 61 MAVVDQLTCVYMLGPREAEVQIDQVLTSESSQEAAMDVRKYPRIYQPAKLTNTKATSN 120

DB 831 MAVVDQLTCVYMLGPREAEVQIDQVLTSESSQEAAMDVRKYPRIYQPAKLTNTKATSN 890
 QY 121 KPRAPAVYDLBEGSSNTLANTDEDAVPYVGGIPDPPELPSRLRPPRYGCIETLDLNN 180
 DB 891 KPTPGVYMDGNSNTLNTLNDPENVFFYVGGYPDPFKLPSRLSPPYKGCIELDLNN 950
 QY 181 VLSLVNFKTTPNLTTEVEPCRRKESDKNYEGGVARIPTQPNAPFPNFIQTITV 240
 DB 951 VLSLVNFKTTPNLTTEVEPCRRKESDKNYEGGVARIPTQPNAPFPNFIQTITV 1010
 QY 241 DRGLLPPAENQDNFISLNTEDGLMVRKYNLSPPPEKGIPTINDGKHSLITIGKQ 300
 DB 1011 DRGLLPPAENQDNFISLNTEDGLMVRKYNLSPPPEKGIPTINDGKHSLITIGKQ 1070
 QY 301 KRMWIVNRSVRIEERIDFSTYYIGIPIAIRERFNISTPAFOCMNKKTSVVNL 360
 DB 1071 KRMWIVNRSVRIEERIDFSTYYIGIPIAIRERFNISTPAFOCMNKKTSVVNL 1130
 QY 361 NDTVGVTKKCSBDMKLVRTASFSRGQMSFTNLDVPTDRPOLSPFGOTFQPSGTLINHQ 420
 DB 1131 NDTVGVTKKCSBDMKLVRTASFSRGQMSFTNLDVPTDRPOLSPFGOTFQPSGTLINHQ 1190
 QY 421 TRTSSLLVTLBDGHELESTRDSNIPFKSPGYMDGLHRSVYISDTSGRLRLIDQVLR 480
 DB 1191 TWTRNLQVTLBEGYIELSTDSGGLPKSPQYMDGLHRSVYISDTSGRLRLIDQVLR 1250
 QY 481 RNQRLPFSNAQSLRGGHPEGICISNVLVQFSGSPYVLDAKSTKDKSLGGCSLN 540
 DB 1251 NSKRLKHISRSQSLTLDGSGNFEGCISNVFQGLSLSPVLDLTSNLSLRKDVSLGCGCSLN 1310
 QY 541 KPEFLMLFKSPKRNKRIENVQL 565
 DB 1311 KPEFLMLFKSTREKTKTIRINQL 1335
 RESULT 10
 ADR87606
 ID ADR87606 standard; protein; 1713 AA.
 XX
 AC ADR87606;
 XX
 DT 02-DEC-2004 (first entry)
 XX
 DB Human laminin alpha 3 (nicein), SEQ ID 10.
 XX
 KM Cytostatic; Gene Therapy; renal cell carcinoma; Wilms tumour; human;
 KM laminin alpha 3; nicein.
 XX
 OS Homo sapiens.
 XX
 PN WO2004075835-A2.
 XX
 PD 10-SEP-2004.
 XX
 PF 20-FEB-2004; 2004MO-US005042.
 XX
 PR 21-FEB-2003; 2003US-00372683.
 XX
 (GETH) GENENTECH INC.
 XX
 PI Gerritsen ME, Peale FV, Wu TD;
 XX
 DR MPI; 2004-676901/66.
 DR N-PSDB; ADR87605.
 XX
 PT New anti-BDRA antibody, useful in preparing a composition for diagnosing
 PT or inhibiting the growth of renal cell carcinoma or Wilms tumor.
 XX
 PS Example 1; SEQ ID NO 10; 257pp; English.
 XX
 CC The present invention relates to novel antibodies which bind to proteins
 CC which are overexpressed in renal cell carcinomas or Wilms tumour. The
 CC antibody can bind to a protein comprising CXCR4 (ADR87598), Laminin alpha

CC 4 (ADR87600), TIMP1 (ADR87602), Type IV collagen alpha 1 (ADR87604),
CC laminin alpha 3 (nicotin) (ADR87606), Adrenomedullin (ADR87608), Type IV
CC collagen alpha 2 (ADR87610), Thrombospondin 2 (ADR87612), Type I collagen
CC alpha 2 (ADR87614), Type VI collagen alpha 3 (ADR87616), Latent TGFbeta
CC binding protein 2 (LMBP2) (ADR87618), Serine or cysteine protease
CC inhibitor heat shock protein 47 (HSP47) (ADR87620), Procollagen-lysine, 2
CC -oxoglutarate 5-dioxygenase (ADR87622), connexin 43 (ADR87624), Type IV
CC collagen alpha 2 (ADR87626), Connexin 37 (ADR87628), Ephrin A1
CC (ADR87630), Laminin beta 2 (ADR87632), Integrin alpha 1, hevin
CC (ADR87635), Stanniocalcin 1 (ADR87637), Thrombospondin 4 (ADR87639), CD36
CC polypeptide (ADR87641), Endothelin receptor A (EDNRA, ADR87643) or
CC Endothelin receptor B (EDNRB, ADR87645). The proteins of ADR87598-ADR87641
CC and ADR87645 are all overexpressed in renal cell carcinoma, and ADR87643
CC (EDNRA) is overexpressed in Wilms tumour. The antibodies are useful in
CC preparing a composition for diagnosing or inhibiting the growth of renal
CC cell carcinoma or Wilms tumour. The present sequence is one such protein
CC of the invention.
XX
XX
SQ Sequence 1713 AA;

Query Match 83.0%; Score 2439; DB 8; Length 1713;
Best Local Similarity 81.9%; Pred. No. 3.1e-215;
Matches 463; Conservative 47; Mismatches 55; Indels 0; Gaps 0;

QY 1 MRFNGSGVEVRLPNDLEDLKGYTSLSLFLQRPDLRENGGTEDMFWYLGAKNDASKDYIG 60
DB 771 MRFNGSGVEVRLPNDLEDLKGYTSLSLFLQRPNSRENGGTENMFYWGAKNDASKDYIG 830
QY 61 MAVVDGQLTCVYNLGDREAEVQIDVLTSESGEAMVDRKPRITQPAKANTKATSN 120
DB 831 MAVVDGQLTCVYNLGDREAEVQIDVLTSESGEAMVDRKPRITQPAKANTKATSN 890
QY 121 KKPAPAVYDLDEGGSSNTLNDPEDAVFYGGYPPDFELPSRLRPPYKGCIELDLNEN 180
DB 891 KKPAPAVYDLDEGGSSNTLNDPEDAVFYGGYPPDFELPSRLRPPYKGCIELDLNEN 950
QY 181 VLSVNFKTFNTLNTTEVEPCRRRKEESDKNYFEGGYARIPQNPAPFPNFIQTITV 240
DB 951 VLSVNFKTFNTLNTTEVEPCRRRKEESDKNYFEGGYARIPQNPAPFPNFIQTITV 1010
QY 241 DRGLFFPANGDNFISLNIEDGNLMRYKLNSEPRKEKGRDITNGKSHLITIGKIQ 300
DB 1011 DRGLFFPANGDNFISLNIEDGNLMRYKLNSEPRKEKGRDITNGKSHLITIGKIQ 1070
QY 301 KRMWNVNRSVRIEGEIPDFSTYYLGIPAIAREFNISTPAFOGCMKLNKKTSGVRL 360
DB 1071 KRMWNVNRSVRIEGEIPDFSTYYLGIPAIAREFNISTPAFOGCMKLNKKTSGVRL 1130
QY 361 NDTVGVTKKCSSEDMKLVRTASFSRGGQMSFTNLDPVSTDRFQLSFGFQTFFQPSGTLNHO 420
DB 1131 NDTVGVTKKCSSEDMKLVRTASFSRGGQMSFTNLDPVSTDRFQLSFGFQTFFQPSGTLNHO 1190
QY 421 TRTSLLVLTEDGHIELSTRDSNIPFKSPGTMDGLHHVSYISTSGILLIDOVLR 480
DB 1191 TRTSLLVLTEDGHIELSTRDSNIPFKSPGTMDGLHHVSYISTSGILLIDOVLR 1250
QY 481 RNORLPSFSNAQOGLRIGGSHFEGGCSISNVLVQRFOSPEVLDLASKSTKDAISLGGCSIN 540
DB 1251 RNORLPSFSNAQOGLRIGGSHFEGGCSISNVLVQRFOSPEVLDLASKSTKDAISLGGCSIN 1310
QY 541 KPPFLMLFKSPKFNKGRIFNVNQL 565
DB 1311 KPPFLMLFKSPKFNKGRIFNVNQL 1335

RESULT 11
AAB48456 standard; protein; 1724 AA.
XX
AC AAB48456;
XX
DT 02-MAR-2001 (first entry)
XX

DE Human laminin 5 polypeptide, SEQ ID NO: 2.
XX Human; laminin 5; vulnery; antilulcer; antiinflammatory; antidiabetic;
KW cell adhesion promoter; wound healing; ulcers; burn; skin graft;
KW periodontitis; gingivitis; Type I diabetes; angiogenesis regulation.
XX
OS Homo sapiens.
XX
PN WO20006731-A2.
XX
PD 09-NOV-2000.
XX
PF 28-APR-2000; 2000MO-US011459.
XX
PR 30-APR-1999; 99US-0131720P.
PR 21-AUG-1999; 99US-0149738P.
PR 24-SEP-1999; 99US-0155945P.
XX
PA (BIOS-) BIOSTATUM INC.
XX
PI Boucard A;
XX
DR MPI: 2000-687538/67.
XX
DR N-PSDB; AAC83717.
XX
PT Laminin 5-expressing cells, used to accelerate wound healing associated
XX with diabetic foot ulcers, venous ulcers, pressure sores, skin surgery,
XX burns, acute wounds and skin grafts.
XX
PS Claim 3; Page 53-59; 232pp; English.
XX
CC The present sequence is a laminin 5 chain polypeptide. Recombinant
CC laminin 5-expressing cells are used to accelerate wound healing,
CC especially diabetic foot ulcers, venous ulcers, pressure sores, skin
CC surgery, burns, acute wounds, skin grafts, corneal ulcerations, gastro-
CC intestinal ulcers, periodontitis, and gingivitis. They are also used to
CC improve the biocompatibility of medical devices, and to promote cell
CC adhesion to a surface. They can be used for the ex vivo treatment of Type
CC I diabetes. Laminin can also be used to regulate angiogenesis. The cell
CC line produces and secretes recombinant heterotrimeric laminin, whereas
CC prior art cell lines have been created that produce but do not secrete
CC only one or two chain laminins
XX
SQ Sequence 1724 AA;

Query Match 83.0%; Score 2439; DB 3; Length 1724;
Best Local Similarity 81.9%; Pred. No. 3.1e-215;
Matches 463; Conservative 47; Mismatches 55; Indels 0; Gaps 0;

QY 1 MRFNGSGVEVRLPNDLEDLKGYTSLSLFLQRPDLRENGGTEDMFWYLGAKNDASKDYIG 60
DB 782 MRFNGSGVEVRLPNDLEDLKGYTSLSLFLQRPNSRENGGTENMFYWGAKNDASKDYIG 841
QY 61 MAVVDGQLTCVYNLGDREAEVQIDVLTSESGEAMVDRKPRITQPAKANTKATSN 120
DB 842 MAVVDGQLTCVYNLGDREAEVQIDVLTSESGEAMVDRKPRITQPAKANTKATSN 901
QY 121 KKPAPAVYDLDEGGSSNTLNDPEDAVFYGGYPPDFELPSRLRPPYKGCIELDLNEN 180
DB 902 KKPAPAVYDLDEGGSSNTLNDPEDAVFYGGYPPDFELPSRLRPPYKGCIELDLNEN 961
QY 181 VLSVNFKTFNTLNTTEVEPCRRRKEESDKNYFEGGYARIPQNPAPFPNFIQTITV 240
DB 962 VLSVNFKTFNTLNTTEVEPCRRRKEESDKNYFEGGYARIPQNPAPFPNFIQTITV 1021
QY 241 DRGLFFPANGDNFISLNIEDGNLMRYKLNSEPRKEKGRDITNGKSHLITIGKIQ 300
DB 1022 DRGLFFPANGDNFISLNIEDGNLMRYKLNSEPRKEKGRDITNGKSHLITIGKIQ 1081
QY 301 KRMWNVNRSVRIEGEIPDFSTYYLGIPAIAREFNISTPAFOGCMKLNKKTSGVRL 360
DB 1082 KRMWNVNRSVRIEGEIPDFSTYYLGIPAIAREFNISTPAFOGCMKLNKKTSGVRL 1141

QY 361 NDTVGVTKKSEBDMKLVRTASFSRGGOMSEFTNLDVPSDRFQSLFSGFQTFQPSGTLNMQ 420
 DB 1142 NDTVGVTKKSEBDMKLVRTASFSRGGOMSEFTNLDVPSDRFQSLFSGFQTFQPSGTLNMQ 1201
 QY 421 TRTSSLVLTLEDGHIETSDSNIPFKSPGYMDGLHHVYSISDTSGLRLIDQVLR 480
 DB 1202 TWTRNLQVLTLEDGHIETSDSNIPFKSPGYMDGLHHVYSISDTSGLRLIDQVLR 1261
 QY 481 RNRQLPSFSAQOSLRLGGHFECCISNVLVQRFSGSPFVLDLASKTKDASIGGCSLN 540
 DB 1262 NSRRLKHISRSRSLRGGSNFECISNVFQRLSLSPVLDLTSNLSKDVSLGGCSLN 1321
 QY 541 KPPEFLMFKSPKPKRPFNKGRIFNVNQL 565
 DB 1322 KPPEFLMFKSGTFRNKTKTRINQL 1346

RESULT 12
 ADE08094
 ID ADE08094 standard; protein; 3332 AA.
 AC ADE08094;
 XX
 DT 29-JAN-2004 (first entry)
 XX
 DE Novel protein (useful for identifying genetic disorders) #249.
 XX
 KW novel gene; novel protein; tissue marker; molecular weight marker;
 KM chromosome marker; genetic disorder.
 XX
 OS Unidentified.
 XX
 EN WO2003054152-A2.
 XX
 PD 03-JUL-2003.
 XX
 PF 10-DEC-2002; 2002WO-US039555.
 XX
 PR 10-DEC-2001; 2001US-0339739P.
 PR 11-DEC-2001; 2001US-0339453P.
 PR 14-MAR-2002; 2002US-0365091P.
 PR 14-MAR-2002; 2002US-0365384P.
 PR 12-APR-2002; 2002US-0372381P.
 PR 12-APR-2002; 2002US-0372615P.
 PR 22-APR-2002; 2002US-00128558.
 PR 24-APR-2002; 2002US-0376045P.
 XX
 PA (HYSE-) HYSEQ INC.
 XX
 PI Tang YT, Aunudi V, Goodrich RW, Ren F, Zhang J, Zhao QA, Wang J,
 PI Ghosh M, Xue AJ, Wehrman T, Weng G, Zhou P, Drmanac RT, Wang Z;
 PI Ma Y, Wang D, Chen R, Xu C, Boyle BJ,
 XX
 DR WPI; 2003-569235/53.
 DR N-PSDB; ADE07183.
 XX
 PT New polynucleotides, useful for expressing recombinant proteins for
 PT analysis, characterization or therapeutic use, or as markers for tissues
 PT in which the corresponding protein is preferentially expressed.
 XX
 PS Claim 20; SEQ ID NO 1160; 1177pp; English.
 XX
 CC The invention comprises the amino acid and coding sequences of novel
 CC proteins. The DNA and protein sequences of the invention are useful as:
 CC markers for tissues in which the corresponding protein is preferentially
 CC expressed; as molecular weight markers on gels; as chromosome markers or
 CC tags; to identify chromosomes or to map related gene positions; and to
 CC compare with endogenous DNA sequences in patients to identify potential
 CC genetic disorders. The present amino acid sequence represents a protein
 CC of the invention.
 XX
 SQ Sequence 3332 AA;

Query Match 83.0%; Score 2439; DB 7; Length 3332;
 Best Local Similarity 81.9%; Pred. No. 8,9e-215;
 Matches 463; Conservative 47; Mismatches 55; Indels 0; Gaps 0;

QY 1 MRFNGSGVEVRLPNLDELKGYTSLSLFQRPDLNENGTEDMFVNTGNKASKDYIG 60
 DB 2390 MRFNGSGVEVRLPNLDELKGYTSLSLFQRPDLNENGTEDMFVNTGNKASKDYIG 2449
 QY 61 MAVVDDQLTCVYMLGPREAVQIDQVLTRESSEDAWDRKFORIQPALNTKATSN 120
 DB 2450 MAVVDDQLTCVYMLGPREAVQIDQVLTRESSEDAWDRKFORIQPALNTKATSN 2509
 QY 121 KPRAPAVDLEGGSSNTLNLADPEDAVFYVGGYPPDFELPSRLRFPYKCIELDLNEN 180
 DB 2510 KPRTPGVYDMDGNSTLNLADPEDAVFYVGGYPPDFELPSRLRFPYKCIELDLNEN 2569
 QY 181 VLSLVNFKTTEFNLTTEVEPCRRKESDKNYEGTGVARIPQPNAPFPNFIQTITV 240
 DB 2570 VLSLVNFKTTEFNLTTEVEPCRRKESDKNYEGTGVARIPQPNAPFPNFIQTITV 2629
 QY 241 DRGLLPPAENQDNFISLNTEDGMLNRYKLSNPPKSGIRDTINDGKHSILITGKQ 300
 DB 2630 DRGLLPPAENQDNFISLNTEDGMLNRYKLSNPPKSGIRDTINDGKHSILITGKQ 2689
 QY 301 KRMWIVNERSVRIEGSIPDSTYYLGGPIAIRERFNISTPAPFGCMKULKXTSGVRL 360
 DB 2690 KRMWIVNERSVRIEGSIPDSTYYLGGPIAIRERFNISTPAPFGCMKULKXTSGVRL 2749
 QY 361 NDTVGVTKKSEBDMKLVRTASFSRGGOMSEFTNLDVPSDRFQSLFSGFQTFQPSGTLNMQ 420
 DB 2750 NDTVGVTKKSEBDMKLVRTASFSRGGOMSEFTNLDVPSDRFQSLFSGFQTFQPSGTLNMQ 2809
 QY 421 TRTSSLVLTLEDGHIETSDSNIPFKSPGYMDGLHHVYSISDTSGLRLIDQVLR 480
 DB 2810 TWTRNLQVLTLEDGHIETSDSNIPFKSPGYMDGLHHVYSISDTSGLRLIDQVLR 2869
 QY 481 RNRQLPSFSAQOSLRLGGHFECCISNVLVQRFSGSPFVLDLASKTKDASIGGCSLN 540
 DB 2870 NSRRLKHISRSRSLRGGSNFECISNVFQRLSLSPVLDLTSNLSKDVSLGGCSLN 2929
 QY 541 KPPEFLMFKSPKPKRPFNKGRIFNVNQL 565
 DB 2930 KPPEFLMFKSGTFRNKTKTRINQL 2954

RESULT 13
 AAR70148
 ID AAR70148 standard; protein; 1713 AA.
 AC AAR70148;
 XX
 DT 25-MAR-2003 (revised)
 DT 05-OCT-1995 (first entry)
 XX
 DE Deduced sequence of cDNA corresp. to the alpha-3BPA transcript.
 XX
 KW E170; epithelial ligand glycoprotein; epiligrin complex;
 KM epithelial cell binding.
 XX
 OS Homo sapiens.
 XX
 EN WO9506660-A1.
 XX
 PD 09-MAR-1995.
 XX
 PF 02-SEP-1994; 94WO-US010261.
 PR 02-SEP-1993; 93US-00115918.
 XX
 PA (HUTC-) HUTCHINSON CANCER RES CENT FRED.
 XX
 PI Carter WG, Gil SG, Ryan MC;
 XX

DR WPI, 1995-115398/15.
 DR N-PSDB; AAQ83236.
 XX
 PT New nucleic acid encoding epiligrin, an epithelial ligand complex - also
 PT related vectors, transformed cells, proteins and antibodies, useful
 PT therapeutically, and diagnostically, e.g., in cases of inflammation and to
 PT induce cancer cell differentiation.
 XX
 XX Claim 12; Fig 15A-F; 187pp; English.
 XX
 CC AAQ83235 depicts the nt. sequence compiled from sequencing cDNA clones
 CC corresp. to the alpha-3 Bpa transcript. The invention includes nt
 CC sequences in the gp. comprising the nt sequence shown in AAQ83235, the
 CC cDNA clone Bp-1 (ATCC No. 75540) shown in AAQ83234, the cDNA clone 1-1
 CC (ATCC No. 75539), and the cDNA clone 8-6 (ATCC No. 75538), or the nt.
 CC sequences shown in AAQ83236. The entire nt region encoding E170 is
 CC depicted in AAQ83236, and corresp. to the SO of alpha-3. AAQ83236
 CC consists of a composite sequence derived from several overlapping clones.
 CC A synthetic polypeptide of at least 5 AAs that corresp. to part or all of
 CC the nt. sequence shown in AAQ83236 is claimed. (Updated on 25-MAR-2003 to
 CC correct PN field.)
 XX
 XX Sequence 1713 AA;
 SQ
 Query Match 82.7%; Score 2431; DB 2; Length 1713;
 Best Local Similarity 81.8%; Pred. No. 1.7e-214;
 Matches 462; Conservative 47; Mismatches 56; Indels 0; Gaps 0;
 QY 1 MRFNGSGVEVRLPNDLEDKGYTSLFLQRPDLRENGTGEMFVMYLGNDKASDXYG 60
 DB 771 MRFNGSGVEVRLPNDLEDKGYTSLFLQRPDRENGTGEMFVMYLGNDKASDXYG 830
 QY 61 MAVVDQQLTCVYNLGDREAEVQIDQVLTSESQEAAMDVRYKFORIYQFALNTKATSN 120
 DB 831 MAVVDQQLTCVYNLGDREAEVQIDQVLTSETKEAVMDRYKFORIYQFALNTKATSN 890
 QY 121 KKPAAVYDLEGSSNTLNLDPEDAVFYGYGPPDELPRLRFPYKCIETLDDLNEN 180
 DB 891 KKPAAVYDLEGSSNTLNLDPEDAVFYGYGPPDELPRLRFPYKCIETLDDLNEN 950
 QY 181 VLSVNFKTFPNTTEVEPCRRKESDKNYEGGVYARIPQPNAPFPNFQITQTV 240
 DB 951 VLSVNFKTFPNTTEVEPCRRKESDKNYEGGVYARIPQPNAPFPNFQITQTV 1010
 QY 241 DRGLFFAENODNFISLNTEDGMLMYRYKLNSEPPKEKIRDTINGKHSILITIGKQ 300
 DB 1011 DRGLFFAENODNFISLNTEDGMLMYRYKLNSEPPKEKIRDTINGKHSILITIGKQ 1070
 QY 301 KRWMIIVNERSVRIEGEIPDFSTYYIGTPIAIRERNISTPAFGQCMKLNKKTSGVRL 360
 DB 1071 KRWMIIVNERSVRIEGEIPDFSTYYIGTPIAIRERNISTPAFGQCMKLNKKTSGVRL 1130
 QY 361 NDTVGVTKKSEDMKLVRTASFSRGGOMFTNLDVSTSRFQUSPFRQFPQSGTLLNQG 420
 DB 1131 NDTVGVTKKSEDMKLVRTASFSRGGOMFTNLDVSTSRFQUSPFRQFPQSGTLLNQG 1190
 QY 421 TRTSSLVLTLEDGHIETSTDSNIPFKSPGTMDGLLHHVYSIPTSGLRLIIDQVLR 480
 DB 1191 TRTSSLVLTLEDGHIETSTDSNIPFKSPGTMDGLLHHVYSIPTSGLRLIIDQVLR 1250
 QY 481 RNORLPSFNAQSLRLGGHFEGCISNVLVQFSGSPYVLDLASKSTKDNASLGCCSLN 540
 DB 1251 NSRKLKRISSRSQSLRLGGHFEGCISNVLVQFSGSPYVLDLASKSTKDNASLGCCSLN 1310
 QY 541 KPEFLMLFKSPKRFNKGRIFFNVQL 565
 DB 1311 KPEFLMLFKSPKRFNKGRIFFNVQL 1335

RESULT 14
 AA26584
 ID AA26584 standard; protein; 770 AA.
 XX

AC AA26584;
 XX
 XX 25-MAR-2003 (revised)
 DT 21-JAN-1998 (first entry)
 XX
 DE Rat hemidesmosome formation inducing protein 154 kDa subunit.
 XX
 KW Hemidesmosome; laminin; epithelial cell; cell attachment; adhesion;
 KW bladder carcinoma; 804G; NBT-II; rat; dental implant.
 XX
 OS Rattus sp.
 XX
 PN US5658789-A.
 XX
 PD 19-AUG-1997.
 XX
 PF 19-MAY-1995; 95US-00445135.
 XX
 PR 12-NOV-1993; 93US-00151134.
 XX
 PA (DESM-) DESMOS INC.
 XX
 PI Horita M, Quaranta V;
 XX
 DR WPI, 1997-424242/39.
 XX
 PT Soluble protein that induces hemidesmosome formation in epithelial cells
 PT - useful for stimulating epithelial cell attachment, e.g. to dental
 PT implants or teeth.
 XX
 XX Claim 2; Col 21-26; 20pp; English.
 XX
 CC This polypeptide comprises the 154 kDa alpha chain of an isolated soluble
 CC protein that induces hemidesmosome formation in epithelial cells normally
 CC unable to form hemidesmosomes. The 146 kD gamma chain (see AA26584) and
 CC the N-terminal portion (see AA26585) of the 139 kDa beta chain sequence
 CC were also determined. The protein has properties including: (a)
 CC solubility in aqueous media; (b) binding by antibodies present in the
 CC serum of rabbits inoculated with an extracellular matrix deposited by
 CC 804G rat bladder carcinoma cells or NBT-II rat bladder carcinoma cells;
 CC (c) being bound by monoclonal antibodies generated against extracellular
 CC matrix; (d) promoting rapid epithelial cell adhesion to substrates coated
 CC with at least one of the three protein chains; and (e) being obtainable
 CC from 804G rat bladder carcinoma cells or NBT-II rat bladder carcinoma
 CC cells. The protein (secreted laminin) is used to induce hemidesmosome
 CC formation in epithelial cells and to facilitate their growth (claimed).
 CC It may be used to promote cell attachment to solid surfaces, e.g. to
 CC dental implants, and may also be of use in studies concerning
 CC hemidesmosome morphogenesis and alpha 6 beta 4 integrin interactions with
 CC the epithelial extracellular matrix. (Updated on 25-MAR-2003 to correct
 CC PF field.)
 XX
 XX Sequence 770 AA;
 SQ
 Query Match 44.6%; Score 1310; DB 2; Length 770;
 Best Local Similarity 90.9%; Pred. No. 2.1e-111;
 Matches 259; Conservative 3; Mismatches 13; Indels 10; Gaps 4;
 QY 1 MRFNGSGVEVRLPNDLEDKGYTSLFLQRPDLRENGTGEMFVMYLGNDKASDXYG 60
 DB 491 MRFNGSGVEVRLPNDLEDKGYTSLFLQRPDLRENGTGEMFVMYLGNDKASDXYG 550
 QY 61 MA---VVDGQLTCVYNLGDREAEVQIDQVLTSESQEAAMDVRYKFORIYQFALNTYK 115
 DB 551 IGGCWPAD---VCLQPGGPR--SVSDSGITSESQEAAMDVRYKFORIYQFALNTYK 605
 QY 116 EATSNKPRAPAVYDLEGSSNTLNLDPEDAVFYGYGPPDELPRLRFPYKCIETL 175
 DB 606 EATSNKPRAPAVYDLEGSSNTLNLDPEDAVFYGYGPPDELPRLRFPYKCIETL 665
 QY 176 DLTENVLSLNFKTFPNTTEVEPCRRKESDKNYEGGVYARIPQPNAPFPNFQIT 235
 DB 666 DLTENVLSLNFKTFPNTTEVEPCRRKESDKNYEGGVYARIPQPNAPFPNFQIT 725

QY 236 IOTVDRGLLFPANODNFISLNIEDGNLAVRYKLANSEPPKXGI 280
 DB 726 IOTVARGLLFPANODNFISLNIEDGNLAVRYKLANSEPPKXGI 770

RESULT 15
 ABB09503
 ID ABB09503 standard; protein; 3597 AA.

AC ABB09503;

DT 01-NOV-2002 (first entry)

DE Human laminin alpha-5-like NOVIC protein, SEQ ID NO:6.

XX Human; NOVIC; neurological disorder; Alzheimer's disease;
 XX Huntington's disease; Parkinson's disease; pain; behavioural disorder;
 XX addition; tuberos sclerosis; cancer; immune disorder; allergy;
 XX autoimmune disease; myasthenia gravis; asthma; arthritis; diabetes;
 XX thyroiditis; cardiovascular disease; hypertension; reproductive disorder;
 XX endometriosis; incontinence; psoriasis; scleroderma; alopecia; ulcer;
 XX pancreatic disease; glomerular endotheiosis; bacterial infection;
 XX polycystic kidney disease; endocrine disorder; obesity; cardiomyopathy;
 XX atherosclerosis; cell signal processing-related disorder;
 XX metabolic pathway regulation disorder; cystostatic; neuroprotective;
 XX antiinflammatory; immunosuppressive; analgesic; antiatherosclerotic;
 XX dermatological; antidiabetic; antiarthritic; hepatotropic; neurogenesis;
 XX differentiation; proliferation; motility; haematopoiesis; wound healing;
 XX angiogenesis; forensic biology; transgenic animal; drug screening;
 XX gene therapy; NOVIC; laminin alpha-5-like; chromosome 20.

OS Homo sapiens.

XX Key Location/Qualifiers

FT Peptide 1..14

FT Protein /label= signal_peptide

FT Protein /note= "Mature NOVIC protein"

XX MO200253742-A2.

XX 11-JUL-2002.

XX 07-JAN-2002; 2002MO-US000375.

XX 05-JAN-2001; 2001US-0260018P.

XX 08-JAN-2001; 2001US-0260360P.

XX 28-FEB-2001; 2001US-0272411P.

XX 02-MAR-2001; 2001US-0272817P.

XX 05-JUL-2001; 2001US-0303231P.

XX 12-JUL-2001; 2001US-0305060P.

XX 10-SEP-2001; 2001US-0318405P.

XX 12-SEP-2001; 2001US-0318700P.

XX 04-JAN-2002; 2002US-00037417.

XX (CURA-) CURAGEN CORP.

XX PA

XX PI

PI Kekuda R, Alsobrook JP, Tchernev VT, Liu X, Spytek KA;

PI Patturajan M, Grosse WM, Lepley DM, Burgess CE, Vernet CAM, Li L;

PI Gorman L, Edinger S, Sciore P, Elleman K, Malyanankar U;

PI Rothenberg M, Stone D, Boldog F, Guo X, Shenoy S, Anderson D;

PI Padigaru M, Taupier RJ, Miller CE, Eissen A;

XX WPI; 2002-583619/62.

XX DR N-PSDB; ABQ93861.

PT Novel polypeptides and nucleic acids homologous to transmembrane

PT receptor, thymosin, neuromodulin-like family of proteins for diagnosing,

PT treating cancer, atherosclerosis, neurological, skin and autoimmune

XX disorders.

XX Claim 1c; Page 20-21; 323pp; English.

XX The invention relates to 24 novel human proteins designated NOVI-NOV14
 CC (ABB09501-ABB09524), collectively referred to as NOVIC proteins, and
 CC nucleic acids encoding them (ABQ93879-ABQ93902). NOVIC proteins and
 CC nucleotides are useful in the treatment, diagnosis or prevention of NOVIC-
 CC associated disorders or in the manufacture of a medicament for treating
 CC such disorders, with specific applications described for each of the 24
 CC NOVIC proteins, based on their homology to known proteins. Various
 CC disorders are associated with NOVIC proteins including neurological
 CC disorders (e.g., Alzheimer's, Huntington's and Parkinson's diseases),
 CC pain, behavioural disorders, addition, tuberos sclerosis, cancers
 CC (e.g., colorectal cancer, leukaemia and osteosarcoma), immune disorders
 CC (e.g., allergies and autoimmune diseases), myasthenia gravis, asthma,
 CC various forms of arthritis, diabetes, thyroiditis, cardiovascular disease
 CC (e.g., hypertension), reproductive disorders, endometriosis,
 CC incontinence, psoriasis, scleroderma, alopecia, ulcers, pancreatitis,
 CC cirrhosis, glomerular endotheiosis, polycystic kidney disease, endocrine
 CC disorders, obesity, bacterial infections and particularly cardiomyopathy,
 CC atherosclerosis, cell signal processing-related disorders and disorders
 CC of metabolic pathway regulation. NOVIC nucleic acids and polypeptides may
 CC be used to identify cellular receptors or downstream effectors which
 CC binds to a NOVIC protein, and are also useful as targets for the
 CC identification of small molecules that modulate or inhibit processes such
 CC as neurogenesis, cell differentiation, cell motility, cellular
 CC proliferation, haematopoiesis, wound healing and angiogenesis. NOVIC
 CC nucleic acid sequences can be used to identify a cell or tissue type and
 CC are useful as a source of primers or probes for forensic biology and for
 CC identifying and cloning NOVIC homologues in other cell types. Cells
 CC comprising NOVIC nucleic acids are useful for producing non-human
 CC transgenic animals which are useful for studying the function and
 CC activity of NOVIC proteins and for identifying and evaluating modulators
 CC of NOVIC activity. The present sequence represents the laminin alpha-5-
 CC like protein NOVIC. The gene encoding NOVIC is located on chromosome 20
 XX

XX Sequence 3597 AA;

XX Query Match 24.4%; Score 717.5; DB 5; Length 3597;

XX Best Local Similarity 31.7%; Pred. No. 1.4e-55;

XX Matches 200; Conservative 100; Mismatches 222; Indels 109; Gaps 22;

QY 1 MRENGKSGVRLNDLBDLKGYSLSLPLQRPDLRENGTDEDMFYLGKNDASNDYIG 60
 DB 2712 MKEKNGSGVQLRFPRLDLADLAAYTALKFYLGHPERPGQTEBDFVMYMGSRQATGDMYG 2771
 QY 61 MAVVDQGLCYVNLGPR-EAEVQIDVLTRESQEAEMVRVKQRITPKALNTYK--- 116
 DB 2772 VSLRDKKVMVYQLGSGAPVLSIDEDIGSQ-----FAVSLDRITLQFGHMSVTEROM 2825
 QY 117 --ATSNKPRAPAYYDLGGSSNTLNLDPEDAVFYVGYPPDELSRLRFPYKGIETL 174
 DB 2826 IQETKADTYAFGA---EG-----LNLRPDDVFYVGGIPSTTPPPLRFPGRGICEM 2877
 QY 175 DDLNENVLILNFKETFNATTEVEPCRRKKE-----SDKNYFEGTGYARIPQNP-AP 228
 DB 2878 DTLNEEVLNENKRFOLDIANDRCARSKSGDPMWDGSLDGTGPARISFDQISIT 2937
 QY 229 FENFIQTIOTVDRGLLFPANODNFISLNIEDGNLAVRYKLANSEPPKXGI 275
 DB 2938 TKRFEQELTLVSYSGVLFPKQSQPLCLAVQSGSLVLYDFAGLKKAVLPLOPPPLTS 2997
 QY 276 KEKGIDTINDGDHSILITIGLQKRMWNVN---SVRIEGLFDFSTYVLGIP- 330
 DB 2998 ASRAIQ-----VPLGSSRRVLRERATVYSVEQNDLELADAYTLGGVPPD 3046
 QY 331 -IAIRERFNISTPAPQCKMNLK---KTSGVVALNDTVGTYKCSSEDMKLVRTASPSRG 386
 DB 3047 QLPSLRLRFPYGSVAGCVKGIKALGVYDKRLN--TTGVSAGCTADLVLRMTFHGIG 3105
 QY 387 --QMSFTNLDPSTDRFQSLFQPTQPSGTLNMQTRTSSLSLTYLEDGHSISTDSNT 444
 DB 3106 FLRLALSNV-APLTGVVSGFPHSADSALTYTPRASPVAPHQVSLQGGVSVSLQLRTVE 3164
 QY 445 PTFKSGTYMDGLLHVSVISDTSGRLRLIDDV--LRNRQRLPFSNQAQGS---LRIG 498

Db	3165	---KTQAGPADGAPHYVAFYSNATGWLYYDDLOQMKEPHRGPPPEIQPQPEGPPRLILG	3221
QY	499	G-----GHFEGCISNVLVQRFPSQSPBEVLDL-----	523
Db	3222	GLPESGTIYNFSCCISNVFVQRLIGFORVFDLQONTGSVNVSTGCAPALQAOTPGIGPRO	3281
QY	524	ASKSTRKDAISLGGCSLNKPPFLMLFKSPKRP	554
Db	3282	ASRRSRQPARHPACWL--PEHLRTTRDSYQF	3310

Search completed: February 22, 2005, 08:18:47
job time : 107.16 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: February 22, 2005, 08:19:00 / Search time 75.7216 Seconds
(without alignments)
2441.722 Million cell updates/sec

Title: US-10-817-423-4

Perfect score: 2940

Sequence: 1 MRNKGSGVVRLPNDLEDL.....MLFKSPKRRFKRIFVNVQL 565

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 1380268 seqs, 327241040 residues

Total number of hits satisfying chosen parameters: 1380268

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database:

Published Applications AA:*

- 1: /cgn2_6/ptodata/2/pubppaa/US07_PUBCOMB.pep:*
- 2: /cgn2_6/ptodata/2/pubppaa/PCT_NEW_PUB.pep:*
- 3: /cgn2_6/ptodata/2/pubppaa/US06_NEW_PUB.pep:*
- 4: /cgn2_6/ptodata/2/pubppaa/US06_PUBCOMB.pep:*
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- 11: /cgn2_6/ptodata/2/pubppaa/US09C_PUBCOMB.pep:*
- 12: /cgn2_6/ptodata/2/pubppaa/US09_NEW_PUB.pep:*
- 13: /cgn2_6/ptodata/2/pubppaa/US10_PUBCOMB.pep:*
- 14: /cgn2_6/ptodata/2/pubppaa/US10C_PUBCOMB.pep:*
- 15: /cgn2_6/ptodata/2/pubppaa/US10D_PUBCOMB.pep:*
- 16: /cgn2_6/ptodata/2/pubppaa/US10E_PUBCOMB.pep:*
- 17: /cgn2_6/ptodata/2/pubppaa/US10F_PUBCOMB.pep:*
- 18: /cgn2_6/ptodata/2/pubppaa/US11_NEW_PUB.pep:*
- 19: /cgn2_6/ptodata/2/pubppaa/US60_NEW_PUB.pep:*
- 20: /cgn2_6/ptodata/2/pubppaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2940	100.0	1694	US-10-603-725-12	Sequence 12, App1
2	2940	100.0	1725	US-10-603-725-10	Sequence 10, App1
3	2439	83.0	1693	US-10-603-725-4	Sequence 4, App1
4	2439	83.0	1693	US-10-603-725-8	Sequence 8, App1
5	2439	83.0	1713	US-10-171-311-113	Sequence 113, App1
6	2439	83.0	1713	US-10-372-683-10	Sequence 10, App1
7	2439	83.0	1713	US-10-603-725-6	Sequence 6, App1
8	2439	83.0	1724	US-10-603-725-2	Sequence 2, App1
9	717.5	24.4	3597	US-10-037-417-6	Sequence 6, App1
10	717.5	24.4	3600	US-10-037-417-2	Sequence 2, App1
11	715	24.3	1634	US-10-112-944-347	Sequence 347, App1
12	715	24.3	1634	US-10-037-417-49	Sequence 49, App1
13	715	24.3	1677	US-10-112-944-801	Sequence 801, App1

14	715	24.3	3695	US-10-312-352-22	Sequence 22, App1
15	715	24.3	3696	US-10-312-088-31	Sequence 31, App1
16	715	24.3	3705	US-10-312-088-30	Sequence 30, App1
17	712	24.2	1640	US-10-037-417-8	Sequence 8, App1
18	712	24.2	3695	US-10-037-182-2	Sequence 2, App1
19	694	23.6	1816	US-10-372-683-4	Sequence 4, App1
20	688	23.4	1823	US-10-363-616-457	Sequence 457, App1
21	686	23.3	1581	US-10-408-765A-154	Sequence 154, App1
22	685	23.3	953	US-09-845-583-4	Sequence 4, App1
23	685	23.3	953	US-10-037-417-50	Sequence 50, App1
24	683	23.2	1816	US-10-299-058-2	Sequence 2, App1
25	681	23.2	1816	US-10-299-058-4	Sequence 2, App1
26	681	23.2	3635	US-09-845-583-2	Sequence 2, App1
27	681	23.2	3635	US-10-037-182-4	Sequence 4, App1
28	681	23.2	3635	US-10-037-417-47	Sequence 47, App1
29	680	23.1	469	US-10-106-698-5877	Sequence 5877, App1
30	578	19.7	908	US-10-037-417-4	Sequence 4, App1
31	395	13.4	3712	US-10-108-605-103	Sequence 103, App1
32	395	13.4	3712	US-10-037-417-48	Sequence 48, App1
33	395	13.4	3712	US-10-037-417-51	Sequence 51, App1
34	322.5	11.0	286	US-10-299-058-5	Sequence 5, App1
35	322.5	11.0	286	US-10-299-058-6	Sequence 6, App1
36	321	10.9	289	US-10-299-058-13	Sequence 13, App1
37	298.5	10.2	3672	US-10-369-493-6146	Sequence 6146, App1
38	280	9.5	3084	US-09-938-275-4	Sequence 4, App1
39	280	9.5	3084	US-10-262-670-2	Sequence 2, App1
40	270	9.2	3075	US-09-938-275-5	Sequence 5, App1
41	252	8.6	3070	US-09-961-403-7	Sequence 7, App1
42	222.5	7.6	2823	US-10-369-493-5220	Sequence 5220, App1
43	222.5	7.6	2823	US-10-369-493-5221	Sequence 5221, App1
44	213.5	7.3	1399	US-10-187-975-26	Sequence 26, App1
45	213.5	7.3	1438	US-10-187-975-22	Sequence 22, App1

ALIGNMENTS

RESULT 1
US-10-603-725-12
; Sequence 12, Application US/10603725
; Publication No. US20040014665A1
; GENERAL INFORMATION:
; APPLICANT: Bontand, Ariel
; TITLE OF INVENTION: Recombinant Laminin 5
; FILE REFERENCES: 99-274-C
; CURRENT APPLICATION NUMBER: US/10/603,725
; CURRENT FILING DATE: 2003-06-25
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 12
; LENGTH: 1694
; TYPE: PRT
; ORGANISM: Rattus norvegicus
US-10-603-725-12

Query Match 100.0%; Score 2940; DB 15; Length 1694;
Best Local Similarity 100.0%; Pred. No. 7.6e-240;
Matches 565; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	MRNKGSGVVRLPNDLEDLKGYSLSLPIORDLRNGSTDMFWYTLGNKASXQYIG 60
DB	751	MRNKGSGVVRLPNDLEDLKGYSLSLPIORDLRNGSTDMFWYTLGNKASXQYIG 810
QY	61	MAVVDGQLTCVNIAGREAEVQIDQVLTESBSGEAVMDRVKFORIQPAKANTTKATSN 120
DB	811	MAVVDGQLTCVNIAGREAEVQIDQVLTESBSGEAVMDRVKFORIQPAKANTTKATSN 870
QY	121	KPRAPAVYDLGEGSSNTLNLDPEDAVFYGGVPPPELPSRLRFPYKCCIELDNDEN 180
DB	871	KPRAPAVYDLGEGSSNTLNLDPEDAVFYGGVPPPELPSRLRFPYKCCIELDNDEN 930
QY	181	VLSTLYPKTFNNATTEVEPCRRRKESDNGVEGTCYARIPTQNAFPNFQIOTQTV 240

Db 931 VLSLNVFKTTFNLTNTTEVEPCRRRKESBDKNVEGTVARIPTQPNAPFPNFIQTITQTV 990
Qy 241 DRGLLFAENODNFISLNIEDGNLWRYKLNSEPPKEKGRDITINDGKHSILITIGKQ 300
Db 991 DRGLLFAENODNFISLNIEDGNLWRYKLNSEPPKEKGRDITINDGKHSILITIGKQ 1050
Qy 301 KKMWINNERSVRIEGBIFDFSTYYLGGIPAIAREFNISTPAFOGCMKLUKKTSGVRL 360
Db 1051 KKMWINNERSVRIEGBIFDFSTYYLGGIPAIAREFNISTPAFOGCMKLUKKTSGVRL 1110
Qy 361 NDTVGVTKCSBDMKLVRTASFSRGQMSFTNLDPSTDRPOLSGFOTPOPSGTLNMQ 420
Db 1111 NDTVGVTKCSBDMKLVRTASFSRGQMSFTNLDPSTDRPOLSGFOTPOPSGTLNMQ 1170
Qy 421 TRTSSLVLTLEBDEHIELSTRDSNIPIFKSPGYMDGLLHHVSVISDTSGLRLIIDQVLR 480
Db 1171 TRTSSLVLTLEBDEHIELSTRDSNIPIFKSPGYMDGLLHHVSVISDTSGLRLIIDQVLR 1230
Qy 481 RNQRLPFSNMQOSLRLGGHFEBCISNVLVORFSQSPVLDLASKSTKQDASLGCCSLN 540
Db 1231 RNQRLPFSNMQOSLRLGGHFEBCISNVLVORFSQSPVLDLASKSTKQDASLGCCSLN 1290
Qy 541 KPPFLMLFKSPKRFNKGRIFNVNQL 565
Db 1291 KPPFLMLFKSPKRFNKGRIFNVNQL 1315

RESULT 2
US-10-603-725-10
/ Sequence 10, Application US/10603725
/ Publication No. US20040014665A1
/ GENERAL INFORMATION:
/ APPLICANT: Bouland, Arlel
/ TITLE OF INVENTION: Recombinant Laminin 5
/ FILE REFERENCE: 99-274-C
/ CURRENT APPLICATION NUMBER: US/10/603,725
/ CURRENT FILING DATE: 2003-06-25
/ NUMBER OF SEQ ID NOS: 36
/ SOFTWARE: PatentIn Ver. 2.0
/ SEQ ID NO 10
/ LENGTH: 1725
/ TYPE: PRP
/ ORGANISM: Rattus norvegicus
US-10-603-725-10

Query Match 100.0%; Score 2940; DB 15; Length 1725;
Best Local Similarity 100.0%; Pred. No. 7.8e-240;
Matches 565; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MRFNKGSGVEVRLPNDLEDKGYTSLFLQRPDLRENGGTEDMFVMTLGNKQDASRDYIG 60
Db 782 MRFNKGSGVEVRLPNDLEDKGYTSLFLQRPDLRENGGTEDMFVMTLGNKQDASRDYIG 841
Qy 61 MAVVDGQLTCVYNLGDREAEVQIDVLTSESOEAVMDRVKFORIYQPAKLNTYKATSN 120
Db 842 MAVVDGQLTCVYNLGDREAEVQIDVLTSESOEAVMDRVKFORIYQPAKLNTYKATSN 901
Qy 121 KKPAPAVYDLEGSSNTLNLDPEDAVFYVGYPPDFELPSRLRPPTYKGCIELDLNEN 180
Db 902 KKPAPAVYDLEGSSNTLNLDPEDAVFYVGYPPDFELPSRLRPPTYKGCIELDLNEN 961
Qy 181 VLSLNVFKTTFNLTNTTEVEPCRRRKESBDKNVEGTVARIPTQPNAPFPNFIQTITQTV 240
Db 962 VLSLNVFKTTFNLTNTTEVEPCRRRKESBDKNVEGTVARIPTQPNAPFPNFIQTITQTV 1021
Qy 241 DRGLLFAENODNFISLNIEDGNLWRYKLNSEPPKEKGRDITINDGKHSILITIGKQ 300
Db 1022 DRGLLFAENODNFISLNIEDGNLWRYKLNSEPPKEKGRDITINDGKHSILITIGKQ 1081
Qy 301 KKMWINNERSVRIEGBIFDFSTYYLGGIPAIAREFNISTPAFOGCMKLUKKTSGVRL 360
Db 1082 KKMWINNERSVRIEGBIFDFSTYYLGGIPAIAREFNISTPAFOGCMKLUKKTSGVRL 1141

Qy 361 NDTVGVTKCSBDMKLVRTASFSRGQMSFTNLDPSTDRPOLSGFOTPOPSGTLNMQ 420
Db 1142 NDTVGVTKCSBDMKLVRTASFSRGQMSFTNLDPSTDRPOLSGFOTPOPSGTLNMQ 1201
Qy 421 TRTSSLVLTLEBDEHIELSTRDSNIPIFKSPGYMDGLLHHVSVISDTSGLRLIIDQVLR 480
Db 1202 TRTSSLVLTLEBDEHIELSTRDSNIPIFKSPGYMDGLLHHVSVISDTSGLRLIIDQVLR 1261
Qy 481 RNQRLPFSNMQOSLRLGGHFEBCISNVLVORFSQSPVLDLASKSTKQDASLGCCSLN 540
Db 1261 RNQRLPFSNMQOSLRLGGHFEBCISNVLVORFSQSPVLDLASKSTKQDASLGCCSLN 1321
Qy 541 KPPFLMLFKSPKRFNKGRIFNVNQL 565
Db 1322 KPPFLMLFKSPKRFNKGRIFNVNQL 1346

RESULT 3
US-10-603-725-4
/ Sequence 4, Application US/10603725
/ Publication No. US20040014665A1
/ GENERAL INFORMATION:
/ APPLICANT: Bouland, Arlel
/ TITLE OF INVENTION: Recombinant Laminin 5
/ FILE REFERENCE: 99-274-C
/ CURRENT APPLICATION NUMBER: US/10/603,725
/ CURRENT FILING DATE: 2003-06-25
/ NUMBER OF SEQ ID NOS: 36
/ SOFTWARE: PatentIn Ver. 2.0
/ SEQ ID NO 4
/ LENGTH: 1693
/ TYPE: PRP
/ ORGANISM: Homo sapiens
US-10-603-725-4

Query Match 83.0%; Score 2439; DB 15; Length 1693;
Best Local Similarity 81.9%; Pred. No. 2.6e-197;
Matches 463; Conservative 47; Mismatches 55; Indels 0; Gaps 0;

Qy 1 MRFNKGSGVEVRLPNDLEDKGYTSLFLQRPDLRENGGTEDMFVMTLGNKQDASRDYIG 60
Db 751 MRFNKGSGVEVRLPNDLEDKGYTSLFLQRPDLRENGGTEDMFVMTLGNKQDASRDYIG 810
Qy 61 MAVVDGQLTCVYNLGDREAEVQIDVLTSESOEAVMDRVKFORIYQPAKLNTYKATSN 120
Db 811 MAVVDGQLTCVYNLGDREAEVQIDVLTSESOEAVMDRVKFORIYQPAKLNTYKATSN 870
Qy 121 KKPAPAVYDLEGSSNTLNLDPEDAVFYVGYPPDFELPSRLRPPTYKGCIELDLNEN 180
Db 871 KKPAPAVYDLEGSSNTLNLDPEDAVFYVGYPPDFELPSRLRPPTYKGCIELDLNEN 930
Qy 181 VLSLNVFKTTFNLTNTTEVEPCRRRKESBDKNVEGTVARIPTQPNAPFPNFIQTITQTV 240
Db 931 VLSLNVFKTTFNLTNTTEVEPCRRRKESBDKNVEGTVARIPTQPNAPFPNFIQTITQTV 990
Qy 241 DRGLLFAENODNFISLNIEDGNLWRYKLNSEPPKEKGRDITINDGKHSILITIGKQ 300
Db 991 DRGLLFAENODNFISLNIEDGNLWRYKLNSEPPKEKGRDITINDGKHSILITIGKQ 1050
Qy 301 KKMWINNERSVRIEGBIFDFSTYYLGGIPAIAREFNISTPAFOGCMKLUKKTSGVRL 360
Db 1051 KKMWINNERSVRIEGBIFDFSTYYLGGIPAIAREFNISTPAFOGCMKLUKKTSGVRL 1110
Qy 361 NDTVGVTKCSBDMKLVRTASFSRGQMSFTNLDPSTDRPOLSGFOTPOPSGTLNMQ 420
Db 1111 NDTVGVTKCSBDMKLVRTASFSRGQMSFTNLDPSTDRPOLSGFOTPOPSGTLNMQ 1170
Qy 421 TRTSSLVLTLEBDEHIELSTRDSNIPIFKSPGYMDGLLHHVSVISDTSGLRLIIDQVLR 480
Db 1171 TRTSSLVLTLEBDEHIELSTRDSNIPIFKSPGYMDGLLHHVSVISDTSGLRLIIDQVLR 1230
Qy 481 RNQRLPFSNMQOSLRLGGHFEBCISNVLVORFSQSPVLDLASKSTKQDASLGCCSLN 540
Db 1230 RNQRLPFSNMQOSLRLGGHFEBCISNVLVORFSQSPVLDLASKSTKQDASLGCCSLN 1290

Db 1231 NSRKLKHSSRSQSLRGSGNFEGCISNVFVQRLSLSPVLDLITNSLAKDVSIGGCSLN 1290
Qy 541 KPPELMLFKSPKRFNKGRIFVNWQL 565
Db 1291 KPPELMLKSGSTRFNKTKTRINQL 1315

RESULT 4

US-10-603-725-8
; Sequence 8, Application US/10603725
; Publication No. US20040014665A1
; GENERAL INFORMATION:
; APPLICANT: Boulant, Ariel
; TITLE OF INVENTION: Recombinant Laminin 5
; FILE REFERENCE: 99-274-C
; CURRENT APPLICATION NUMBER: US/10/603,725
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 8
; LENGTH: 1693
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-603-725-8

Query Match 83.0%; Score 2439; DB 15; Length 1693;
Best Local Similarity 81.9%; Pred. No. 2.6e-197;

Matches 463; Conservative 47; Mismatches 55; Indels 0; Gaps 0;

Qy 1 MRENGSGVEVRLPNDLEDKGYTSLFLQRPDLRENGGTEDMFVYVLGNKDKASXDYIG 60
Db 751 MRENGSGVEVRLPNDLEDKGYTSLFLQRPDLRENGGTEDMFVYVLGNKDKASRYIG 810
Qy 61 MAVVDQQLTCVYMLGDBAEAVQIDVLTSESOEAVMDRYKFORIYOPALANTYKATSN 120
Db 811 MAVVDQQLTCVYMLGDBAEAVQIDVLTSESKAVMDRYKFORIYOPALANTYKATSS 870
Qy 121 KPAKPAVYDLEGSSNTLNLDPEDAVFYVGGYPPDELPRLRFPYKGCIELDLINEN 180
Db 871 KPTPGYVDMGNSNTLNLDPENAVFYVGGYPPDKLPRLRFPYKGCIELDLINEN 930
Qy 181 VLSLYNFKTFNNTTEVEBCRRKESDKNYFEGTGVARIPQPNAPFPNFIQTITV 240
Db 931 VLSLYNFKTFNNTTEVEBCRRKESDKNYFEGTGVARIPQPNAPFPNFIQTITV 990
Qy 241 DRGLLFFAENQDNFISLNIEDGMLMVRKYKLNSEBPYKGIADTINDKHSILITIGKLQ 300
Db 991 DRGLLFFAENQDNFISLNIEDGMLMVRKYKLNSEBPYKGIADTINDKHSILITIGKLQ 1050
Qy 301 KRWMINVNSVRIEGEIPDPSTYYLGGIPAIAREFNISTPAFQCGMKLKTSGVRL 360
Db 1051 KRWMINVNSVRIEGEIPDPSTYYLGGIPAIAREFNISTPAFQCGMKLKTSGVRL 1110
Qy 361 NDVYGVTKKCSBDMKLVRTASFSRGGOMSFNTLDVSTDRFQSLFGFOTPOPGSTLLNHQ 420
Db 1111 NDVYGVTKKCSBDMKLVRTASFSRGGOMSFNTLDVSTDRFQSLFGFOTPOPGSTLLNHQ 1170
Qy 421 TRTSSLLVLTLEDGHIESTSDSNIPFKSPGYTMDGLLHHVYSISDTSGRLIIDQVLR 480
Db 1171 TWTRNLQVLTLEDGHIESTSDSGPIFKSPQTYMDGLLHHVYSISDTSGRLIIDQVLR 1230
Qy 481 RNQRLSPSNAQOSLRLGGGHFEGCISNVLYVQFSQSPRYLDLASKSTKCDASIGGCSLN 540
Db 1231 NSRKLKHSSRSQSLRGSGNFEGCISNVFVQRLSLSPVLDLITNSLAKDVSIGGCSLN 1290
Qy 541 KPPELMLFKSPKRFNKGRIFVNWQL 565
Db 1291 KPPELMLKSGSTRFNKTKTRINQL 1315

RESULT 5
US-10-171-311-113
; Sequence 113, Application US/10171311

; Publication No. US20030087270A1

; GENERAL INFORMATION:

; APPLICANT: Schlegel, Robert

; APPLICANT: Chen, Yan

; APPLICANT: Zhao, Xumei

; APPLICANT: Monahan, John

; APPLICANT: Kamackar, Shubhangi

; APPLICANT: Glatz, Karen

; APPLICANT: Ganavarapu, Manjula

; APPLICANT: Hoersch, Sebastian

; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR

; IDENTIFICATION, ASSESSMENT, PREVENTION, AND THERAPY

; TITLE OF INVENTION: OF CERVICAL CANCER

; FILE REFERENCE: MRI-035

; CURRENT APPLICATION NUMBER: US/10/171,311

; CURRENT FILING DATE: 2002-06-12

; PRIOR APPLICATION NUMBER: US 60/298,159

; PRIOR FILING DATE: 2001-06-13

; PRIOR APPLICATION NUMBER: US 60/298,155

; PRIOR FILING DATE: 2001-06-13

; PRIOR APPLICATION NUMBER: US 60/335,936

; PRIOR FILING DATE: 2001-11-14

; NUMBER OF SEQ ID NOS: 238

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 113

; LENGTH: 1713

; TYPE: PRT

; ORGANISM: Homo sapiens

US-10-171-311-113

Query Match 83.0%; Score 2439; DB 14; Length 1713;
Best Local Similarity 81.9%; Pred. No. 2.6e-197;

Matches 463; Conservative 47; Mismatches 55; Indels 0; Gaps 0;

Qy 1 MRENGSGVEVRLPNDLEDKGYTSLFLQRPDLRENGGTEDMFVYVLGNKDKASXDYIG 60
Db 771 MRENGSGVEVRLPNDLEDKGYTSLFLQRPDLRENGGTEDMFVYVLGNKDKASRYIG 830
Qy 61 MAVVDQQLTCVYMLGDBAEAVQIDVLTSESOEAVMDRYKFORIYOPALANTYKATSN 120
Db 831 MAVVDQQLTCVYMLGDBAEAVQIDVLTSESKAVMDRYKFORIYOPALANTYKATSS 890
Qy 121 KPAKPAVYDLEGSSNTLNLDPEDAVFYVGGYPPDELPRLRFPYKGCIELDLINEN 180
Db 891 KPTPGYVDMGNSNTLNLDPENAVFYVGGYPPDKLPRLRFPYKGCIELDLINEN 950
Qy 181 VLSLYNFKTFNNTTEVEBCRRKESDKNYFEGTGVARIPQPNAPFPNFIQTITV 240
Db 951 VLSLYNFKTFNNTTEVEBCRRKESDKNYFEGTGVARIPQPNAPFPNFIQTITV 1010
Qy 241 DRGLLFFAENQDNFISLNIEDGMLMVRKYKLNSEBPYKGIADTINDKHSILITIGKLQ 300
Db 1011 DRGLLFFAENQDNFISLNIEDGMLMVRKYKLNSEBPYKGIADTINDKHSILITIGKLQ 1070
Qy 301 KRWMINVNSVRIEGEIPDPSTYYLGGIPAIAREFNISTPAFQCGMKLKTSGVRL 360
Db 1071 KRWMINVNSVRIEGEIPDPSTYYLGGIPAIAREFNISTPAFQCGMKLKTSGVRL 1130
Qy 361 NDVYGVTKKCSBDMKLVRTASFSRGGOMSFNTLDVSTDRFQSLFGFOTPOPGSTLLNHQ 420
Db 1131 NDVYGVTKKCSBDMKLVRTASFSRGGOMSFNTLDVSTDRFQSLFGFOTPOPGSTLLNHQ 1190
Qy 421 TRTSSLLVLTLEDGHIESTSDSNIPFKSPGYTMDGLLHHVYSISDTSGRLIIDQVLR 480
Db 1191 TWTRNLQVLTLEDGHIESTSDSGPIFKSPQTYMDGLLHHVYSISDTSGRLIIDQVLR 1250
Qy 481 RNQRLSPSNAQOSLRLGGGHFEGCISNVLYVQFSQSPRYLDLASKSTKCDASIGGCSLN 540
Db 1251 NSRKLKHSSRSQSLRGSGNFEGCISNVFVQRLSLSPVLDLITNSLAKDVSIGGCSLN 1310
Qy 541 KPPELMLFKSPKRFNKGRIFVNWQL 565
Db 1311 KPPELMLKSGSTRFNKTKTRINQL 1335

```
RESULT 6
US-10-372-683-10
; Sequence 10, Application US/10372683
; Publication No. US20040009171A1
; GENERAL INFORMATION:
; APPLICANT: GERRITSEN, MARY E.
; APPLICANT: BEALE JR., FRANKLIN V.
; APPLICANT: WU, THOMAS D.
; TITLE OF INVENTION: METHODS FOR THE TREATMENT OF CARCINOMA
; FILE REFERENCE: P1928R1P1
; CURRENT APPLICATION NUMBER: US/10/372,683
; CURRENT FILING DATE: 2003-02-21
; PRIOR APPLICATION NUMBER: US 10/271,690
; PRIOR FILING DATE: 2002-10-16
; PRIOR APPLICATION NUMBER: US 60/344,534
; PRIOR FILING DATE: 2001-10-18
; NUMBER OF SEQ ID NOS: 49
; SEQ ID NO 10
; LENGTH: 1713
; TYPE: PRT
; ORGANISM: Homo sapien
US-10-372-683-10

Query Match      83.0%; Score 2439; DB 15; Length 1713;
Best Local Similarity 81.9%; Pred. No. 2.6e-197;
Matches 463; Conservative 47; Mismatches 55; Indels 0; Gaps 0;

QY      1 MRFNGSGVEVRLPNDLEDKGYTSLFLQRPDLRENGTEPMFVMTLGNDAASKDYIG 60
DB      771 MRFNGSGVEVRLPNDLEDKGYTSLFLQRPNSRENGTEPMFVMTLGNDAASRDYIG 830
QY      61 MAVVDGQLTCVYNLDREAEVQIDQVLTBESQEAAMDVKFORIYQPAKLNTYKATSN 120
DB      831 MAVVDGQLTCVYNLDREAEVQIDQILTSEKAEAMDVKFORIYQPARLNTYKATSS 890
QY      121 KPRAPAVYDLDEGSSNTLLNIDREDAVYVGGYPPDFELPSRLRPPYKGCIELDLNEN 180
DB      891 KPEPQVYDMGDRNSNTLLNIDPENVVFYVGGYPPDFKLPSSLRPPYKGCIELDLNEN 950
QY      181 VLSVNFKTFPLNTTEVEPCRRRKEESDKNYFEGGYARLPTQPNAPFPNFQTIQTTV 240
DB      951 VLSVNFKTFPLNTTEVEPCRRRKEESDKNYFEGGYARVPTQPNAPLPTFGQTIQTTV 1010
QY      241 DRGLLFFAENQDNFISLNIEDGNLMVRYKLNSEPPKEKGIKRTINDGKHSILITIGKQ 300
DB      1011 DRGLLFFAENQDRFISLNIEDGKLMVRYKLNSELPEKRGVGDALNNGRHSIQIKIGKQ 1070
QY      301 KKMWINVNERSVRIEGEIPDFSTYYLGGIPIAIRERFNISTPAFQCGMKNLKKTSGVRL 360
DB      1071 KKMWINVDVQNTIIDGEVDFSTYYLGGIPIAIRERFNISTPAFQCGMKNLKKTSGVRL 1130
QY      361 NDVGVATKCSBDMKLVRTASFSRGGQMSFTNLDVSTDRFQLSFGQTFQPSGTLINHQ 420
DB      1131 NDVGVATKCSBDMKLVRSASFSRGGQLSFTDLGIPPTHQASFGQTFQPSGTLIDHQ 1190
QY      421 TRTSSLVTLBEDGHELSSTRDSNIPFKSPGYMDGLLHVAVISDTSGRLIIDQVLR 480
DB      1191 TWTRNIQVTLBEDGYIELSTSDSGGPIFKSPQTYMDGLLHVAVISDNISGLRLIIDQVLR 1250
QY      481 RNQRLPSFNAQOSRLRGGHREGCISNVLVQFQSPEVLDLASKTKKASLGCCSLN 540
DB      1251 NSKRLKHISRSQSLRLGGSNPEGCISNVFQRLSLSPVLDLTSNLSLRDVS LGCCSLN 1310
QY      541 KPPFLMLFKSPKRFNKGRIFFNVNQL 565
DB      1311 KPPFLMLKSGSTRFNKTKTFRINQL 1335

RESULT 7
US-10-603-725-6
; Sequence 6, Application US/10603725
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; Publication No. US20040014665A1
; GENERAL INFORMATION:
; APPLICANT: Boutand, Arlet
; TITLE OF INVENTION: Recombinant Laminin 5
; FILE REFERENCE: 99-274-C
; CURRENT APPLICATION NUMBER: US/10/603,725
; CURRENT FILING DATE: 2003-06-25
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 6
; LENGTH: 1713
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-603-725-6

Query Match      83.0%; Score 2439; DB 15; Length 1713;
Best Local Similarity 81.9%; Pred. No. 2.6e-197;
Matches 463; Conservative 47; Mismatches 55; Indels 0; Gaps 0;

QY      1 MRFNGSGVEVRLPNDLEDKGYTSLFLQRPDLRENGTEPMFVMTLGNDAASKDYIG 60
DB      771 MRFNGSGVEVRLPNDLEDKGYTSLFLQRPNSRENGTEPMFVMTLGNDAASRDYIG 830
QY      61 MAVVDGQLTCVYNLDREAEVQIDQVLTBESQEAAMDVKFORIYQPAKLNTYKATSN 120
DB      831 MAVVDGQLTCVYNLDREAEVQIDQILTSEKAEAMDVKFORIYQPARLNTYKATSS 890
QY      121 KPRAPAVYDLDEGSSNTLLNIDREDAVYVGGYPPDFELPSRLRPPYKGCIELDLNEN 180
DB      891 KPEPQVYDMGDRNSNTLLNIDPENVVFYVGGYPPDFKLPSSLRPPYKGCIELDLNEN 950
QY      181 VLSVNFKTFPLNTTEVEPCRRRKEESDKNYFEGGYARLPTQPNAPFPNFQTIQTTV 240
DB      951 VLSVNFKTFPLNTTEVEPCRRRKEESDKNYFEGGYARVPTQPNAPLPTFGQTIQTTV 1010
QY      241 DRGLLFFAENQDNFISLNIEDGNLMVRYKLNSEPPKEKGIKRTINDGKHSILITIGKQ 300
DB      1011 DRGLLFFAENQDRFISLNIEDGKLMVRYKLNSELPEKRGVGDALNNGRHSIQIKIGKQ 1070
QY      301 KKMWINVNERSVRIEGEIPDFSTYYLGGIPIAIRERFNISTPAFQCGMKNLKKTSGVRL 360
DB      1071 KKMWINVDVQNTIIDGEVDFSTYYLGGIPIAIRERFNISTPAFQCGMKNLKKTSGVRL 1130
QY      361 NDVGVATKCSBDMKLVRTASFSRGGQMSFTNLDVSTDRFQLSFGQTFQPSGTLINHQ 420
DB      1131 NDVGVATKCSBDMKLVRSASFSRGGQLSFTDLGIPPTHQASFGQTFQPSGTLIDHQ 1190
QY      421 TRTSSLVTLBEDGHELSSTRDSNIPFKSPGYMDGLLHVAVISDTSGRLIIDQVLR 480
DB      1191 TWTRNIQVTLBEDGYIELSTSDSGGPIFKSPQTYMDGLLHVAVISDNISGLRLIIDQVLR 1250
QY      481 RNQRLPSFNAQOSRLRGGHREGCISNVLVQFQSPEVLDLASKTKKASLGCCSLN 540
DB      1251 NSKRLKHISRSQSLRLGGSNPEGCISNVFQRLSLSPVLDLTSNLSLRDVS LGCCSLN 1310
QY      541 KPPFLMLFKSPKRFNKGRIFFNVNQL 565
DB      1311 KPPFLMLKSGSTRFNKTKTFRINQL 1335

RESULT 8
US-10-603-725-2
; Sequence 2, Application US/10603725
; Publication No. US20040014665A1
; GENERAL INFORMATION:
; APPLICANT: Boutand, Arlet
; TITLE OF INVENTION: Recombinant Laminin 5
; FILE REFERENCE: 99-274-C
; CURRENT APPLICATION NUMBER: US/10/603,725
; CURRENT FILING DATE: 2003-06-25
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
```

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; LENGTH: 1724
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-603-725-2

Query Match      83.0%; Score 2439; DB 15; Length 1724;
Best Local Similarity 81.9%; Pred. No. 2.6e-197;
Matches 463; Conservative 47; Mismatches 55; Indels 0; Gaps 0;

QY 1 MRRNGSGVAVRLPNDLEDKGYTSLFLQRPDLRNGTDMFVYLGKDKASKYIG 60
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 782 MRRNGSGVAVRLPNDLEDKGYTSLFLQRPDLRNGTDMFVYLGKDKASKYIG 841

QY 61 MAVVDGQLTCVYNGDREAEVQIDVLTSESSQSAVMDRVKFORIYQPAKLTAKTSN 120
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 842 MAVVDGQLTCVYNGDREAEVQIDVLTSESSQSAVMDRVKFORIYQPAKLTAKTSN 901

QY 121 KPRPAVYDLEGGSSNTLNLMDPEDAVYVGYGPPDFELPSRLFPYKGCIELDLNEN 180
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 902 KPETPGYDMDGNSNTLNLMDPENAVFYVGYGPPDFELPSRLFPYKGCIELDLNEN 961

QY 181 VLSLYNFKTFNLTTEVEPCRRKESDKXVYEGTGYANIPTQPNAPFNFITQITTV 240
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 962 VLSLYNFKTFNLTTEVEPCRRKESDKXVYEGTGYAVPTQPHAPIPTFGQITQITV 1021

QY 241 DRGLLPAENQDPIFINITDQNLNRYKLNSEPRKGIKRPITNDKDSILITGKIQ 300
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 1022 DRGLLPAENGDRPISINIDGKLMVRYKLNSELPKRGVGDALNNRDSHIOIKIGKIQ 1081

QY 301 KRWMINNERSVRLIEGIPDFSTYLLGIPLAIRERFNIPTAPQGGKMLKTSGVVRL 360
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 1082 KRWMINVDVQNTIIDGVPPSTYLLGIPLAIRERFNIPTAPQGGKMLKTSGVVRL 1141

QY 361 NDTVGVTKKCEBWKLVRTASFSRQMSFTNLDPSTDRQLSFGFTQPSGTLINHQ 420
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 1142 NDTVGVTKKCEBWKLVRTASFSRQMSFTNLDPSTDRQLSFGFTQPSGTLINHQ 1201

QY 421 TRPSLLVLTEDGHIESTDSNIPFKSPGTVDGLHNVSVSDSGRLITIDPOVR 480
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 1202 TWRNLDVLTEDGHIESTDSNIPFKSPGTVDGLHNVSVSDSGRLITIDPOVR 1261

QY 481 RNORLSPSNAQOSLRIGGHEGECISNVLVQRFSGSEVYDLASKSTKQDASIGGSLN 540
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 1262 NSKRLKHISRSRSLRIGGHEGECISNVLVQRFSGSEVYDLASKSTKQDASIGGSLN 1321

QY 541 KPPLMLFKSPKRPKRGIRFNVQL 565
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 1322 KPPLMLFKSGTRFNKTKTRINQL 1346

RESULT 9
US-10-037-417-6
; Sequence 6, Application US/10037417
; Publication No. US20040052806A1
; GENERAL INFORMATION:
; APPLICANT: Kekuda, Rameesh
; APPLICANT: Alsebrook II, John P
; APPLICANT: Tchernev, Velizar T
; APPLICANT: Liu, Xiaohong
; APPLICANT: Szytek, Kimberly A
; APPLICANT: Paturajan, Meera
; APPLICANT: Groese, William M
; APPLICANT: Lepley, Denise M
; APPLICANT: Burgess, Catherine E
; APPLICANT: Vermet, Corine A.M.
; APPLICANT: Li, Li
; APPLICANT: Gorman, Linda
; APPLICANT: Edinger, Shlomit R
; APPLICANT: Sciore, Paul
; APPLICANT: Ellerman, Karen
; APPLICANT: Malyankar, Uriel M
; APPLICANT: Rothenberg, Mark
; APPLICANT: Stone, David J
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; APPLICANT: Boldog, Ferenc L
; APPLICANT: Guo, Xiaojia
; APPLICANT: Shenoy, Suresh G
; APPLICANT: Anderson, David W
; APPLICANT: Padigaru, Muralidhara
; APPLICANT: Raupler Jr, Raymond J
; APPLICANT: Miller, Charles E
; APPLICANT: Bisen, Andrew J
; TITLE OR INVENTION: Proteins and Nucleic Acids Encoding Same
; FILE REFERENCE: 21402-235
; CURRENT APPLICATION NUMBER: US/10/037,417
; CURRENT FILING DATE: 2002-09-20
; PRIOR APPLICATION NUMBER: 60/260,018
; PRIOR FILING DATE: 2001-01-05
; PRIOR APPLICATION NUMBER: 60/260,360
; PRIOR FILING DATE: 2001-01-08
; PRIOR APPLICATION NUMBER: 60/272,411
; PRIOR FILING DATE: 2001-02-28
; PRIOR APPLICATION NUMBER: 60/272,817
; PRIOR FILING DATE: 2001-03-02
; PRIOR APPLICATION NUMBER: 60/291,186
; PRIOR FILING DATE: 2001-05-15
; PRIOR APPLICATION NUMBER: 60/303,231
; PRIOR FILING DATE: 2001-07-05
; PRIOR APPLICATION NUMBER: 60/305,060
; PRIOR FILING DATE: 2001-07-12
; PRIOR APPLICATION NUMBER: 60/318,405
; PRIOR FILING DATE: 2001-09-10
; PRIOR APPLICATION NUMBER: 60/318,700
; PRIOR FILING DATE: 2001-09-12
; NUMBER OF SEQ ID NOS: 227
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
; LENGTH: 3597
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-037-417-6

Query Match      24.4%; Score 717.5; DB 15; Length 3597;
Best Local Similarity 31.7%; Pred. No. 1.1e-50;
Matches 200; Conservative 100; Mismatches 222; Indels 109; Gaps 22;

QY 1 MRRNGSGVAVRLPNDLEDKGYTSLFLQRPDLRNGTDMFVYLGKDKASKYIG 60
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 2712 MRRNGSGVAVRLPNDLEDKGYTSLFLQRPDLRNGTDMFVYLGKDKASKYIG 2771

QY 61 MAVVDGQLTCVYNGDREAEVQIDVLTSESSQSAVMDRVKFORIYQPAKLTAKTSN 116
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 2772 VSLRDKKXHVYVQLEAGRAVLSDIDIGRQ-----FAVSLDRITLQFGHMSVTVBRQM 2825

QY 117 -ATSNKPRPAVYDLEGGSSNTLNLMDPEDAVYVGYGPPDFELPSRLFPYKGCIEL 174
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 2826 IQETKDPVAPGA-----EG-----LNLNRPDDFVYVGYGPPDFELPSRLFPYKGCIEL 2877

QY 175 DDNLNENVLSTYNKTFNLTTEVEPCRRKES-----SKNYFEGGVARIPTQPNAP 228
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 2878 DTNNEEVSLYNKTFNLTTEVEPCRRKES-----SKNYFEGGVARIPTQPNAP 2937

QY 229 PPNFIQITQTVDRGLLPAENQDPIFINITDQNLNRYKLNSEPRKGIKRPITNDKDS 275
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 2938 TKRFEGELRIVSVGYFLFKQSQFLCLAVGSGSLVLYDPAGLKKAVPLQPPPLTSS 2997

QY 276 KERGINDTNDGKHSILITIGLQKRWMINVNER--SVRIGEIPIFSTYLLGIP-- 330
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 2998 ASRAIQ-----VFLLGSGSRKXVLRVERATVYSVEQNDDELADAYLIGVPPD 3046

QY 331 -IARERFNISTAPQGGKMLKTSGVNLNMDPEDAVYVGYGPPDFELPSRLFPYKGCIEL 386
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 3047 QLPGLRLFLPTGSGVAGVIGIALGKYVDLKLIN--TTGVSAGCTADLVGRAMTFRHG 3105

QY 387 --QMSFTNLDPSTDRFQSLSGFTQPSGTLNHNQRTSSLLVLTEDGHIESTDSNIT 444
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 3106 FLRLALSNV-APLTGNVYSGFGFHSAGDSALLYYRASPVAPPHGVSLQGGVAVSLQLETRV 3164
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QY 445 PIFSPGYMGLLHHVVISDTSGLRLIPDOV--LRNRRLPEFSNAQS---LRLG 498
Db 3165 ---KTQAGFADGAPHYVAIFYSNATSVMLYVDQLQOMKPHRGPEPELOPQBBGPRLLUG 3221
QY 499 G-----GHEFGCISNLYVORFSQSPEVLDL----- 523
Db 3222 GLPESGITYNSGCSISNVFORLLGQKRVFDIQNLGSVNVSTGCAPALQATPELGPRQ 3281
QY 524 ASKSTKDDASLGCGSLNKPPELMLFKSEKRP 554
Db 3282 ASRSRQPARHPACML--PPLKRTTRDSYQF 3310

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RESULT 10
US-10-037-417-2
Sequence 2, Application US/10037417
Publication No. US20040052806A1
GENERAL INFORMATION:
APPLICANT: Kekuda, Ramesh
APPLICANT: Alsobrook II, John P
APPLICANT: Tchernev, Velizar T
APPLICANT: Liu, Xiaohong
APPLICANT: Spytek, Kimberly A
APPLICANT: Patureajan, Meera
APPLICANT: Grose, William M
APPLICANT: Lepley, Denise M
APPLICANT: Burgess, Catherine B
APPLICANT: Vernet, Corine A.M.
APPLICANT: Li, Li
APPLICANT: Gorman, Linda
APPLICANT: Edinger, Shlomit R
APPLICANT: Sciore, Paul
APPLICANT: Ellerman, Karen
APPLICANT: Malyankar, Uriel M
APPLICANT: Rothenberg, Mark
APPLICANT: Stone, David J
APPLICANT: Boldog, Ferenc L
APPLICANT: Guo, Xiaojia
APPLICANT: Shenoy, Suresh G
APPLICANT: Anderson, David W
APPLICANT: Padigaru, Muralidhara
APPLICANT: Taupier Jr, Raymond J
APPLICANT: Miller, Charles E
APPLICANT: Eissen, Andrew J
TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same
FILE REFERENCE: 21402-235
CURRENT APPLICATION NUMBER: US/10/037,417
CURRENT FILING DATE: 2002-09-20
PRIOR APPLICATION NUMBER: 60/260,018
PRIOR FILING DATE: 2001-01-05
PRIOR APPLICATION NUMBER: 60/260,360
PRIOR FILING DATE: 2001-01-08
PRIOR APPLICATION NUMBER: 60/272,411
PRIOR FILING DATE: 2001-02-28
PRIOR APPLICATION NUMBER: 60/272,817
PRIOR FILING DATE: 2001-03-02
PRIOR APPLICATION NUMBER: 60/291,186
PRIOR FILING DATE: 2001-05-15
PRIOR APPLICATION NUMBER: 60/303,231
PRIOR FILING DATE: 2001-07-05
PRIOR APPLICATION NUMBER: 60/305,060
PRIOR FILING DATE: 2001-07-12
PRIOR APPLICATION NUMBER: 60/318,405
PRIOR FILING DATE: 2001-09-10
PRIOR APPLICATION NUMBER: 60/318,700
PRIOR FILING DATE: 2001-09-12
NUMBER OF SEQ ID NOS: 227
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 2
LENGTH: 3600
TYPE: PRT
ORGANISM: Homo sapiens

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US-10-037-417-2

Query Match	Score	DB	Length
24.4%	717.5	15	3600
21.7%	110.50		

Matches 200; Conservative 100; Mismatches 222; Indels 109; Gaps 22;

1 MRFNGSKSGVEVRLPNLDELKGYTSLSLFLQRPDLRENGGTEDMFVMYLGKNDASKDYIC 60

2715 MKFNGRSGVQLRTPRDLADLAAYTALKFYLLQGPEPEPGGTEDRFVMMGSRQATGDYMG 2774

61 MAVVDGOLTCVYNLGR-BAEVQIDVLTESESGEAVMDRVKFORIYQFAKNTYTK----- 116

2775 VSLRDKVHVYQLGEAGPAVLSIDEDIGEÖ-----FAAVSLDRTLQFGHMSVTVERQM 2828

117 -ATSNKPAPAVYDLEGGSSNTLLNLDPEDAVFYVGGYPPDFELPSRLRFPYKGCIEL 174

2829 IQETKGDVAPGA---EG----LNLRPDDFVFVGGYPSTFTPPPLLRFPGRGCIEM 2880

175 DDINENVLSLYNFKTTFNLTTEVEPCRRKEE-----SDKNYFEGTGYARIPTQPN-AP 228

2881 DTINEEVSLYNFERTQDLTAVDRCARSKSTGDPWLTDGSYLDGTGFARISFDSQIST 2940

229 FPNFIQTIVDRGLLFAENQDNFISLNIEDGNLMVRKLS-----EPP----- 275

2941 TKRFQELRLVSYSGVLFPLKQSQFLCLAVQEGSLVLLYDFGAGLKKAVPLQPPPLTS 3000

276 KEGIRDTINDGKDSILITIGKLOKRWINVER--SVRIEGEIFDFSTYYLGIP-- 330

3001 ASKAIQ-----VFLLGSRKRVLRVERATVYSVEQDNDLELADAYYLGGVPPD 3045

331 -IAIRERNISTPAFGCMKLNK--KTSGVRLNDTVGVTKKCSSEDKLVRTASFSRG 386

3050 QLPRLRRLPPTGGSVRCVKIKALGKYVDLKRLN-TTGVSAAGCTADLLVGRAMTFHGHG 3108

387 --QMSFTNLDPSTDRFQLSFGFQTFQPSGTLNHQTRTSSLVTLLEDGHIILSTRDSNI 444

3109 FLRLALSNV-APLTGNVSGFGFHSAQDSALLYRASPVPHQVSLQQGRVSLQLRTEV 3167

445 PIFKSPGTYMDGLHHVSISDTSGRLRIDQV--LRNQRLPSFSNAQS----LRIG 498

3168 ---KTQAGFADGAPHYVAFYSNATGWLYVDDQLQMKPHRGPPPELQRPREGPPRLLG 3224

499 G-----GHFEGCISNVLQRFSSQSP EVDL----- 523

3225 GLPESGTYNFGSCISNVFQRLGLGPQRVFDLQQLGSVNVSTGCAPALQAQTPGLGPRQ 3284

524 ASKSTKDALGGCSLNKPPFLMLFKSPKRF 554

3 285 ASRRSRQPARHPACML--PPHLRTTRDSYQF 3313

RESULT 11
US-10-112-944-347

Publication No. US20040048249A1
Sequence 347, Application US/10112944

GENERAL INFORMATION:
APPLICANT: TANDY TOM

APPLICANT: yang, Yonghong
APPLICANT: Weng, Gezhi

APPLICANT: Zhang, Jie
APPLICANT: Ren, Feiyun

APPLICANT: Xue, Aidong J.
APPLICANT: Wang, Jian-Pui

APPLICANT: Ghosh, Malabika

APPLICANT: wang, duntui
APPLICANT: Zhao, Qing A.

APPLICANT: wang, zhiwei
TITLE OF INVENTION: NO. US20040048249A1e] Nucleic acids and

TITLE OF INVENTION: Secreted Polypeptides

FILE REFERENCE: A05A

CURRENT FILING DATE: 2002-03-28
CURRENT APPLICATION NUMBER: US/10/112,944


```

QY 117 --ATSNKPKAPAVYDLBEGSSNTLLNLDPEDAVFYVGYPPDFELSPRLRPPYKCIETL 174
DB 790 IORTKADTVAPGA---EG-----LNLNRPDDVFYVGYPSFTFPLRLRPPYKCIEM 841
QY 175 DDLNENVSLYNKTKTNNTTEVEPCRRKEE-----SDKNPFGTGARYIPTQPN-AP 228
DB 842 DTLNBEVSLYNKERTFOLDTAVDRPCASKSTGDPMLTDGSLDGTGFARISFDSQIST 901
QY 229 FPNFIQTITQTVDRGLLPPAENQDNFISLNIEDGNLMVRYKLS-----EPP----- 275
DB 902 TRFEGELRLVSYSGVLFLLKQOSQFLCLAVQSGSLVLYDPGALKKAVPLQPPPLPS 961
QY 276 KEGGIDRTINDKDHSLITIGLQKRMWINVER---SVRIEGRIPFSTYLLGI--- 329
DB 962 ASKAID-----VFLGSGSRKRVLYVERATVYSVEQDNDELADAYLGGVPPD 1010
QY 330 --PIAIRERFNISTPAFGCMKLNK---KTSGVRLNDTVGYTKKCSDEMKLVRTASFSR 384
DB 1011 QLPPLRLRFP--TGSSVRCGVKGIKALKYVDLKRNLN--TGVSACTADLLVGRAMTFHG 1068
QY 385 GG--QMSFTNLDPVSTDRFQLSFGFOTFQPSGTLNHNQRTSSLLVLTEDGHIETSDS 442
DB 1069 HGFRLALASNV-APLITGVNYSFGFHSADDSALLYRASPDGLCOVSLQOGVSVSLQLRT 1127
QY 443 NIPFSPGTWMDGLHHVSVISDTSGLRLIDDV--LRNQRLPSFSNAQOS---LR 496
DB 1128 EV---KTOAGFADGAPHYAFYSNATGWMLYDDQLQMKPHRGPPPLQPPBEPRL 1184
QY 497 LGG-----GHFEGCISNVLVQRFSGSPREVLDLASKSTKDDASLG 535
DB 1185 LGGLPESGTYVNFSGCISNVFQRLGPRVFDLQONLGSVNVSTG 1230

```

RESULT 13

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US-10-112-944-801
; Sequence 801, Application US/10112944
; Publication No. US20040048249A1
; GENERAL INFORMATION:
; APPLICANT: Tang, Y. Tom
; APPLICANT: Yang, Yonghong
; APPLICANT: Weng, Gezhi
; APPLICANT: Zhang, Jie
; APPLICANT: Ren, Feiyan
; APPLICANT: Xue, Aidong J.
; APPLICANT: Wang, Jian-Rui
; APPLICANT: Wehrman, Tom
; APPLICANT: Ghosh, Malabika
; APPLICANT: Wang, Dunrui
; APPLICANT: Zhao, Qing A.
; APPLICANT: Wang, Zhiwei
; TITLE OF INVENTION: No. US20040048249A1 Nucleic Acids and
; FILE REFERENCE: 805A
; CURRENT APPLICATION NUMBER: US/10/112,944
; PRIOR FILING DATE: 2002-03-28
; PRIOR APPLICATION NUMBER: US 09/488,725
; PRIOR FILING DATE: 2000-01-21
; PRIOR APPLICATION NUMBER: US 09/491,404
; PRIOR FILING DATE: 2000-01-25
; PRIOR APPLICATION NUMBER: US 09/496,914
; PRIOR FILING DATE: 2000-02-03
; PRIOR APPLICATION NUMBER: US 09/515,126
; PRIOR FILING DATE: 2000-02-28
; PRIOR APPLICATION NUMBER: US 09/519,705
; PRIOR FILING DATE: 2000-03-07
; PRIOR APPLICATION NUMBER: US 09/540,217
; PRIOR FILING DATE: 2000-03-31
; PRIOR APPLICATION NUMBER: US 09/552,929
; PRIOR FILING DATE: 2000-04-18
; PRIOR APPLICATION NUMBER: US 09/577,408
; PRIOR FILING DATE: 2000-05-18
; NUMBER OF SEQ ID NOS: 924
; SOFTWARE: pt_fl_genes Version 5.0

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; SEQ ID NO 801
; LENGTH: 1677
; TYPE: PRF
; ORGANISM: Homo sapiens
US-10-112-944-801

```

Query Match 24.3%; Score 715; DB 15; Length 1677;
 Best Local Similarity 33.1%; Pred. No. 5,7e-51;
 Matches 194; Conservative 96; Mismatches 214; Indels 82; Gaps 21;

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QY 1 MAFNKGSGYEVNLPDLDELKGTSLSLFLQRPDLRENGCTEDMVMYLGAKDASKDYIG 60
DB 687 MAFNKGSGYEVNLPDLDELKGTSLSLFLQRPDLRENGCTEDMVMYLGAKDASKDYIG 746
QY 61 MAVVQGLTCVNLGDR--EAEVQIDOVLTSSSGAAMDVRYFORIYOPAKNRYKE--- 116
DB 747 VSLRDKKAMWVQLSGAGPAVLSIDEDIGEQ-----FAVSLDITLQPGHNSVTEROM 800
QY 117 --ATSNKPKAPAVYDLBEGSSNTLLNLDPEDAVFYVGYPPDFELSPRLRPPYKCIETL 174
DB 801 IORTKADTVAPGA---EG-----LNLNRPDDVFYVGYPSFTFPLRLRPPYKCIEM 852
QY 175 DDLNENVSLYNKTKTNNTTEVEPCRRKEE-----SDKNPFGTGARYIPTQPN-AP 228
DB 853 DTLNBEVSLYNKERTFOLDTAVDRPCASKSTGDPMLTDGSLDGTGFARISFDSQIST 912
QY 229 FPNFIQTITQTVDRGLLPPAENQDNFISLNIEDGNLMVRYKLS-----EPP----- 275
DB 902 TRFEGELRLVSYSGVLFLLKQOSQFLCLAVQSGSLVLYDPGALKKAVPLQPPPLPS 961
QY 276 KEGGIDRTINDKDHSLITIGLQKRMWINVER---SVRIEGRIPFSTYLLGI--- 329
DB 962 ASKAID-----VFLGSGSRKRVLYVERATVYSVEQDNDELADAYLGGVPPD 1010
QY 330 --PIAIRERFNISTPAFGCMKLNK---KTSGVRLNDTVGYTKKCSDEMKLVRTASFSR 384
DB 1011 QLPPLRLRFP--TGSSVRCGVKGIKALKYVDLKRNLN--TGVSACTADLLVGRAMTFHG 1068
QY 385 GG--QMSFTNLDPVSTDRFQLSFGFOTFQPSGTLNHNQRTSSLLVLTEDGHIETSDS 442
DB 1069 HGFRLALASNV-APLITGVNYSFGFHSADDSALLYRASPDGLCOVSLQOGVSVSLQLRT 1127
QY 443 NIPFSPGTWMDGLHHVSVISDTSGLRLIDDV--LRNQRLPSFSNAQOS---LR 496
DB 1128 EV---KTOAGFADGAPHYAFYSNATGWMLYDDQLQMKPHRGPPPLQPPBEPRL 1184
QY 497 LGG-----GHFEGCISNVLVQRFSGSPREVLDLASKSTKDDASLG 535
DB 1185 LGGLPESGTYVNFSGCISNVFQRLGPRVFDLQONLGSVNVSTG 1241

```

RESULT 14

```

US-10-312-352-22
; Sequence 22, Application US/10312352
; Publication No. US20040053824A1
; GENERAL INFORMATION:
; APPLICANT: INCYTE GENOMICS, INC.; TANG, Y. Tom
; APPLICANT: YUE, Henry; AKIMZAI, Yalda
; APPLICANT: HE, Amy; BATRA, Sajeev
; APPLICANT: LO, Terence P.; NGUYEN, Daniel B.
; APPLICANT: BURRILL, John D.; MARCUS, Gregory A.
; APPLICANT: ZINGLER, Kurt A.; GANDHI, Ameena R.
; APPLICANT: LAL, Preeti G.; KEARNEY, Liam
; APPLICANT: BURFORD, Neil; YAO, Monique G.
; APPLICANT: CHANLA, Narinder K.; ELIOT, Vicki S.
; APPLICANT: ARVIZU, Chandra S.; KHAN, Farrah A.
; APPLICANT: BAUGHN, Mariah R.; HAFALIA, April, J.A.
; APPLICANT: POLICKY, Jennifer L.; AV-YOUNG, Janice K.
; APPLICANT: LU, Yan; BOROWSKY, Mark L.
; APPLICANT: LU, Dyrung Aina M.; RAMKUMAR, Jayalaxmi
; APPLICANT: YANG, Junming; GURURAJAN, Rajagopal
; APPLICANT: WARREN, Bridget A.; GIETZEN, Kimberly J.
; APPLICANT: XU, Yuning; KALLICK, Deborah A.

```

```
APPLICANT: LEE, Ernestine A.; THANGAVELU, Kavitha
APPLICANT: DELBEARE, Angelo M.; LEE, Sally
TITLE OF INVENTION: EXTRACELLULAR MATRIX AND CELL ADHESION MOLECULES
FILE REFERENCE: EP-0794 USN
CURRENT APPLICATION NUMBER: US/10/312,352
PRIOR FILING DATE: 2002-12-18
PRIOR APPLICATION NUMBER: PCT/US01/21067
PRIOR FILING DATE: 2001-06-29
PRIOR APPLICATION NUMBER: US 60/215,454
PRIOR FILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: US 60/219,462
PRIOR FILING DATE: 2000-07-18
PRIOR APPLICATION NUMBER: US 60/240,111
PRIOR FILING DATE: 2000-10-12
PRIOR APPLICATION NUMBER: US 60/240,106
PRIOR FILING DATE: 2000-10-12
PRIOR APPLICATION NUMBER: US 60/244,021
PRIOR FILING DATE: 2000-10-27
PRIOR APPLICATION NUMBER: US 60/248,887
PRIOR FILING DATE: 2000-11-14
PRIOR APPLICATION NUMBER: US 60/249,570
PRIOR FILING DATE: 2000-11-16
NUMBER OF SEQ ID NOS: 72
SOFTWARE: PERL Program
SEQ ID NO 22
LENGTH: 3695
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc feature
OTHER INFORMATION: Incyte ID No. US20040053824A1 6382722CD1
US-10-312-352-22

Query Match      24.3%; Score 715; DB 15; Length 3695;
Best Local Similarity 33.1%; Pred. No. 1.9e-50;
Matches 194; Conservative 96; Mismatches 214; Indels 82; Gaps 21;

QY      1 MRNNGSGVEVRLPNLEDLKGTYSLSLPIQRPDLRENGTDMFWYLGKNAKSDYIG 60
DB      2737 MKNNGSGVQLRTPRLADIATAATLALFYLGEPPEPGQTEPRFVWYMGSRQATYDYM 2796
QY      61 MAVVDQLTCVNYLGNDR-EAEVQIDQVLTSESQEAVMRVKQRIYQFAKLNTYKE--- 116
DB      2797 VSLRDKKVMYVQLGEGRAVLSDIDIGHQ-----FAVSLDRTLQFGHMYTVYRQM 2850
QY      117 --ATSNKPKAPAVYDLEGGSSNTLLNDPEDAVFYVGGYPPDELPBRLRPPYKGI 174
DB      2851 IQETKGDYVAPGA---EG-----LNLNRPDQVFFYVGGYSTPTPLLPFGYRGCI 2902
QY      175 DDLNENVLSLNKKTTPNLTTEVEPCRRKEE-----SPKNTFEGYGIARIPQRP-AP 228
DB      2903 DTLNEBVSILYNBERFQDLTAVDRCARSKSTGDPWLTGGSYLDGTGPARISFDQIST 2962
QY      229 FPNFIQTIQTVDRGLLFPANODNFI SLNIDGNLMVRKLS-----BPP----- 275
DB      2963 TKRFBQLRIVSVSGVLFKQOSQFLCLAVQESLVLDPGAGLKAAPLQPPPLTS 3022
QY      276 KKKGIQDITNDKDHSLITIGKLQKRMWVNER---SVRIEGEIFDFSTYLLGFI--- 329
DB      3023 ASRAIQ-----VFLIGSRKRVLVREBAITYVSVEQNDDELADAYILGVPPD 3071
QY      330 --PLAIRERNISTPAFOGCMKNIK---KTSGVRLNDTVGVTKKSEDMKLVRTASFSR 384
DB      3072 QLPESLRRLFP-TGSGVRCGVKGIKALGKYVDLKRLL-TTGVSAGCTADLLVGRAMTFHG 3129
QY      385 GG--QMSFTMLDVPSTDRFOLSPFQTFOPSGTLLNHQRTSSILVLTLEDGHIELSTRDS 442
DB      3130 HGFLRLALSNV-ALITGVNYSGFPHSAQDSALLYTAASPDGLQGVSLQGRVSLQTLRT 3188
QY      443 NIPIFKSPGTYMGGLLHHSVISDTSGLRLLIDQV--LRRNQLPSFSNAQOS---LR 496
DB      3189 EV---KTQAGPADCAAPHYVAFVSNATGVMLVYDDQLQMKPHRGPPELQPPGPPRL 3245
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QY      497 LGG-----GHFEGCISNVLVQRFQSPQSEVLDLASKSTKQASLG 535
DB      3246 LGGLPESGTYNPFSSGISNVFQRLGLGPRVFLQNMISVNVSTG 3291

RESULT 15
US-10-312-088-31
Sequence 31, Application US/10312088
Publication No. US20030219862A1
GENERAL INFORMATION:
APPLICANT: Agarwal, Pankaj
APPLICANT: Cogswell, John P.
APPLICANT: Kohnic, Karen S.
APPLICANT: Lai, Ying-Ta
APPLICANT: Martensen, Shelby A.
APPLICANT: Murdoch, Paul R.
APPLICANT: Smith, Randall P.
APPLICANT: Strum, Jay C.
APPLICANT: Xiang, Zhaoying
APPLICANT: Xie, Qing
APPLICANT: Rizni, Safia K.
TITLE OF INVENTION: NOVEL COMPOUNDS
FILE REFERENCE: GP50029
CURRENT FILING DATE: 2002-12-20
PRIOR APPLICATION NUMBER: PCT/US01/19929
PRIOR FILING DATE: 2001-06-22
PRIOR APPLICATION NUMBER: 60/213,161
PRIOR FILING DATE: 2000-06-22
PRIOR APPLICATION NUMBER: 60/213,156
PRIOR FILING DATE: 2000-06-22
NUMBER OF SEQ ID NOS: 44
SOFTWARE: Pascal for Windows Version 4.0
SEQ ID NO 31
LENGTH: 3696
TYPE: PRT
ORGANISM: Homo sapiens
US-10-312-088-31

Query Match      24.3%; Score 715; DB 15; Length 3696;
Best Local Similarity 33.1%; Pred. No. 1.9e-50;
Matches 194; Conservative 96; Mismatches 214; Indels 82; Gaps 21;

QY      1 MRNNGSGVEVRLPNLEDLKGTYSLSLPIQRPDLRENGTDMFWYLGKNAKSDYIG 60
DB      2738 MKNNGSGVQLRTPRLADIATAATLALFYLGEPPEPGQTEPRFVWYMGSRQATYDYM 2797
QY      61 MAVVDQLTCVNYLGNDR-EAEVQIDQVLTSESQEAVMRVKQRIYQFAKLNTYKE--- 116
DB      2798 VSLRDKKVMYVQLGEGRAVLSDIDIGHQ-----FAVSLDRTLQFGHMYTVYRQM 2851
QY      117 --ATSNKPKAPAVYDLEGGSSNTLLNDPEDAVFYVGGYPPDELPBRLRPPYKGI 174
DB      2852 IQETKGDYVAPGA---EG-----LNLNRPDQVFFYVGGYSTPTPLLPFGYRGCI 2903
QY      175 DDLNENVLSLNKKTTPNLTTEVEPCRRKEE-----SPKNTFEGYGIARIPQRP-AP 228
DB      2904 DTLNEBVSILYNBERFQDLTAVDRCARSKSTGDPWLTGGSYLDGTGPARISFDQIST 2963
QY      229 FPNFIQTIQTVDRGLLFPANODNFI SLNIDGNLMVRKLS-----BPP----- 275
DB      2964 TKRFBQLRIVSVSGVLFKQOSQFLCLAVQESLVLDPGAGLKAAPLQPPPLTS 3023
QY      276 KKKGIQDITNDKDHSLITIGKLQKRMWVNER---SVRIEGEIFDFSTYLLGFI--- 329
DB      3024 ASRAIQ-----VFLIGSRKRVLVREBAITYVSVEQNDDELADAYILGVPPD 3072
QY      330 --PLAIRERNISTPAFOGCMKNIK---KTSGVRLNDTVGVTKKSEDMKLVRTASFSR 384
DB      3073 QLPESLRRLFP-TGSGVRCGVKGIKALGKYVDLKRLL-TTGVSAGCTADLLVGRAMTFHG 3130
QY      385 GG--QMSFTMLDVPSTDRFOLSPFQTFOPSGTLLNHQRTSSILVLTLEDGHIELSTRDS 442
```

```
Db      3131 HGFRLALSNV-APLTGNVYSGFGFHSADDSALLTYRASPDGICQVSLQGRVSLQLRT 3189
Qy      443 NIPFSPGTMYDGLHNVSVISDTSGLRLIIDQV--LRNQRLPSPSNAQOS---LR 496
      :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
Db      3190 BV---KTQAGFADGAPHYVAFYSNATGWLVYDDQLQMKPHRGPPPELQPQEGPPRL 3246
Qy      497 LGG-----GHEGCTSNVLVORFSQSPPEVLDLASKSTKQASLG 535
      :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
Db      3247 LGGLPESGTIYNFSGCISNVFYORLGPQRFVFDLQONLGSVNVSTG 3292
```

Search completed: February 22, 2005, 08:44:42
Job time : 78.7216 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: February 22, 2005, 08:13:40 ; Search time 26.3827 Seconds
(without alignments)
1598.653 Million cell updates/sec

Title: US-10-817-423-4

Perfect score: 2940

Sequence: 1 MRNGKSGVRLPNLEDL.....MLFKSPKPKRIFPVNQL 565

Scoring table:

BLOSUM62

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database : Issued Patents AA:*
1: /cgn2_6/ptodata/1/1aa/5A COMB.pep:*
2: /cgn2_6/ptodata/1/1aa/5B COMB.pep:*
3: /cgn2_6/ptodata/1/1aa/6A COMB.pep:*
4: /cgn2_6/ptodata/1/1aa/6B COMB.pep:*
5: /cgn2_6/ptodata/1/1aa/PTUS COMB.pep:*
6: /cgn2_6/ptodata/1/1aa/backfile1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Result No.	Score	Query Match	Length	ID	Description
1	2940	100.0	1694	US-09-560-385A-12	Sequence 12, Appl
2	2940	100.0	1725	US-09-560-385A-10	Sequence 10, Appl
3	2439	83.0	1693	US-09-560-385A-4	Sequence 4, Appl
4	2439	83.0	1693	US-09-560-385A-8	Sequence 8, Appl
5	2439	83.0	1713	US-08-600-982-24	Sequence 24, Appl
6	2439	83.0	1713	US-09-560-385A-6	Sequence 6, Appl
7	2439	83.0	1713	US-09-538-092-1359	Sequence 1359, Ap
8	2439	83.0	1713	PCT-US94-10261A-24	Sequence 24, Appl
9	2439	83.0	1724	US-09-560-385A-2	Sequence 2, Appl
10	1310	44.6	770	US-08-445-135-2	Sequence 2, Appl
11	715	24.3	3647	US-09-949-016-10932	Sequence 10932, A
12	694	23.6	1792	US-09-561-818A-4	Sequence 4, Appl
13	694	23.6	1800	US-09-561-818A-8	Sequence 8, Appl
14	694	23.6	1816	US-09-561-818A-2	Sequence 2, Appl
15	694	23.6	1824	US-09-561-818A-6	Sequence 6, Appl
16	685	23.3	953	US-09-845-583A-4	Sequence 4, Appl
17	683	23.2	1792	US-09-561-818A-12	Sequence 12, Appl
18	683	23.2	1816	US-09-561-818A-10	Sequence 10, Appl
19	681	23.2	3635	US-09-845-583A-2	Sequence 2, Appl
20	302	10.3	3084	US-09-562-702A-12	Sequence 12, Appl
21	302	10.3	3106	US-09-562-702A-10	Sequence 10, Appl
22	297	10.1	5444	US-09-562-702A-2	Sequence 2, Appl
23	297	10.1	5444	US-09-562-702A-4	Sequence 4, Appl
24	294	10.0	1130	US-08-460-309-2	Sequence 2, Appl
25	294	10.0	1130	US-08-125-077-2	Sequence 2, Appl
26	294	10.0	3088	US-09-562-702A-8	Sequence 8, Appl
27	294	10.0	3089	US-09-562-702A-4	Sequence 4, Appl

28	294	10.0	3110	US-09-562-702A-2	Sequence 2, Appl
29	294	10.0	3110	US-09-562-702A-6	Sequence 6, Appl
30	294	10.0	3110	US-09-561-709B-7	Sequence 7, Appl
31	294	10.0	3110	US-09-917-254-86	Sequence 86, Appl
32	294	10.0	3110	US-09-949-016-5937	Sequence 5937, Ap
33	294	10.0	3111	US-08-460-309-4	Sequence 4, Appl
34	294	10.0	3111	US-08-125-077-4	Sequence 4, Appl
35	270	9.2	3075	US-08-460-309-5	Sequence 5, Appl
36	270	9.2	3075	US-08-125-077-5	Sequence 5, Appl
37	252	8.6	3070	US-09-961-403-7	Sequence 7, Appl
38	182	6.2	1384	US-09-949-016-7814	Sequence 7814, Ap
39	153	5.2	705	US-10-006-011A-3	Sequence 3, Appl
40	153	5.2	4391	US-10-006-011A-2	Sequence 2, Appl
41	144	4.9	1331	US-09-949-016-6861	Sequence 6861, Ap
42	144	4.9	1523	US-09-182-024A-2	Sequence 2, Appl
43	139	4.7	1384	US-08-826-134-2	Sequence 2, Appl
44	139	4.7	1384	US-09-949-016-6395	Sequence 6395, Ap
45	139	4.7	1525	US-09-191-647-2	Sequence 2, Appl

ALIGNMENTS

RESULT 1
US-09-560-385A-12

; Sequence 12, Application US/09560385A

; Patent No. 6703363

; GENERAL INFORMATION:

; APPLICANT: Bouland, Arlet

; TITLE OF INVENTION: Recombinant Laminin 5

; FILE REFERENCE: 99-274-C

; CURRENT APPLICATION NUMBER: US/09/560,385A

; CURRENT FILING DATE: 2000-04-28

; NUMBER OF SEQ ID NOS: 36

; SOFTWARE: Patent In Ver. 2.0

; SEQ ID NO 12

; LENGTH: 1694

; TYPE: PRT

; ORGANISM: Rattus norvegicus

; US-09-560-385A-12

QY	1	MRNGKSGVRLPNLEDLKGYTSLFLQRPDLRNGGTEDMFVYLGAKDSKDYIG	60
DB	751	MRNGKSGVRLPNLEDLKGYTSLFLQRPDLRNGGTEDMFVYLGAKDSKDYIG	810
QY	61	MAVVDQQLTCVNLGPREAEVQIDQVLTSESGEAYMDYKFORITQFALNTTKATSN	120
DB	811	MAVVDQQLTCVNLGPREAEVQIDQVLTSESGEAYMDYKFORITQFALNTTKATSN	870
QY	121	KPRAPVYDLGGSSNTLNLDPEDAVFYVGVPPFELPSRLRPPYKGCIELDLNEN	180
DB	871	KPRAPVYDLGGSSNTLNLDPEDAVFYVGVPPFELPSRLRPPYKGCIELDLNEN	930
QY	181	VLSVNFKTFNLTTEVEPCRRRKESEDKNYEGTYARIPQPNAPPNFIQTITQV	240
DB	931	VLSVNFKTFNLTTEVEPCRRRKESEDKNYEGTYARIPQPNAPPNFIQTITQV	990
QY	241	DRGLLPPAEQNDPFIISLNTEDGNLMRYKLSNPPYKGRITDINDKSHIITIGKIQ	300
DB	991	DRGLLPPAEQNDPFIISLNTEDGNLMRYKLSNPPYKGRITDINDKSHIITIGKIQ	1050
QY	301	KRMVNVNERSVRIEISIFDFTYVGGTPIAIRERFNISTPAFOGCMKRLKKTSGVRL	360
DB	1051	KRMVNVNERSVRIEISIFDFTYVGGTPIAIRERFNISTPAFOGCMKRLKKTSGVRL	1110
QY	361	NDTVGVTKKCSSEDMKLVRTASFSRGQMSFTNLDVPSDTRFOLSPFGQTFQPSGTLINQ	420
DB	1111	NDTVGVTKKCSSEDMKLVRTASFSRGQMSFTNLDVPSDTRFOLSPFGQTFQPSGTLINQ	1170

QY 421 TRTSSLLVLTLEDHGIELSTDSNIP1FKSPGTMDGLHHVSVISPTSGRLIIDQVLR 480
| | | | |
Db 1171 TRTSSLLVLTLEDHGIELSTDSNIP1FKSPGTMDGLHHVSVISPTSGRLIIDQVLR 1230
| | | | |
QY 481 RNQRLPSFSAQOSSLRLGGHFEBCISNVLVORFSQSPVLDLASKSTKDAISLGGCSLN 540
| | | | |
Db 1231 RNQRLPSFSAQOSSLRLGGHFEBCISNVLVORFSQSPVLDLASKSTKDAISLGGCSLN 1290
| | | | |
QY 541 KPPFLMLFKSPKRFNKGRIFFNVNQL 565
| | | | |
Db 1291 KPPFLMLFKSPKRFNKGRIFFNVNQL 1315
| | | | |
RESULT 2
US-09-560-385A-10
; Sequence 10, Application US/09560385A
; Patent No. 6703363
; GENERAL INFORMATION:
; APPLICANT: Bouland, Arlet
; TITLE OF INVENTION: Recombinant Laminin 5
; FILE REFERENCE: 99-274-C
; CURRENT APPLICATION NUMBER: US/09/560,385A
; CURRENT FILING DATE: 2000-04-28
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 10
; LENGTH: 1725
; TYPE: PRT
; ORGANISM: Rattus norvegicus
US-09-560-385A-10

Query Match 100.0%; Score 2940; DB 4; Length 1725;
Best Local Similarity 100.0%; Pred. No. 8.3e-285;
Matches 565; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRPNKSGVEVRLPNDLEDKGYTSLSLFQRPDLRENGTEDMFVMTLGNKDAKDYIG 60
| | | | |
Db 782 MRPNKSGVEVRLPNDLEDKGYTSLSLFQRPDLRENGTEDMFVMTLGNKDAKDYIG 841
| | | | |
QY 61 MAVVDGOLTCVYNLGDREAEVQIDQVLTSEBSQEAAMDVKFORIYQPAKLNTYKATSN 120
| | | | |
Db 842 MAVVDGOLTCVYNLGDREAEVQIDQVLTSEBSQEAAMDVKFORIYQPAKLNTYKATSN 901
| | | | |
QY 121 KPRAPAVYDLGGSSNTLNLDPEDAVFYVGYPPDFELPSRLRPPYKGCIELDLNEN 180
| | | | |
Db 902 KPRAPAVYDLGGSSNTLNLDPEDAVFYVGYPPDFELPSRLRPPYKGCIELDLNEN 961
| | | | |
QY 181 VLSLVNFKTFNLTTEVEPCRRKRESDKNYFEGTGYARIPTOQNAFPNFIQTITTV 240
| | | | |
Db 962 VLSLVNFKTFNLTTEVEPCRRKRESDKNYFEGTGYARIPTOQNAFPNFIQTITTV 1021
| | | | |
QY 241 DRGLLFFAENQDNFISLNIEDGNLMRYKLNSEPPKEKGRDITINDGKHSILITIGKQ 300
| | | | |
Db 1022 DRGLLFFAENQDNFISLNIEDGNLMRYKLNSEPPKEKGRDITINDGKHSILITIGKQ 1081
| | | | |
QY 301 KRWMINVNERSVIRIEGIFDPSTYYLGGIPAIARERFNISTPAFQGCNKLKKTSGVRL 360
| | | | |
Db 1082 KRWMINVNERSVIRIEGIFDPSTYYLGGIPAIARERFNISTPAFQGCNKLKKTSGVRL 1141
| | | | |
QY 361 NDTVGVTKKCSSEWMLVKTASFSRGQMSFTNLDPSTDRFQLSFGQTFQPSGTLINQ 420
| | | | |
Db 1142 NDTVGVTKKCSSEWMLVKTASFSRGQMSFTNLDPSTDRFQLSFGQTFQPSGTLINQ 1201
| | | | |
QY 421 TRTSSLLVLTLEDHGIELSTDSNIP1FKSPGTMDGLHHVSVISPTSGRLIIDQVLR 480
| | | | |
Db 1202 TRTSSLLVLTLEDHGIELSTDSNIP1FKSPGTMDGLHHVSVISPTSGRLIIDQVLR 1261
| | | | |
QY 481 RNQRLPSFSAQOSSLRLGGHFEBCISNVLVORFSQSPVLDLASKSTKDAISLGGCSLN 540
| | | | |
Db 1262 RNQRLPSFSAQOSSLRLGGHFEBCISNVLVORFSQSPVLDLASKSTKDAISLGGCSLN 1321
| | | | |
QY 541 KPPFLMLFKSPKRFNKGRIFFNVNQL 565
| | | | |

Db 1322 KPPFLMLFKSPKRFNKGRIFFNVNQL 1346
| | | | |
RESULT 3
US-09-560-385A-4
; Sequence 4, Application US/09560385A
; Patent No. 6703363
; GENERAL INFORMATION:
; APPLICANT: Bouland, Arlet
; TITLE OF INVENTION: Recombinant Laminin 5
; FILE REFERENCE: 99-274-C
; CURRENT APPLICATION NUMBER: US/09/560,385A
; CURRENT FILING DATE: 2000-04-28
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 4
; LENGTH: 1693
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-560-385A-4

Query Match 83.0%; Score 2439; DB 4; Length 1693;
Best Local Similarity 81.9%; Pred. No. 1.4e-234;
Matches 463; Conservative 47; Mismatches 35; Indels 0; Gaps 0;

QY 1 MRPNKSGVEVRLPNDLEDKGYTSLSLFQRPDLRENGTEDMFVMTLGNKDAKDYIG 60
| | | | |
Db 751 MRPNKSGVEVRLPNDLEDKGYTSLSLFQRPDLRENGTEDMFVMTLGNKDAKDYIG 810
| | | | |
QY 61 MAVVDGOLTCVYNLGDREAEVQIDQVLTSEBSQEAAMDVKFORIYQPAKLNTYKATSN 120
| | | | |
Db 811 MAVVDGOLTCVYNLGDREAEVQIDQVLTSEBSQEAAMDVKFORIYQPAKLNTYKATSN 870
| | | | |
QY 121 KPRAPAVYDLGGSSNTLNLDPEDAVFYVGYPPDFELPSRLRPPYKGCIELDLNEN 180
| | | | |
Db 871 KPRAPAVYDLGGSSNTLNLDPEDAVFYVGYPPDFELPSRLRPPYKGCIELDLNEN 930
| | | | |
QY 181 VLSLVNFKTFNLTTEVEPCRRKRESDKNYFEGTGYARIPTOQNAFPNFIQTITTV 240
| | | | |
Db 931 VLSLVNFKTFNLTTEVEPCRRKRESDKNYFEGTGYARIPTOQNAFPNFIQTITTV 990
| | | | |
QY 241 DRGLLFFAENQDNFISLNIEDGNLMRYKLNSEPPKEKGRDITINDGKHSILITIGKQ 300
| | | | |
Db 991 DRGLLFFAENQDNFISLNIEDGNLMRYKLNSEPPKEKGRDITINDGKHSILITIGKQ 1050
| | | | |
QY 301 KRWMINVNERSVIRIEGIFDPSTYYLGGIPAIARERFNISTPAFQGCNKLKKTSGVRL 360
| | | | |
Db 1051 KRWMINVNERSVIRIEGIFDPSTYYLGGIPAIARERFNISTPAFQGCNKLKKTSGVRL 1110
| | | | |
QY 361 NDTVGVTKKCSSEWMLVKTASFSRGQMSFTNLDPSTDRFQLSFGQTFQPSGTLINQ 420
| | | | |
Db 1111 NDTVGVTKKCSSEWMLVKTASFSRGQMSFTNLDPSTDRFQLSFGQTFQPSGTLINQ 1170
| | | | |
QY 421 TRTSSLLVLTLEDHGIELSTDSNIP1FKSPGTMDGLHHVSVISPTSGRLIIDQVLR 480
| | | | |
Db 1171 TRTSSLLVLTLEDHGIELSTDSNIP1FKSPGTMDGLHHVSVISPTSGRLIIDQVLR 1230
| | | | |
QY 481 RNQRLPSFSAQOSSLRLGGHFEBCISNVLVORFSQSPVLDLASKSTKDAISLGGCSLN 540
| | | | |
Db 1231 RNQRLPSFSAQOSSLRLGGHFEBCISNVLVORFSQSPVLDLASKSTKDAISLGGCSLN 1290
| | | | |
QY 541 KPPFLMLFKSPKRFNKGRIFFNVNQL 565
| | | | |
Db 1291 KPPFLMLFKSPKRFNKGRIFFNVNQL 1315
| | | | |
RESULT 4
US-09-560-385A-8
; Sequence 8, Application US/09560385A
; Patent No. 6703363
; GENERAL INFORMATION:
; APPLICANT: Bouland, Arlet
; TITLE OF INVENTION: Recombinant Laminin 5

FILE REFERENCE: 99-274-C
CURRENT APPLICATION NUMBER: US/09/560,385A
CURRENT FILING DATE: 2000-04-28
NUMBER OF SEQ ID NOS: 36
SOFTWARE: Patent In Ver. 2.0
SEQ ID NO 8
LENGTH: 1693
TYPE: PRT
ORGANISM: Homo sapiens
US-09-560-385A-8

Query Match 83.0%; Score 2439; DB 4; Length 1693;
Best Local Similarity 81.9%; Pred. No. 1.4e-234;
Matches 463; Conservative 47; Mismatches 55; Indels 0; Gaps 0;

1 MRNFGSGVRLPNLEDKGTSLSLFLQRPDLRENGTDMFWYLGAKDASDYIG 60
751 MRNFGSGVRLPNLEDKGTSLSLFLQRPDLRENGTDMFWYLGAKDASDYIG 810

61 MAVVDQQLTCVYMLGDRBAEVDQVLTSESEQAAMDVKFQRIYQFALNTTKATSN 120
811 MAVVDQQLTCVYMLGDRBAEVDQVLTSESEQAAMDVKFQRIYQFALNTTKATSN 870

121 KKPAPAVYDLEGGSSNTLNLADPEDAVFYGGYPPDFELPSRLRFPYKGCIELDLNEN 180
871 KKPAPAVYDLEGGSSNTLNLADPEDAVFYGGYPPDFELPSRLRFPYKGCIELDLNEN 930

181 VLSLYNFKTFTNLTTEVEBCRRRKEESDNVFEGETGVARIPTQPNAPFPNFLOTIQTIV 240
931 VLSLYNFKTFTNLTTEVEBCRRRKEESDNVFEGETGVARIPTQPNAPFPNFLOTIQTIV 990

241 DRGLLFAENQDNFISLNTEDGMLNRYKLNSEPPKEGIRDTINDGKHSILITGKQ 300
991 DRGLLFAENQDNFISLNTEDGMLNRYKLNSEPPKEGIRDTINDGKHSILITGKQ 1050

301 KRWMINNERSVRIEGEIPDFTYYLGGIPAIIRERNISTPAFQCGMKLTKTSGVRL 360
1051 KRWMINNERSVRIEGEIPDFTYYLGGIPAIIRERNISTPAFQCGMKLTKTSGVRL 1110

361 NDTVGYTKKSEDMKLVRTASFSRGQMSFTNLDVSTDRFOLSGFGQTQPSGTLTLMQ 420
1111 NDTVGYTKKSEDMKLVRTASFSRGQMSFTNLDVSTDRFOLSGFGQTQPSGTLTLMQ 1170

421 TRTSSLLVTEDEGHIESTDSNIPFKSPGTMDGLHHVSYISDTSGLRLIDQVLR 480
1171 TRTSSLLVTEDEGHIESTDSNIPFKSPGTMDGLHHVSYISDTSGLRLIDQVLR 1230

481 RNQRLPSFNAOQSLRIGGHPFGCISNVLVORPSQPEVLDLASKSTKQDASLGCCSLN 540
1231 RNQRLPSFNAOQSLRIGGHPFGCISNVLVORPSQPEVLDLASKSTKQDASLGCCSLN 1290

541 KPPFLMLFKSPKRFNKGRIFNVNQL 565
1291 KPPFLMLFKSPKRFNKGRIFNVNQL 1315

RESULT 5
US-08-600-982-24
Sequence 24, Application US/08600982
Patent No. 6120991
GENERAL INFORMATION:
APPLICANT: Carter, William G.
APPLICANT: Gili, Susana A.
APPLICANT: Ryan, Maureen C.
TITLE OF INVENTION: Epiligrin, an Epithelial Ligand for
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
ADDRESSEE: Christensen, O'Connor, Johnson, and Kindness
STREET: 1420 Fifth Avenue
CITY: Seattle
STATE: WA
COUNTRY: USA

ZIP: 98101-8100
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/600,982
FILING DATE: 02-SEP-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Shelton, Dennis K.
REGISTRATION NUMBER: 26,997
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 682-8100
TELEFAX: (206) 224-0779
INFORMATION FOR SEQ ID NO: 24:
SEQUENCE CHARACTERISTICS:
LENGTH: 1713 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULAR TYPE: protein
DESCRIPTION: E170 protein as translated from sequence
of FIGURES 15A-15F, and as shown also in FIGURES
DESCRIPTION: 19A-19R
US-08-600-982-24

Query Match 83.0%; Score 2439; DB 3; Length 1713;
Best Local Similarity 81.9%; Pred. No. 1.4e-234;
Matches 463; Conservative 47; Mismatches 55; Indels 0; Gaps 0;

1 MRNFGSGVRLPNLEDKGTSLSLFLQRPDLRENGTDMFWYLGAKDASDYIG 60
771 MRNFGSGVRLPNLEDKGTSLSLFLQRPDLRENGTDMFWYLGAKDASDYIG 830

61 MAVVDQQLTCVYMLGDRBAEVDQVLTSESEQAAMDVKFQRIYQFALNTTKATSN 120
831 MAVVDQQLTCVYMLGDRBAEVDQVLTSESEQAAMDVKFQRIYQFALNTTKATSN 890

121 KKPAPAVYDLEGGSSNTLNLADPEDAVFYGGYPPDFELPSRLRFPYKGCIELDLNEN 180
891 KKPAPAVYDLEGGSSNTLNLADPEDAVFYGGYPPDFELPSRLRFPYKGCIELDLNEN 950

181 VLSLYNFKTFTNLTTEVEBCRRRKEESDNVFEGETGVARIPTQPNAPFPNFLOTIQTIV 240
951 VLSLYNFKTFTNLTTEVEBCRRRKEESDNVFEGETGVARIPTQPNAPFPNFLOTIQTIV 1010

241 DRGLLFAENQDNFISLNTEDGMLNRYKLNSEPPKEGIRDTINDGKHSILITGKQ 300
1011 DRGLLFAENQDNFISLNTEDGMLNRYKLNSEPPKEGIRDTINDGKHSILITGKQ 1070

301 KRWMINNERSVRIEGEIPDFTYYLGGIPAIIRERNISTPAFQCGMKLTKTSGVRL 360
1071 KRWMINNERSVRIEGEIPDFTYYLGGIPAIIRERNISTPAFQCGMKLTKTSGVRL 1130

361 NDTVGYTKKSEDMKLVRTASFSRGQMSFTNLDVSTDRFOLSGFGQTQPSGTLTLMQ 420
1131 NDTVGYTKKSEDMKLVRTASFSRGQMSFTNLDVSTDRFOLSGFGQTQPSGTLTLMQ 1190

421 TRTSSLLVTEDEGHIESTDSNIPFKSPGTMDGLHHVSYISDTSGLRLIDQVLR 480
1191 TRTSSLLVTEDEGHIESTDSNIPFKSPGTMDGLHHVSYISDTSGLRLIDQVLR 1250

481 RNQRLPSFNAOQSLRIGGHPFGCISNVLVORPSQPEVLDLASKSTKQDASLGCCSLN 540
1251 RNQRLPSFNAOQSLRIGGHPFGCISNVLVORPSQPEVLDLASKSTKQDASLGCCSLN 1310

541 KPPFLMLFKSPKRFNKGRIFNVNQL 565
1311 KPPFLMLFKSPKRFNKGRIFNVNQL 1335

RESULT 6

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US-09-560-385A-6
; Sequence 6, Application US/09560385A
; Patent No. 6703363
; GENERAL INFORMATION:
; APPLICANT: Bontand, Ariel
; TITLE OF INVENTION: Recombinant Laminin 5
; FILE REFERENCE: 99-274-C
; CURRENT APPLICATION NUMBER: US/09/560,385A
; NUMBER OF SEQ ID NOS: 2000-04-28
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 6
; LENGTH: 1713
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-560-385A-6

Query Match      83.0%; Score 2439; DB 4; Length 1713;
Best Local Similarity 81.9%; Pred. No. 1.4e-234;
Matches 463; Conservative 47; Mismatches 55; Indels 0; Gaps 0;

QY      1 MRFNKSGVYVRLPNLDLBDLKGYSLSFLQRPDLRENGSTEDMFVMTLGNKDAKDYIG 60
DB      771 MRFNKSGVYVRLPNLDLBDLKGYSLSFLQRPDRNENGTENMFVMTLGNKDAKRDYIG 830
QY      61 MAVVDGQLTCVYNLDGREAEVQIDVLTSESSQEAAMDVRVYQRIYQPAKNTYTKATSN 120
DB      831 MAVVDGQLTCVYNLDGREAEVQIDVLTSESSQEAAMDVRVYQRIYQPAKNTYTKATSS 890
QY      121 KKPAPAVYDLEGSSNTLNLDPEDAVFYGGYPPDFELBRLRPPYKGCIELDLNLN 180
DB      891 KKPAPAVYDMDRNSNTLNLDPENVVYVGGYPPDFELBRLRPPYKGCIELDLNLN 950
QY      181 VLSLNFKTFYNTLNTVEVPCRRKESDKYFEGTGVARIPYQNAFPNFIQTIQTV 240
DB      951 VLSLNFKTFYNTLNTVEVPCRRKESDKYFEGTGVARIPYQNAFPNFIQTIQTV 1010
QY      241 DRGLLPPAENQDNFISLNIEDGNLMVRYKLNSEPPKKGIRDTINDGKHSILITIGKQ 300
DB      1011 DRGLLPPAENGDRFISLNIEDGKLMVRYKLNSELPKRGVGDALNNGRHSIQIKIGKQ 1070
QY      301 KKMWINVAKRSVRIEGEIPDEFTYLLGGIPLAIRERNISTPAFGCKMNLKKTSGVYRL 360
DB      1071 KKMWINVDQNTIIDGEVDFSTYLLGGIPLAIRERNISTPAFGCKMNLKKTSGVYRL 1130
QY      361 NDTVGYTKKCSSEDMKLVRTASFSRGGOMSFYTLDPVSTDRFQLSPFGOTFOPSGTILNHQ 420
DB      1131 NDTVGYTKKCSSEDMKLVRSASFSRGGQLSTYDLGLPETHLQASFGQTFFQPSGILNDHQ 1190
QY      421 TRTSSLLVTLDEGHIELSTRDSNIPFKSPGYMDGLLHHVSVISDTSGLRLIIDQVLR 480
DB      1191 TWTRNLQVTLDEGYIELSTDSGGPIFKSPGYMDGLLHHVSVISDNGSLRLIIDQQLR 1250
QY      481 RNRQLPSPSNAQOSRLGGGHEGICISNVLVQRFQSGSEFVLDLAKSTYKDAALGGCSLN 540
DB      1251 NSKRRLKHISRSQSLRLLGSGNFEGCISNVFQRLISPBEVLDTNSNLKRDVSLGGCSLN 1310
QY      541 KPPFLMLFKSPKPKGRIFPNVNL 565
DB      1311 KPPFLMLKSGTFRNKTKTFRINQL 1335

RESULT 7
US-09-538-092-1359
; Sequence 1359, Application US/09538092
; Patent No. 6753314
; GENERAL INFORMATION:
; APPLICANT: Glot, Loic
; APPLICANT: Mansfield, Traci A.
; TITLE OF INVENTION: Protein-Protein Complexes and Method of Using Same
; FILE REFERENCE: 15966-542
; CURRENT APPLICATION NUMBER: US/09/538,092
; CURRENT FILING DATE: 2000-03-29
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; PRIOR APPLICATION NUMBER: 60/127,352
; PRIOR FILING DATE: 1999-04-01
; PRIOR APPLICATION NUMBER: 60/178,965
; PRIOR FILING DATE: 2000-02-01
; NUMBER OF SEQ ID NOS: 1387
; SOFTWARE: CurafastSeqFormatter Version 0.9
; SEQ ID NO 1359
; LENGTH: 1713
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (0) ... (0)
; OTHER INFORMATION: Polypeptide Accession Number Q16787
US-09-538-092-1359

Query Match      83.0%; Score 2439; DB 4; Length 1713;
Best Local Similarity 81.9%; Pred. No. 1.4e-234;
Matches 463; Conservative 47; Mismatches 55; Indels 0; Gaps 0;

QY      1 MRFNKSGVYVRLPNLDLBDLKGYSLSFLQRPDLRENGSTEDMFVMTLGNKDAKDYIG 60
DB      771 MRFNKSGVYVRLPNLDLBDLKGYSLSFLQRPDRNENGTENMFVMTLGNKDAKRDYIG 830
QY      61 MAVVDGQLTCVYNLDGREAEVQIDVLTSESSQEAAMDVRVYQRIYQPAKNTYTKATSN 120
DB      831 MAVVDGQLTCVYNLDGREAEVQIDVLTSESSQEAAMDVRVYQRIYQPAKNTYTKATSS 890
QY      121 KKPAPAVYDLEGSSNTLNLDPEDAVFYGGYPPDFELBRLRPPYKGCIELDLNLN 180
DB      891 KKPAPAVYDMDRNSNTLNLDPENVVYVGGYPPDFELBRLRPPYKGCIELDLNLN 950
QY      181 VLSLNFKTFYNTLNTVEVPCRRKESDKYFEGTGVARIPYQNAFPNFIQTIQTV 240
DB      951 VLSLNFKTFYNTLNTVEVPCRRKESDKYFEGTGVARIPYQNAFPNFIQTIQTV 1010
QY      241 DRGLLPPAENQDNFISLNIEDGNLMVRYKLNSEPPKKGIRDTINDGKHSILITIGKQ 300
DB      1011 DRGLLPPAENGDRFISLNIEDGKLMVRYKLNSELPKRGVGDALNNGRHSIQIKIGKQ 1070
QY      301 KKMWINVAKRSVRIEGEIPDEFTYLLGGIPLAIRERNISTPAFGCKMNLKKTSGVYRL 360
DB      1071 KKMWINVDQNTIIDGEVDFSTYLLGGIPLAIRERNISTPAFGCKMNLKKTSGVYRL 1130
QY      361 NDTVGYTKKCSSEDMKLVRTASFSRGGOMSFYTLDPVSTDRFQLSPFGOTFOPSGTILNHQ 420
DB      1131 NDTVGYTKKCSSEDMKLVRSASFSRGGQLSTYDLGLPETHLQASFGQTFFQPSGILNDHQ 1190
QY      421 TRTSSLLVTLDEGHIELSTRDSNIPFKSPGYMDGLLHHVSVISDTSGLRLIIDQVLR 480
DB      1191 TWTRNLQVTLDEGYIELSTDSGGPIFKSPGYMDGLLHHVSVISDNGSLRLIIDQQLR 1250
QY      481 RNRQLPSPSNAQOSRLGGGHEGICISNVLVQRFQSGSEFVLDLAKSTYKDAALGGCSLN 540
DB      1251 NSKRRLKHISRSQSLRLLGSGNFEGCISNVFQRLISPBEVLDTNSNLKRDVSLGGCSLN 1310
QY      541 KPPFLMLFKSPKPKGRIFPNVNL 565
DB      1311 KPPFLMLKSGTFRNKTKTFRINQL 1335

RESULT 8
PCT-US94-10261A-24
; Sequence 24, Application PC/TUS9410261A
; GENERAL INFORMATION:
; APPLICANT: Carter, William G.
; APPLICANT: Gali, Susanna A.
; APPLICANT: Ryan, Maureen C.
; TITLE OF INVENTION: Integrin, an Epithelial Ligand for
; TITLE OF INVENTION: Integrins
; NUMBER OF SEQUENCES: 30
; CORRESPONDENCE ADDRESS:
; ADDRESSER: Christensen, O'Connor, Johnson, and Kindness
```

STREET: 1420 Fifth Avenue
 CITY: Seattle
 STATE: WA
 COUNTRY: USA
 ZIP: 98101-8100
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: PCT/US94/10261A
 FILING DATE: 02-SEP-1994
 CLASSIFICATION:
 ATTORNEY/AGENT INFORMATION:
 NAME: Shelton, Dennis K.
 REGISTRATION NUMBER: 26,997
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (206) 682-8100
 TELEFAX: (206) 224-0779
 INFORMATION FOR SEQ ID NO: 24:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 1713 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 DESCRIPTION: E170 protein as translated from sequence of
 DESCRIPTION: FIGURES 15A-15F, and as shown also in FIGURES 19A-19R
 PCT-US94-10261A-24

Query Match 83.0%; Score 2439; DB 5; Length 1713;
 Best Local Similarity 81.9%; Pred. No. 1.4e-234;

Matches 463; Conservative 47; Mismatches 55; Indels 0; Gaps 0;

1 MRFGKSGVEVRLPNDLEDKGYTSLFLQRPDLRNGGTEDMFVYTLGNKQASRDYIG 60
 771 MRFGKSGVEVRLPNDLEDKGYTSLFLQRPDLRNGGTEDMFVYTLGNKQASRDYIG 830
 61 MAVVDGQLTCVYNIAGREAEVQIDQVLTSESGQEAAMDVKFORIYQPAKANTYKATSN 120
 831 MAVVDGQLTCVYNIAGREAEVQIDQVLTSESGQEAAMDVKFORIYQPAKANTYKATSN 890
 121 KPRAPAVYDIEGGSSNTLNLDPEDAVFYGYGYPDPFELPSRLRFPYKGCIEILDNEN 180
 891 KPRAPAVYDIEGGSSNTLNLDPEDAVFYGYGYPDPFELPSRLRFPYKGCIEILDNEN 950
 181 VLSLYNFKTFNLTTEVEPCRRRKEESDKNYFEGTGYARIPTQPNAPFNFIQTQITV 240
 951 VLSLYNFKTFNLTTEVEPCRRRKEESDKNYFEGTGYARIPTQPNAPFNFIQTQITV 1010
 241 DRGLLFFAENQDNFISLNIEDGNLMVRYKLNSEPPKEKGIKRTINDGKHSILITIGKQ 300
 1011 DRGLLFFAENQDNFISLNIEDGNLMVRYKLNSEPPKEKGIKRTINDGKHSILITIGKQ 1070
 301 KRWMINNERSVRIEGLIPDSFTYLLGIPAIIRERNISTPAPQGMKMLKKTSGVRL 360
 1071 KRWMINNERSVRIEGLIPDSFTYLLGIPAIIRERNISTPAPQGMKMLKKTSGVRL 1130
 361 NDTVGVTKKCSSEDMKLVRSASFSGQMSFTNLDVSTDRFQLSFGFOTQPSGTLINHQ 420
 1131 NDTVGVTKKCSSEDMKLVRSASFSGQMSFTNLDVSTDRFQLSFGFOTQPSGTLINHQ 1190
 421 TRTSSSLVLTLEDGHIESTDSNIPFKSPGTMDGILHHVSVISDPSGLRLIDQVLR 480
 1191 TRTSSSLVLTLEDGHIESTDSNIPFKSPGTMDGILHHVSVISDPSGLRLIDQVLR 1250
 481 RNORLPFSNAQOSLRIGGHEFGCISNVLYQRFSSQSEVYLDLASKSTKQDASIGGCSLN 540
 1251 RNORLPFSNAQOSLRIGGHEFGCISNVLYQRFSSQSEVYLDLASKSTKQDASIGGCSLN 1310
 541 KPEPLMLFKSPKRNKRIFNVNQL 565
 1311 KPEPLMLFKSTRENTKTRINQL 1335

RESULT 9

US-09-560-385A-2
 ; Sequence 2, Application US/09560385A
 ; Patent No. 6703363
 ; GENERAL INFORMATION:
 ; APPLICANT: Bouland, Ariel
 ; TITLE OF INVENTION: Recombinant Laminin 5
 ; FILE REFERENCE: 99-274-C
 ; CURRENT APPLICATION NUMBER: US/09/560,385A
 ; NUMBER OF SEQ ID NOS: 36
 ; SOFTWARE: Patentin Ver. 2.0
 ; SEQ ID NO 2
 ; LENGTH: 1724
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-09-560-385A-2

Query Match 83.0%; Score 2439; DB 4; Length 1724;
 Best Local Similarity 81.9%; Pred. No. 1.4e-234;

Matches 463; Conservative 47; Mismatches 55; Indels 0; Gaps 0;

1 MRFGKSGVEVRLPNDLEDKGYTSLFLQRPDLRNGGTEDMFVYTLGNKQASRDYIG 60
 782 MRFGKSGVEVRLPNDLEDKGYTSLFLQRPDLRNGGTEDMFVYTLGNKQASRDYIG 841
 61 MAVVDGQLTCVYNIAGREAEVQIDQVLTSESGQEAAMDVKFORIYQPAKANTYKATSN 120
 842 MAVVDGQLTCVYNIAGREAEVQIDQVLTSESGQEAAMDVKFORIYQPAKANTYKATSN 901
 121 KPRAPAVYDIEGGSSNTLNLDPEDAVFYGYGYPDPFELPSRLRFPYKGCIEILDNEN 180
 902 KPRAPAVYDIEGGSSNTLNLDPEDAVFYGYGYPDPFELPSRLRFPYKGCIEILDNEN 961
 181 VLSLYNFKTFNLTTEVEPCRRRKEESDKNYFEGTGYARIPTQPNAPFNFIQTQITV 240
 962 VLSLYNFKTFNLTTEVEPCRRRKEESDKNYFEGTGYARIPTQPNAPFNFIQTQITV 1021
 241 DRGLLFFAENQDNFISLNIEDGNLMVRYKLNSEPPKEKGIKRTINDGKHSILITIGKQ 300
 1022 DRGLLFFAENQDNFISLNIEDGNLMVRYKLNSEPPKEKGIKRTINDGKHSILITIGKQ 1081
 301 KRWMINNERSVRIEGLIPDSFTYLLGIPAIIRERNISTPAPQGMKMLKKTSGVRL 360
 1082 KRWMINNERSVRIEGLIPDSFTYLLGIPAIIRERNISTPAPQGMKMLKKTSGVRL 1141
 361 NDTVGVTKKCSSEDMKLVRSASFSGQMSFTNLDVSTDRFQLSFGFOTQPSGTLINHQ 420
 1142 NDTVGVTKKCSSEDMKLVRSASFSGQMSFTNLDVSTDRFQLSFGFOTQPSGTLINHQ 1201
 421 TRTSSSLVLTLEDGHIESTDSNIPFKSPGTMDGILHHVSVISDPSGLRLIDQVLR 480
 1202 TRTSSSLVLTLEDGHIESTDSNIPFKSPGTMDGILHHVSVISDPSGLRLIDQVLR 1261
 481 RNORLPFSNAQOSLRIGGHEFGCISNVLYQRFSSQSEVYLDLASKSTKQDASIGGCSLN 540
 1262 RNORLPFSNAQOSLRIGGHEFGCISNVLYQRFSSQSEVYLDLASKSTKQDASIGGCSLN 1321
 541 KPEPLMLFKSPKRNKRIFNVNQL 565
 1322 KPEPLMLFKSTRENTKTRINQL 1346

RESULT 10

US-08-445-135-2
 ; Sequence 2, Application US/08445135
 ; Patent No. 5638789
 ; GENERAL INFORMATION:
 ; APPLICANT: Quaranta, Vito
 ; APPLICANT: Hormia, Marketta
 ; TITLE OF INVENTION: Promotion of Epithelial Cell Adhesion


```
Query Match      23.6%; Score 694; DB 4; Length 1816;
Best Local Similarity 32.1%; Pred. No. 1.4e-59;
Matches 193; Conservative 101; Mismatches 246; Indels 62; Gaps 20;

QY 1 MRNGSGVRLNPNLEDLKGYTSLPLP-----QPDLENGGTDMFMVTLGNDAK 56
DB 829 MAFDQSAVEVSRSTMDLKAFTSLTYMKPVRKPELTETADQFLIYLSKNKK 885
QY 57 DYIGMAVVDGQLTCVYNLGDREAEVQIDQVLTESQAEAVMDRVKQRIYQAKLNTYKE 116
DB 886 EYMGALIKNDNLVYVYNLGTQVEIPLDS--KPVSWPAPVSYIVKIERVGRKGVFLTP 943
QY 117 ATSNKPKAPAVVDLEGGSSNTLLNPDPAVYVGYPPDFELPSRLRPPYKCIETLD 176
DB 944 SLSSTAEKFKIKGFEFGSDSLDLPEDTFFYVGVGSNFKLPTSLNPGFVGLIELAT 1003
QY 177 LNEENVLSYNEKTFENLTTEVEPCRRK-----ESDKNYFEGTGARIPQPN----A 227
DB 1004 LNNDVISLYNFKHIYNNMDPSTSVPCARDKLAFTQSRASYPFDGSGYAVVRDIPRGRKG 1063
QY 228 PPFNFITQITVDRGLLFFAENQDNFISLNEGNLWRY-----KLNSEPPKEGI 280
DB 1064 QVTRPDIEVRTPADNGLILLMVGSMFRLERNGYLHVFPYDFGSSGRVHLEDTLKA- 1122
QY 281 RDTINDGKDSILITIGKLOKRMWVNNERSVRI---EGEIFDFSTYYIAGIP-----I 331
DB 1123 --QINDAKYHEISI-IYHNDKMLVDRRHVKSMDNEKKKIPFTDIYIGGAPPEILQSR 1179
QY 332 AIRERFNISTPAFGCMKNL---KTSGVRLNDTVGYTKCSDEWKLVRTASFSRGQM 388
DB 1180 ALRAHLPLDI-NFRGCMKGFOQKDFNLQETETLGVGCGCEDSLISRAYFN--GQS 1236
QY 389 SFTNLD-VPSTDRFQLSFGFQFPQSGTLLNHQRTSSLLVTLDEGHIELSTRDSNIPF 447
DB 1237 FLASIOKISFPQFEGGFNRTIQPNGLLFYVASSGDVFSISLNDGTVMQK--GIRYQ 1294
QY 448 KSPGTVMGDLAHVVISDTSGLR--LLID-DQVLRNRQRLPSFSNAQSLR---LGG-- 499
DB 1295 SVDKQYNDGLSHF--VISSVSPTRYELIVDKSRVGSKNPTKGIQGTQASEKKFVFGSP 1352
QY 500 -----GHFEGCISNVLVORFQSPEVLDLASKSTKQDASLGCSLAKPPFLMFKSPRF 554
DB 1353 ISAOYANFTGCISNAYFTRVDVDEVEDFORYTEKVTSLYECPIESSPLFLHKKGNL 1412
QY 555 NK 556
DB 1413 SK 1414

RESULT 15
US-09-561-818A-6
; Sequence 6, Application US/09561818A
; Patent No. 6638907
; GENERAL INFORMATION:
; APPLICANT: Korteemaa, Jarko
; APPLICANT: Tiysvaabon, Karl
; TITLE OF INVENTION: Laminin 8 and Methods For Its Use
; FILE REFERENCES: 99,274-D
; CURRENT APPLICATION NUMBER: US/09/561,818A
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 6
; LENGTH: 1824
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-561-818A-6

Query Match      23.6%; Score 694; DB 4; Length 1824;
Best Local Similarity 32.1%; Pred. No. 1.4e-59;
Matches 193; Conservative 101; Mismatches 246; Indels 62; Gaps 20;

QY 1 MRNGSGVRLNPNLEDLKGYTSLPLP-----QPDLENGGTDMFMVTLGNDAK 56
```

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DB 829 MAFDQSAVEVSRSTMDLKAFTSLTYMKPVRKPELTETADQFLIYLSKNKK 885
QY 57 DYIGMAVVDGQLTCVYNLGDREAEVQIDQVLTESQAEAVMDRVKQRIYQAKLNTYKE 116
DB 886 EYMGALIKNDNLVYVYNLGTQVEIPLDS--KPVSWPAPVSYIVKIERVGRKGVFLTP 943
QY 117 ATSNKPKAPAVVDLEGGSSNTLLNPDPAVYVGYPPDFELPSRLRPPYKCIETLD 176
DB 944 SLSSTAEKFKIKGFEFGSDSLDLPEDTFFYVGVGSNFKLPTSLNPGFVGLIELAT 1003
QY 177 LNEENVLSYNEKTFENLTTEVEPCRRK-----ESDKNYFEGTGARIPQPN----A 227
DB 1004 LNNDVISLYNFKHIYNNMDPSTSVPCARDKLAFTQSRASYPFDGSGYAVVRDIPRGRKG 1063
QY 228 PPFNFITQITVDRGLLFFAENQDNFISLNEGNLWRY-----KLNSEPPKEGI 280
DB 1064 QVTRPDIEVRTPADNGLILLMVGSMFRLERNGYLHVFPYDFGSSGRVHLEDTLKA- 1122
QY 281 RDTINDGKDSILITIGKLOKRMWVNNERSVRI---EGEIFDFSTYYIAGIP-----I 331
DB 1123 --QINDAKYHEISI-IYHNDKMLVDRRHVKSMDNEKKKIPFTDIYIGGAPPEILQSR 1179
QY 332 AIRERFNISTPAFGCMKNL---KTSGVRLNDTVGYTKCSDEWKLVRTASFSRGQM 388
DB 1180 ALRAHLPLDI-NFRGCMKGFOQKDFNLQETETLGVGCGCEDSLISRAYFN--GQS 1236
QY 389 SFTNLD-VPSTDRFQLSFGFQFPQSGTLLNHQRTSSLLVTLDEGHIELSTRDSNIPF 447
DB 1237 FLASIOKISFPQFEGGFNRTIQPNGLLFYVASSGDVFSISLNDGTVMQK--GIRYQ 1294
QY 448 KSPGTVMGDLAHVVISDTSGLR--LLID-DQVLRNRQRLPSFSNAQSLR---LGG-- 499
DB 1295 SVDKQYNDGLSHF--VISSVSPTRYELIVDKSRVGSKNPTKGIQGTQASEKKFVFGSP 1352
QY 500 -----GHFEGCISNVLVORFQSPEVLDLASKSTKQDASLGCSLAKPPFLMFKSPRF 554
DB 1353 ISAOYANFTGCISNAYFTRVDVDEVEDFORYTEKVTSLYECPIESSPLFLHKKGNL 1412
QY 555 NK 556
DB 1413 SK 1414
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Search completed: February 22, 2005, 08:40:55
Job time : 29.3827 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: February 22, 2005, 08:05:49 / Search time 5.81686 Seconds
(without alignments)
3605.942 Million cell updates/sec

Title: US-10-817-423-6

Perfect score: 1118
Sequence: 1 MNKLKKTSGVRLNDTVGVLT.....MLFKSPKRFKRGRIFFVNLQ 218

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	850	76.0	1713	2 A55347	adhesive ligand ep
2	187	16.7	1816	1 S68960	laminin alpha-4 ch
3	186	16.6	3635	2 T10053	laminin alpha-5 ch
4	173.5	15.5	3712	2 S18253	laminin alpha-1 ch
5	144.5	12.9	3106	1 S53868	laminin alpha-2 ch
6	134.5	12.0	1751	1 M6H0M	laminin alpha-2 ch
7	115.5	10.3	3102	2 T43291	laminin alpha-1 ch
8	111.5	10.0	3084	1 M6MGA	laminin alpha-1 ch
9	107	9.6	3097	2 T00021	DN-cadherin - fru1
10	105	9.4	5147	1 IJFPTM	cadherin-related t
11	101.5	9.1	3075	2 S14458	laminin alpha-1 ch
12	99.5	8.9	3672	2 T23433	hypothetical prote
13	99.5	8.9	3704	2 T73716	probable laminin a
14	99	8.9	1158	2 E86327	protein F18014.19
15	94.5	8.5	675	1 KXBO5	plasma protein S p
16	94	8.4	1722	2 E89753	protein F11C7.4 [1
17	92.5	8.3	487	2 P00259	hypothetical prote
18	91.5	8.2	403	2 A26371	sex steroid-bindin
19	91.5	8.2	714	2 S68603	hypothetical prote
20	91.5	8.2	882	2 A39030	androgen-binding p
21	91	8.1	206	2 P84459	hypothetical prote
22	91	8.1	510	1 S56640	ferredoxin-nitrite
23	91	8.1	729	2 P86308	similar to disease
24	91	8.1	2833	2 T23064	protein T22A3.8 [1
25	91	8.1	2833	2 T23064	hypothetical prote
26	91	8.1	4351	2 T00252	MEGF1 protein - ra
27	90.5	8.1	2325	2 A61208	chondroitin sulfat
28	89.5	8.0	272	2 T30305	dnaf protein - lac
29	89.5	8.0	1381	2 T31083	paranodin - rat

30	88	7.9	1264	2 T19545	hypothetical prote
31	87.5	7.8	1283	2 T13799	neurexin IV - fru1
32	86.5	7.7	642	2 S53433	plasma protein S p
33	86.5	7.7	1531	2 T42218	slit-1 protein hom
34	85.5	7.6	935	2 A64608	exonuclease ABC c
35	84.5	7.6	776	2 T19900	hypothetical prote
36	84.5	7.6	1385	2 T14158	neurexin IV - mus
37	84	7.5	629	2 S63369	hypothetical prote
38	82.5	7.4	307	2 D90394	purine nucleosidas
39	82.5	7.4	468	2 B40228	neurexin I-beta pr
40	82.5	7.4	1530	2 I45944	neurexin I-alpha pr
41	82	7.3	428	1 E69044	diaminopimelate de
42	81.5	7.3	336	2 T27762	hypothetical prote
43	81.5	7.3	446	2 D64210	replicative DNA he
44	81.5	7.3	1365	2 A41483	glucosyltransferas
45	81.5	7.3	1507	2 A40228	neurexin I-alpha p

ALIGNMENTS

```
RESULT 1
A55347
adhesive ligand epiligrin, alpha-3 chain form A precursor - human
C/Species: Homo sapiens (man)
C/Date: 06-Feb-1995 #sequence_revision 06-Feb-1995 #text_change 09-Jul-2004
C/Accession: A55347
R/Ryan, M.C.; Tizard, R.; Vandevanter, D.R.; Carter, W.G.
J. Biol. Chem. 269, 22779-22787, 1994
A/Title: Cloning of the lam3 gene encoding the alpha3 chain of the adhesive ligand epi
A/Reference number: A55347, MIMD:94357926, PMID:8077230
A/Accession: A55347
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-1713 <RVA>
C/Superfamilies: UNIPROT:016787; GB:U34155; NID:9551596; PID:9551597
C/Keywords: alternative splicing
F/67-114/Domain: laminin-type EGF-like homology <LE2>
F/1392-1534/Domain: laminin G repeat homology <LG4>

Query Match          76.0%; Score 850; DB 2; Length 1713;
Best local similarity 76.6%; Pred. No. 1.1e-69;
Matches 167; Conservative 18; Mismatches 33; Indels 0; Gaps 0;

QY 1 MNKLKKTSGVRLNDTVGVTKKCEDWKLVRASFGGQMSFTNLDVPETRFQLSFGF 60
DB 1118 MNKLKKTSGVRLNDTVGVTKKCEDWKLVRASFGGQLSFTDGLPPTDHLQASFGF 1177
QY . 61 QTFPESGTLNMQTRTSLLVTLQDGHIELSTRDSNIPFKASGCTTMDGILLHVSVISDT 120
DB 1178 QTFPESGTLNMQTRTSLLVTLQDGHIELSTRDSNIPFKASGCTTMDGILLHVSVISDN 1237
QY 121 SGRLIIDQVLRBNRLSPFSAOQSLRLGGHFGGCSNNVYVDFSSPEVLDLASKS 180
DB 1238 SGRLIIDQVLRBNRLSPFSAOQSLRLGGHFGGCSNNVYVDFSSPEVLDLASKS 1297
QY 181 TKKDAISLGGCSLNKPPFLMLFKSPKRFKRGRIFFVNLQ 218
DB 1298 LKRDSVLGGCSLNKPPFLMLFKSPKRFKRGRIFFVNLQ 1335

RESULT 2
S68960
laminin alpha-4 chain precursor - human
N/Alternate names: laminin Ah
C/Species: Homo sapiens (man)
C/Date: 21-Aug-1998 #sequence_revision 21-Aug-1998 #text_change 09-Jul-2004
C/Accession: S68960; S65926; S49149; S40150; I53516
R/Richards, A.; Al-Imara, L.; Pope, F.M.
Eur. J. Biochem. 238, 813-821, 1996
A/Title: The complete cDNA sequence of laminin alpha-4 and its relationship to the othe
A/Reference number: S68960, MIMD:96300249, PMID:8706685
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A/Accession: S66960
 A/Molecule type: mRNA
 A/Residues: 1-1816 <RIC>
 A/Cross-references: UNIPROT:Q16363; UNIPROT:Q14731; EMBL:X91171; NID:G1212962; PIDN:CAAG
 A/Experimental source: tissue type heart
 R:/Livanainen, A.; Sainio, K.; Sariola, H.; Tryggvason, K.
 FEBS Lett. 365, 183-188, 1995
 A/Title: Primary structure and expression of a novel human laminin alpha-4 chain.
 A/Reference number: 153516; MUID:95300971; PMID:7781776
 A/Accession: S65926
 A/Molecule type: mRNA
 A/Residues: 1-142, 'P', 144-177, 'P', 179-490, 'Y', 492-1056, 'P', 1058-1816 <ITV>
 A/Cross-references: EMBL:S78569; NID:G1042081; PIDN:AA34635.1; PID:G1042082
 R:/Richard, A.J.; Al-Imara, L.; Carter, N.; Leverisha, M.; Lloyd, J.C.; Pope, F.M.
 submitted to the EMBL Data Library, December 1993
 A/Description: Localisation of the gene (LAMA4) to chromosome 6q21 and isolation of a p
 A/Reference number: S49149
 A/Accession: S49149
 A/Molecule type: mRNA
 A/Residues: 236-1816 <R12>
 A/Cross-references: EMBL:X76939; NID:G509805; PIDN:CA54258.1; PID:G509806
 R:/Richard, A.J.; Al-Imara, L.; Carter, N.; Lloyd, J.C.; Pope, F.M.
 submitted to the EMBL Data Library, February 1993
 A/Description: Isolation of a partial cDNA encoding a protein homologous to laminin A. A
 A/Reference number: S40150
 A/Accession: S40150
 A/Molecule type: mRNA
 A/Residues: 1403-1541, 'S', 1543-1816 <R13>
 A/Cross-references: EMBL:X70904; NID:G437804; PIDN:CA50261.1; PID:G437805
 C/Genetics:
 A/Gene: GDB:LAMA4; LAMA3
 A/Cross-references: GDB:203904; OMIM:600133
 A/Map position: 6q21-6q21
 C/Complex: Laminins are trimers of an alpha-type, a beta-type, and a gamma-type laminin
 C/Function: Laminins are trimers of an alpha-type, a beta-type, and a gamma-type laminin
 A/Description: interact with cells and with other basement membrane proteins to promote
 C/Superfamily: laminin alpha-4 chain; laminin G repeat homology; laminin-type EGF-like h
 C/Keywords: basement membrane; cell binding; coiled coil; extracellular matrix; glycopro
 F:/1-24/Domain: signal sequence #status predicted <SIG>
 F:/25-1816/Product: laminin alpha-4 chain #status predicted <MAT>
 F:/82-129/Domain: laminin-type EGF-like homology <LE1>
 F:/132-184/Domain: laminin-type EGF-like homology <LE2>
 F:/187-338/Domain: laminin-type EGF-like homology <LE3>
 F:/241-265/Domain: laminin-type EGF-like homology #status atypical <LE4>
 F:/717-719/Region: cell attachment (R-G-D) motif
 F:/662-1031/Domain: laminin G repeat homology <LG1>
 F:/1068-1223/Domain: laminin G repeat homology <LG2>
 F:/1252-1398/Domain: laminin G repeat homology <LG3>
 F:/1488-1636/Domain: laminin G repeat homology <LG4>
 F:/1665-1816/Domain: laminin G repeat homology <LG5>
 F:/104, 215, 308, 458, 524, 550, 571, 574, 631, 639, 735, 751, 754, 780, 803, 1086, 1086, 1281, 1359, 1411/Bindin
 F:/266, 269/Disulfide bonds: interchain #status predicted

Query Match 16.6%; Score 186; DB 2; Length 3635;
 Best Local Similarity 29.2%; Pred. No. 5.2e-08;
 Matches 59; Conservative 34; Mismatches 91; Indels 18; Gaps 6;

RESULT 3
 T10053
 laminin alpha 5 chain - mouse (fragment)
 C/Species: Mus musculus (house mouse)
 C/Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 09-Jul-2004
 C/Accession: T10053
 R:/Miner, J.H.; Lewis, R.M.; Sane, J.R.
 submitted to the EMBL Data Library, November 1997
 A/Reference number: Z16923
 A/Accession: T10053
 A/Status: preliminary; translated from GB/EMBL/DBJ
 A/Molecule type: mRNA
 A/Residues: 1-3635 <MIN>
 A/Cross-references: UNIPROT:Q61001; EMBL:U37501; NID:G2599231; PID:G2599232
 C/Genetics:
 A/Gene: LAMA5
 C/Keywords: basement membrane; cell binding; extracellular matrix
 F:/1888-1939/Domain: laminin-type EGF-like homology <LEG>
 F:/1942-1970/Domain: EGF homology <EGF>

Query Match 16.6%; Score 186; DB 2; Length 3635;
 Best Local Similarity 29.2%; Pred. No. 5.2e-08;
 Matches 59; Conservative 34; Mismatches 91; Indels 18; Gaps 6;

1 MKNLKTSGVRLNDVTGVTKKCSSEDMKLVETASFSRGOMFTNLDV-PSTDRFQLSFG 59
 Db 3015 IKALGKYVDLKRIN-TTGISFGCTADLLVGRMTFHHGFLPLPDAFPTREVYSGFG 3073
 Qy 60 FQTPQSGTLNHQRTSSLVLTLEDGHEISTDSNIPFKSPGTMDGLHVSYSID 119
 Db 3074 FRGTDDNNLLYRTSPDPSPYQVSLREGHVTLRFNQEV---ETQVFADGAPHYAFYSN 3130
 Qy 120 TSGRLTLD--QVRRNRQLPSFSNAQ-----QSLRLG3-----GHREGCISNVLVQR 166
 Db 3131 VTGVALVYDDQLQVLSHRTTPMLQLPBPBSRLLLGLPVSGTFNNFSGCISNVFQR 3190
 Qy 167 FQSGPEVLDLASKSTKCDASIG 188
 Db 3191 LRGPVRVFDLHQMGSVAVSVG 3212

RESULT 4
 S18253
 laminin alpha-1 chain precursor - fruit fly (Drosophila melanogaster)
 C/Species: Drosophila melanogaster
 C/Date: 16-Sep-1992 #sequence_revision 24-Jul-1997 #text_change 09-Jul-2004
 C/Accession: S28399; S18253
 R:/Kusche-Guliberg, M.; Garrison, K.; Mackrell, A.J.; Fessler, J.H.
 EMBO J. 11, 4519-4527, 1992
 A/Title: Laminin A chain: expression during Drosophila development and genomic sequence
 A/Reference number: S28399; MUID:93049203; PMID:1425586
 A/Accession: S28399
 A/Status: preliminary
 A/Molecule type: nucleic acid
 A/Residues: 1-3712 <KUS>
 A/Cross-references: UNIPROT:Q00174; GB:M96388; NID:G157799; PIDN:AAA28662.1; PID:G157800
 R:/Garrison, K.; Mackrell, A.J.; Fessler, J.H.
 J. Biol. Chem. 266, 22899-22904, 1991
 A/Title: Drosophila laminin A chain sequence, inter-species comparison, and domain struct
 A/Reference number: S18253; MUID:92078147; PMID:1744083
 A/Accession: S18253
 A/Molecule type: mRNA
 A/Residues: 1762-3712 <GAR>
 A/Cross-references: EMBL:M75882; NID:G157797; PIDN:AAA28661.1; PID:G157798
 C/Genetics:
 A/Gene: FlyBase:iana
 A/Cross-references: FlyBase:FBgn0002526
 C/Superfamily: laminin alpha-1 chain; laminin G repeat homology; laminin-type EGF-like h
 C/Keywords: basement membrane; cell binding; coiled coil; disulfide bond; extracellular
 F:/273-330/Domain: laminin-type EGF-like homology <LEG>
 F:/333-400/Domain: laminin-type EGF-like homology <LEG2>
 F:/541-584/Domain: laminin-type EGF-like homology <LEG1>

F/1776-2115/Domain: III <DOM3>
 F/1776-1866/Domain: laminin-type EGF-like homology #status atypical <LE1>
 F/1809-1866/Domain: laminin-type EGF-like homology <LE2>
 F/1859-1914/Domain: laminin-type EGF-like homology <LE3>
 F/1917-1967/Domain: laminin-type EGF-like homology <LE4>
 F/1970-2014/Domain: laminin-type EGF-like homology <LE5>
 F/2017-2061/Domain: laminin-type EGF-like homology <LE6>
 F/2064-2109/Domain: laminin-type EGF-like homology <LE7>
 F/2116-2697/Domain: I/II, heptad repeats <DOM2>
 F/2698-3712/Domain: G <DOM3>
 F/2698-2863/Domain: repeat G1 <RG1>
 F/2864-3048/Domain: repeat G2 <RG2>
 F/3049-3223/Domain: repeat G3 <RG3>
 F/3079-3200/Domain: laminin G repeat homology <LG3>
 F/3334-3528/Domain: repeat G4 <RG4>
 F/3529-3712/Domain: repeat G5 <RG5>
 F/1847,1850,1943,2024,2196,2215,2267,2301,2323,2482,2524,2538,2569,2699,2720,2890,2938,3

Query Match 15.5%; Score 173.5; DB 2; Length 3712;
 Best Local Similarity 27.9%; Pred. No. 7.6e-07;
 Matches 65; Conservative 43; Mismatches 66; Indels 59; Gaps 12;

3 NLKKTSGVVLNDTV---GVTKKCSBDKLVRTASPSRGQMSFTNLDVPSDTRFOLSPG 59
 NVVINGGVVDLTREYVVGGVBECSAKFTVVSVAPEHYGFLRNNN--VSDNNLHVVLH 3082

60 FQTRPSGTLT---NHQTRSSLVLTEDGHISLSTDSNIPFKSPGYMDGLH--- 112
 FKTTPGVVLPYANMD-QSSTIGLSQDGLKLNKMSGSLVLI-----DRIANDGED 3134

113 HVEVISTSG-LRLLDIDQVLRNORLPSFNAQSLRLGG----- 153
 HVTVQHTGELRLTVDDV---DNKRIGS---PQPLILSGDIFPAGLPDNTRTPPNAL 3187

154 ----HFEGCTSNLVORFOSPEVLDLASKTKKDALGCGSLNKPFLMLFK 202
 ASLAFVPGCISDVTV-----NEELINFANSAEKKNGINNC-----PPIVLAYE 3231

RESULT 5
 553868
 laminin alpha-2 chain precursor - mouse
 N/Alternate names: laminin M chain; merosin heavy chain
 C/Species: Mus musculus (house mouse)
 C/Date: 21-Aug-1998 #sequence revision 21-Aug-1998 #text change 09-Jul-2004
 C/Accession: I49077; S50829; I48655; S31576; S53868
 R/Bernier, S.M.; Utani, A.; Sugiyama, S.; Dol, T.; Polletina, C.; Yamada, Y.
 Matrix Biol. 14, 447-455, 1995
 A/Title: Cloning and expression of laminin alpha 2 chain (M-chain) in the mouse.
 A/Reference number: I49077; MUID:95316259; PMID:7795883
 A/Accession: I49077
 A/Status: preliminary; translated from GB/EMBL/DBD
 A/Molecule type: mRNA
 A/Residues: 1-3106 <RES>
 A/Cross-references: UNIPROT:Q60675; EMBL:U12147; NID:9699109; PIDN:AA652165.1; PID:96991
 R/Xu, H.; Wu, X.R.; Wewer, U.M.; Engvall, E.
 Nature Genet. 8, 297-302, 1994
 A/Title: Murine muscular dystrophy caused by a mutation in the laminin alpha-2 (lama2) g
 A/Reference number: S50829; MUID:95179178; PMID:7874173
 A/Accession: S50829
 A/Status: preliminary
 A/Molecule type: mRNA
 A/Residues: 64-281 <XNH>
 A/Cross-references: GB:S75315; NID:9833929; PIDN:AA33573.1; PID:9833930
 R/Chang, A.C.; Madeworth, S.; Colligan, J.E.
 J. Immunol. 151, 1789-1801, 1993
 A/Title: Expression of merosin in the thymus and its interaction with thymocytes.
 A/Reference number: I48655; MUID:93346725; PMID:8345183
 A/Accession: I48655
 A/Status: preliminary; translated from GB/EMBL/DBD
 A/Molecule type: mRNA
 A/Residues: 2162-2204; 'D', 2206-2213, 'EY', 2216-2279 <RES>
 A/Residues: 2162-2204; 'D', 2206-2213, 'EY', 2216-2279 <RES>
 A/Cross-references: EMBL:X69869; NID:953055; PIDN:CAA9502.1; PID:953056

C/Complex: Laminins are trimers of an alpha-type, a beta-type, and a gamma-type laminin
 C/Function:
 A/Description: Interact with cells and with other basement membrane proteins to promote
 C/Superfamily: laminin alpha-1 chain; laminin G repeat homology; laminin-type EGF-like
 C/Keywords: Basement membrane; calcium binding; coiled coil; extracellular matrix; glyco
 F/1-22/Domain: signal sequence #status predicted <SIG>
 F/23-3106/Product: laminin alpha-2 chain #status predicted <MAT>
 F/283-337/Domain: laminin-type EGF-like homology <LE01>
 F/340-407/Domain: laminin-type EGF-like homology <LE02>
 F/410-462/Domain: laminin-type EGF-like homology <LE03>
 F/465-511/Domain: laminin-type EGF-like homology <LE04>
 F/514-523/Domain: laminin-type EGF-like homology #status atypical <LE05>
 F/720-750/Domain: laminin-type EGF-like homology <LE06>
 F/753-800/Domain: laminin-type EGF-like homology <LE07>
 F/803-858/Domain: laminin-type EGF-like homology <LE08>
 F/861-911/Domain: laminin-type EGF-like homology <LE09>
 F/914-960/Domain: laminin-type EGF-like homology <LE10>
 F/963-1007/Domain: laminin-type EGF-like homology <LE11>
 F/1010-1053/Domain: laminin-type EGF-like homology <LE12>
 F/1056-1099/Domain: laminin-type EGF-like homology <LE13>
 F/1102-1121/Domain: laminin-type EGF-like homology #status atypical <LE14>
 F/1123-1159/Domain: laminin-type EGF-like homology #status atypical <LE15>
 F/1162-1171/Domain: laminin-type EGF-like homology #status atypical <LE16>
 F/1376-1413/Domain: laminin-type EGF-like homology #status atypical <LE17>
 F/1416-1462/Domain: laminin-type EGF-like homology <LE18>
 F/1465-1500/Domain: laminin-type EGF-like homology <LE19>
 F/1523-1567/Domain: laminin-type EGF-like homology <LE20>
 F/2166-2327/Domain: laminin G repeat homology <LG3>
 F/2260-2520/Domain: laminin G repeat homology <LG3>
 F/2546-2709/Domain: laminin G repeat homology <LG4>
 F/2785-2933/Domain: laminin G repeat homology <LG4>
 F/2960-3106/Domain: laminin G repeat homology <LG5>

Query Match 12.9%; Score 144.5; DB 1; Length 3106;
 Best Local Similarity 25.4%; Pred. No. 0.00028;
 Matches 61; Conservative 34; Mismatches 86; Indels 59; Gaps 11;

3 NLKKTSG-----VRLNDTVGVTKKCSBDKLVRTASPSRG--QMSFTNLD 47
 NVKRYSGCLKLDIEISRPYNILSSPDYGVTKGS--LEVNVTVSPPKPEVLAVID 2541

48 VPESTRFOLSGFQTRPSGTLT-----NHQTRSSLVLTEDG---HIEL 90
 ETLNSTNBSGIIILGSGGITPRRRKQTYAVAFILKNGLEVLSS 2542

91 STED-SNIPFKSPGYMDGLHRSVISTSGRLRLIDQVLRNORLPSFNAQ-QSL 148
 GRTMKRIVAKPEPNLFHDSRESHVY-ERTGIFVQIDEDRRHQLNTEQPIEVKCL 2656

149 RLGG-----HFEGCTSNLVORFOSPEVLDLASKTKKDALGCGSLNKP 195
 FVGGAPPEPSPFLRNIPAFQGCVMVLVINSIP---MDPAPIAFKNADIRCTYQKP 2711

RESULT 6
 578704
 laminin alpha-2 chain - human (fragment)
 N/Alternate names: laminin M chain; merosin heavy chain
 C/Species: Homo sapiens (man)
 C/Date: 30-Sep-1991 #sequence revision 21-Aug-1998 #text change 09-Jul-2004
 C/Accession: PX0082; A35899; A38970; S14461
 R/Hori, H.; Kanamori, T.; Mizuta, T.; Yamaguchi, N.; Liu, Y.; Nagai, Y.
 J. Biochem. 116, 1212-1219, 1994
 A/Title: Human laminin M chain: Epitope analysis of its monoclonal antibodies by immuno-
 A/Reference number: PX0082; MUID:95221315; PMID:7535762
 A/Accession: PX0082
 A/Molecule type: mRNA
 A/Residues: 11751 <HOR>
 A/Cross-references: UNIPROT:P24043
 A/Experimental source: Placenta
 R/Enrig, K.; Lelivo, I.; Argaves, W.S.; Ruoslahti, E.; Engvall, E.
 Proc. Natl. Acad. Sci. U.S.A. 87, 3264-3268, 1990
 A/Title: Merosin, a tissue-specific basement membrane membrane protein, is a laminin-like protein.

A:Molecule type: protein
 A:Residues: 630-642, 'D', 644; 2690-2704 <F0J>
 R:Deuzmann, R.; Huber, J.; Schmetz, K.A.; Oberbaumer, I.; Hartl, L.
 Eur. J. Biochem. 177, 35-45, 1988
 A>Title: Structural study of long arm fragments of laminin. Evidence for repetitive C-
 A:Reference number: S01790; PMID:89030693; PMID:3181157
 A:Accession: S01790
 A:Molecule type: mRNA
 A:Residues: 2538-3084 <DEU>
 A:Cross-references: EMBL:X13459; NID:G55499; PIDD:CA31807.1; PIDD:G818014
 A:Accession: A30451
 A:Molecule type: protein
 A:Residues: 1911-1929; 1997-2006; 2033-2045, 'X', 2047-2054, 'X', 2056-2066, 'X', 2068-2105; 2120-
 470; 2487-2498; 2502-2525; 2538-2557; 2561-2591, 'X', 2593-2594; 2600-2610; 2616-2645; 2648-2655;
 93; 2998-3005, 'A', 3007-3033, 'V', 3035; 3068-3083 <DE2>
 A:Note: 2256-Val was also found
 R:Olsson, D.; Nagayoshi, T.; Fazio, M.; Peltonen, J.; Jaakkola, S.; Sanborn, D.; Sasaki, L.
 Lab. Invest. 60, 772-782, 1989
 A>Title: Human laminin: cloning and sequence analysis of cDNAs encoding A, B1 and B2 cha
 A:Reference number: A34961; PMID:89280632; PMID:2733383
 A:Accession: S14670
 A:Molecule type: protein
 A:Residues: 2424-2436; 2440-2451; 2461-2467; 2487-2525; 2550-2557; 2561-2593; 2600-2610; 2616-2-
 -2942, 'T', 2944-2964; 2969-2976; 2980-2993; 2998-3000, 'T', 3002-3018, 'V', 3020-3034; 3068-3083
 C:Complex: Laminins are trimers of an alpha-type, a beta-type, and a gamma-type laminin
 C:Function:
 A:Description: interact with cells and with other basement membrane proteins to promote
 C:Superfamily: laminin alpha-1 chain; laminin G repeat homology; laminin-type EGF-like h
 C:Keywords: basement membrane; calcium binding; cell binding; coiled coil; extracellular
 F:1-24/Domain: signal sequence #status predicted <SIG>
 F:25-1084/Product: laminin alpha-1 chain #status predicted <MAT>
 F:25-277/Domain: VI <DOM6>
 F:277-331/Domain: laminin-type EGF-like homology <LE01>
 F:378-519/Domain: V <DOM5>
 F:334-401/Domain: laminin-type EGF-like homology <LE02>
 F:404-458/Domain: laminin-type EGF-like homology <LE03>
 F:461-507/Domain: laminin-type EGF-like homology <LE04>
 F:510-519/Domain: laminin-type EGF-like homology #status atypical <LE05>
 F:520-715/Domain: IVB <DOM4B>
 F:716-1166/Domain: IIIB <DOM3B>
 F:716-746/Domain: laminin-type EGF-like homology #status atypical <LE06>
 F:749-795/Domain: laminin-type EGF-like homology <LE07>
 F:798-853/Domain: laminin-type EGF-like homology <LE08>
 F:830-834/Domain: cell adhesion #status predicted
 F:856-906/Domain: laminin-type EGF-like homology <LE09>
 F:909-955/Domain: laminin-type EGF-like homology <LE10>
 F:958-1002/Domain: laminin-type EGF-like homology <LE11>
 F:1005-1048/Domain: laminin-type EGF-like homology <LE12>
 F:1051-1094/Domain: laminin-type EGF-like homology <LE13>
 F:1097-1116/Domain: laminin-type EGF-like homology #status atypical <LE14>
 F:1118-1134/Domain: laminin-type EGF-like homology #status atypical <LE15>
 F:1147-1149/Region: cell attachment (R-G-D) motif
 F:1157-1166/Domain: laminin-type EGF-like homology #status atypical <LE16>
 F:1167-1368/Domain: IVA <DOM4A>
 F:1369-1561/Domain: IIA <DOM3A>
 F:1369-1407/Domain: laminin-type EGF-like homology #status atypical <LE17>
 F:1410-1456/Domain: laminin-type EGF-like homology <LE18>
 F:1459-1513/Domain: laminin-type EGF-like homology <LE19>
 F:1516-1560/Domain: laminin-type EGF-like homology <LE20>
 F:1562-2133/Region: I/II <DOM2>
 F:1562-2133/Region: heparin repeats
 F:2134-3084/Domain: G <DOM6>
 F:2150-2308/Domain: laminin G repeat homology <LG1>
 F:2337-2492/Domain: laminin G repeat homology <LG2>
 F:2518-2683/Domain: laminin G repeat homology <LG3>
 F:2748-2897/Domain: laminin G repeat homology <LG4>
 F:2925-3082/Domain: laminin G repeat homology <LG5>
 F:25/Modified site: pyrolysine carboxylic acid (Gln) (in mature form) #status predicted
 F:45,79,370,374,531,562,672,808,914,959,969,1052,1344,1414,1586,1603,1659,1686,1706,1718
 e (Aasn) (covalent) #status predicted
 F:304-312/Diulfide bonds: #status experimental
 F:770,857,1999,2055,2067,2835/Binding site: carbohydrate (Aasn) (covalent) #status absent
 F:845,2102/Binding site: carbohydrate (Aasn) (covalent) #status absent

Query Match 10.0%; Score 111.5; DB 1; Length 3084;
 Best Local Similarity 20.2%; Pred. No. 0.31; Mismatches 75; Indels 95; Gaps 11;
 Matches 53; Conservative 39; Mismatches 75; Indels 95; Gaps 11;
 1 MKKLR-KTSGVRLNDVTGVTYKCSSEDMKLVRTASFSRGQMSFTNLDVSTDRFQSPQFQPSGTL----- 101
 2466 IKRLISRSSTPDLRLNSYGRKCA--LEPIQVSFLRGY-----VEMPP----- 2509
 60 FQFQPSGTL-NHQRTSS--LVTLBEGHILSTRDSNIPFK----- 101
 2510 -KSLSPSSILATFPAKNSGTLVAGDAEAGAAQHPFSSIMLEGRIVHNSG 2568
 102 -----SPGYMDGLHNVISDTSGLRLIDQVLRNRQRLPSFSNAQGSAR 149
 2569 DGTSLKALHAPTSYSDGQHSISLVNRNRVITQVE-----NSFEVKA 2615
 150 LG-----GG-----HPECISNVLVGRFSQSPVLDASKS 180
 2616 LQPLTEGKTIDISNLXIGLPEDKATPMLKMTSFGCIKNVLT-----DAQLDPTHTAT 2670
 181 TKKDSLGGCSLNKPPFLMFK 202
 2671 GSEQVELDTCILAEHPMOSLHR 2692
 RESULT 9
 T00021
 DN-cadherin - fruit fly (Drosophila melanogaster)
 C:Species: Drosophila melanogaster
 C:Date: 22-Jan-1999 #sequence_revision 22-Jan-1999 #ext_change 09-Jul-2004
 C:Accession: T00021
 R:Ival, X.; Deul, T.; Hirano, S.; Steward, R.; Takeichi, M.; Temure, T.
 Neuron 19, 77-89, 1997
 A>Title: Axon patterning requires DN-cadherin, a novel neuronal adhesion receptor, in t
 A:Reference number: Z14058; PMID:97388431; PMID:9247265
 A:Accession: T00021
 A>Status: preliminary; translated from GB/EMBL/DDBL
 A:Molecule type: mRNA
 A:Residues: 1-3097 <IMA>
 A:Note: 1(2)36Da
 A:Experimental source: whole embryo and adult head
 C:Genetics:
 A:Cross-references: FlyBase:FBgn015609
 A:Map position: 36D
 F:2346-2377/Domain: EGF homology <EGF>
 F:2869-2902/Domain: EGF homology <EGF1>
 Query Match 9.6%; Score 107; DB 2; Length 3097;
 Best Local Similarity 21.1%; Pred. No. 0.81; Mismatches 69; Indels 84; Gaps 11;
 Matches 50; Conservative 34; Mismatches 69; Indels 84; Gaps 11;
 17 VGVY-KKSGEDMKLVRTASFSRGQMSFTNLDVSTDRFQSPQFQPSGTL----- 70
 2370 VGVYGRQQ-----TTRSFKNGMAYRPLEK--CDSSHLSLFTTRKPDGLITNGPI 2422
 71 ---NHQRTSS-----LVTLBEGHILSTRDSNIPFKSPGYMDGLHNV 114
 2423 VPPERETLISDRIALBGRVRLIDPQSGTLRLV-----KTKKTLDDGEWHR 2474
 115 SVISDTSGLRLI-----DDQVLRNRQRLPSFS--NAQSLRLG 152
 2475 DLEFMDTESIRMVDPFKSABIAEMEDGTPPEFDMSCQARQIPPNEXYLVNAPLQVGG 2534
 153 GH-----FEGCISNVLVGRFSQSPVLDASGSKTKDASLGGC 190
 2535 LVHEQDQSLYKTHVWPTAKGPDGICRLNV-----HNSKLYDLAHGSLRN-SVAGC 2585
 RESULT 10
 IJFPTM
 cadherin-related tumor suppressor precursor - fruit fly (Drosophila melanogaster)

C:\Species: Drosophila melanogaster
C\Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Feb-1997
C\Accession: A41087, B41087
R\Name: P.A.; Weber, U.; Onofrechuk, P.; Biesemann, H.; Bryant, P.J.; Goodman, C.S.
Cell 67, 853-868, 1991
A>Title: The fat tumor suppressor gene in Drosophila encodes a novel member of the cadherin family
A\Reference number: A41087; MUID:92069752; PMID:1959133
A\Molecule type: mRNA
A\Molecule type: mRNA
A\Residues: 143-485;1279-5147 <MA>
A\Cross-references: B41087
A\Accession: B41087
A\Molecule type: DNA
A\Residues: 1-142;487-1278 <MA2>
A\Cross-references: GB:M0537
A>Note: 1229-Gly and 1233-Ser were also found
C\Genetics:
A\Gene: fat
A\Cross-references: FlyBase:FBgn0001075
C\Superfamily: cadherin-related tumor suppressor; cadherin repeat homology; EGF homology
C\Keywords: calcium binding, cell adhesion, duplication, cadherin, transmembrane protein
F11-35/Domain: signal sequence #status predicted <SIG>
F136-5147/Product: cadherin-related tumor suppressor #status predicted <MAT>
F136-4583/Domain: extracellular #status predicted <EXT>
F151-156/Domain: cadherin repeat homology <CR1>
F159-270/Domain: cadherin repeat homology <CR2>
F1271-382/Domain: cadherin repeat homology <CR3>
F1390-494/Domain: cadherin repeat homology <CR4>
F1497-599/Domain: cadherin repeat homology <CR5>
F1602-708/Domain: cadherin repeat homology <CR6>
F1718-822/Domain: cadherin repeat homology <CR7>
F1831-942/Domain: cadherin repeat homology <CR8>
F1948-1049/Domain: cadherin repeat homology <CR9>
F11052-1153/Domain: cadherin repeat homology <C10>
F1136-1278/Domain: cadherin repeat homology <C11>
F11281-1384/Domain: cadherin repeat homology <C12>
F11387-1489/Domain: cadherin repeat homology <C13>
F11492-1601/Domain: cadherin repeat homology <C14>
F11607-1713/Domain: cadherin repeat homology <C15>
F11717-1823/Domain: cadherin repeat homology <C16>
F11826-1922/Domain: cadherin repeat homology <C17>
F1195-2027/Domain: cadherin repeat homology <C18>
F12028-2167/Domain: cadherin repeat homology <C19>
F12159-2278/Domain: cadherin repeat homology <C20>
F12281-2384/Domain: cadherin repeat homology <C21>
F12387-2491/Domain: cadherin repeat homology <C22>
F12494-2596/Domain: cadherin repeat homology <C23>
F12599-2703/Domain: cadherin repeat homology <C24>
F12707-2810/Domain: cadherin repeat homology <C25>
F12813-2913/Domain: cadherin repeat homology <C26>
F12915-3013/Domain: cadherin repeat homology <C27>
F13014-3124/Domain: cadherin repeat homology <C28>
F13177-3229/Domain: cadherin repeat homology <C29>
F13232-3334/Domain: cadherin repeat homology <C30>
F13337-3439/Domain: cadherin repeat homology <C31>
F13442-3545/Domain: cadherin repeat homology <C32>
F13548-3651/Domain: cadherin repeat homology <C33>
F13654-3756/Domain: cadherin repeat homology <C34>
F13954-4010/Domain: EGF homology <EG1>
F14017-4048/Domain: EGF homology <EG2>
F14056-4089/Domain: EGF homology <EG3>
F14096-4127/Domain: EGF homology <EG4>
F14584-4609/Domain: transmembrane #status predicted <TM>
F14610-5147/Domain: intracellular #status predicted <INT>

Oy 93 RDS---NIPFKSPGTMDELHHVSYISTSGTSLRLLIDQVLRRAQRPLPSFMAQQS--147
| : | : | : | : | : | : | : | : | : | : | : | : | :
Db 4465 KOHHTINMY-QETSTINDSKMHNVLPSFSRSRLRVLDKROYGDLELDIGVTDFDPYL 4523

Oy 148 --LRIAGHEEGCISNVLYORFSQS-----PEV 173
| : | : | : | : | : | : | : | : | : | : | : | : | :
Db 4524 TLIVNGEAFVGCLANTYNNELQLPINGSGISPFEEV 4559

RESULT 11

S14458 laminin alpha-1 chain precursor - human
CSpecies: Homo sapiens (man)
CDate: 30-Sep-1991 #sequence_revision 30-Sep-1991 #cext_change 09-Jul-2004
CAccession: S14458; S14663; A34961
RNAparaneta, T.; Uitto, J.; Engvall, E.
Matrix 11, 151-160, 1991
A>Title: Molecular cloning of the cDNA encoding human laminin A chain.
AReference number: S14458; MUID:91333420; PMID:1714537
AAccession: S14458
A>Status: not compared with conceptual translation
AMolecule type: mRNA
A.Residues: 1-3075 <HA>
ACross-references: UNIPROT:P25391
RNAsistent, M.; Violeleaho, R.; Boot-Handford, R.; Kallunki, P.; Tryggvason, K.
Biochem. J. 276, 369-379, 1991
A>Title: Primary structure of the human laminin A chain. Limited expression in human tis
A.Reference number: S14663; MUID:91264789; PMID:2049067
AAccession: S14663
AMolecule type: mRNA
A.Residues: 1-227, 'FE', 230-251, 'MLP', 255-418, 'E', 420-518, 'L', 520-1022, 'V', 1024-1074, 'V',
ACross-references: EMBL:X8553; NID:g34225; PID:NCAA1418.1; PID:g34226
ROlsen, D.; Nagayoshi, T.; Fazio, M.; Peltonen, J.; Jaakkola, S.; Sandorn, D.; Saeki,
Lab. Invest. 60, 772-782, 1989
A>Title: Human laminin: cloning and sequence analysis of CDNA's encoding A, B1 and B2 cha
A.Reference number: A34961; MUID:89280632; PMID:2733363
AAccession: A34961
A>Status: not compared with conceptual translation
AMolecule type: mRNA
A.Residues: 'W', 2297-2745, 'L', 2747-3053, 'L', 3055-3072, 'PSG'
ANote: the authors translated the codon AGA for residue 2692 as Pro
CGenetics:

A:Gene: GDB:LAMA1, LMA
A:CROSS-references: GDB:120135, OMIM:150320
A:Map position: 16p11.32-18p11.22
C:Superfamily: laminin alpha-1 chain; laminin G repeat homology; laminin-type EGF-like h
C:Keywords: basement membrane; calcium binding; cell binding; coiled coil; disulfide bon
F:1-17/Domains: signal sequence #status predicted <SIG>
F:18-3075/Product: laminin alpha-1 chain #status predicted <MAT>
F:18-269/Domains: VI <DOM6>
F:1270-516/Domains: V <DOM5>
F:327-334/Domains: laminin-type EGF-like homology <LE1>
F:320-334/Domains: laminin-type EGF-like homology <LE2>
F:337-451/Domains: laminin-type EGF-like homology <LE3>
F:454-500/Domains: laminin-type EGF-like homology <LE4>
F:503-512/Domains: laminin-type EGF-like homology #status atypical <LE5>
F:517-708/Domains: IVD <DOA>
F:709-1159/Domains: IIIB <DOJ3B>
F:709-729/Domains: laminin-type EGF-like homology #status atypical <LE6>
F:747-788/Domains: laminin-type EGF-like homology <LE7>
F:771-846/Domains: laminin-type EGF-like homology <LE8>
F:849-899/Domains: laminin-type EGF-like homology <LE9>
F:902-948/Domains: laminin-type EGF-like homology <LE10>
F:951-995/Domains: laminin-type EGF-like homology <LE11>
F:998-1041/Domains: laminin-type EGF-like homology <LE12>
F:1044-1087/Domains: laminin-type EGF-like homology <LE13>
F:1090-1109/Domains: laminin-type EGF-like homology #status atypical <LE14>
F:1111-1147/Domains: laminin-type EGF-like homology #status atypical <LE15>
F:1150-1159/Domains: laminin-type EGF-like homology #status atypical <LE16>
F:1160-1361/Domains: IVA <DOA>
F:1362-1553/Domains: IIIA <DOJA>
F:1362-1400/Domains: laminin-type EGF-like homology #status atypical <LE17>
F:1403-1449/Domains: laminin-type EGF-like homology <LE18>

F:1452-1506/Domain: laminin-type EGF-like homology <LE19>
 F:1509-1553/Domain: laminin-type EGF-like homology <LE20>
 F:1554-2125/Domain: I/II, heptad repeats <DOM2>
 F:2116-2120/Region: cell adhesion #status predicted
 F:2126-3075/Domain: G <DOM3>
 F:2142-2300/Domain: laminin G repeat homology <LG1>
 F:2329-2484/Domain: laminin G repeat homology <LG2>
 F:2510-2676/Domain: laminin G repeat homology <LG3>
 F:2534-2536/Region: cell attachment (R-G-D) motif
 F:2739-2888/Domain: laminin G repeat homology <LG4>
 F:2916-3073/Domain: laminin G repeat homology <LG5>
 F:38,164,555,665,763,801,838,926,952,1045,1407,1579,1596,1678,1689,1698,1717,1804,1894,1 rate (km) (covale) #status predicted
 F:297-305/Disulfide bonds: #status predicted

Query Match 9.1%; Score 101.5; DB 2; Length 3075;
 Best Local Similarity 21.3%; Pred. No. 2.6;
 Matches 53; Conservative 43; Mismatches 102; Indels 51; Gaps 10;

QY 1 MKQLK-KTSGVRLNDVGVTKKSEDMKLVRTASFGSGMSTFNDVSTDRFQSLFG 59
 DB 2458 IKMLKSRSTFDDLRLNRYGVKGL--LEPIRSVFLKGGYILPPKSLPSESEMLVTF 2515
 QY 60 FQTFQPSGTL-----NHQRTSSLVTLLEDGHELESTRDSN-----IPIFKS 102
 DB 2516 --TTNSSGIIILALGDEVKRGDEBAHVPPFSVMLIGNIEVAVNFGDGTGLKALLHA 2573
 QY 103 P-GTYMDGLLHVSVISDTSGRLIIDQ---VLRRNQLPFSFNAQSLRGG----- 152
 DB 2574 PTGCSGQASHISILVNRRIITQVDENNPEVKLGTLVESRTINSLVYGGIPGEG 2633
 QY 153 -----GHEGCSNVLVQRFSGSPVLDLASKSTKQASLGCCSLANKPPL----- 198
 DB 2634 TSLITWERSHPCIKNLI-----NRLDPSNAGHGYVDLDTQWLSERPCLAPDAEDS 2688
 QY 199 MLFSPKPF 207
 DB 2689 KILREPPAF 2697

RESULT 12

T23433
 hypothetical protein K08C7.3 - Caenorhabditis elegans

C/Species: Caenorhabditis elegans
 C/Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
 C/Accession: T23433
 R/Berke, M.

submitted to the EMBL Data Library, March 1996
 A/Reference number: Z19740

A/Accession: T23433
 A/Status: preliminary; translated from GB/EMBL/DBJ

A/Molecule type: DNA
 A/Residues: 1-3672 <MIL>
 A/Cross-references: UNIPROT:Q21313; EMBL:Z70286; PIDD:CAA4293.1; GSPDB:GN00022; CESP:K08C7

A/Experimental source: clone K08C7
 A/Genetic: CESP:K08C7.3
 A/Map position: 4

A/Insertions: 66/1; 284/3; 563/1; 1187/3; 1248/3; 1300/1; 1460/1; 1623/3; 2361/3; 2988/3; 3 C/Superfamily: laminin alpha-1 chain; laminin G repeat homology; laminin-type EGF-like

Query Match 8.9%; Score 99.5; DB 2; Length 3672;
 Best Local Similarity 27.1%; Pred. No. 5;
 Matches 60; Conservative 31; Mismatches 79; Indels 51; Gaps 12;

QY 1 MKNLKKTSGVRLND--TVGVTKKSEDMKLVRTASFGSGMSTFNDVSTDRFQSL 56
 DB 3041 IKSVKLGSDNVDLSSHASGVRGSC--PLHSVTVTFSLDRTTASFNMTRESFD--VSV 3097
 QY 57 SFGFQT---FQPSGTLNMQRTSSLVTL-EDGHIELSTRD--SNPIFKSPGTMDGL 110
 DB 3098 TFKFKTRISIRQPSLFTVNDDESVLVSINEDGILVTSGEDIATLELAASP----DEK 3153

QY 111 LHHVSVISDPTSGRLIIDQVLRNRNQLPFSFNAQSLRGCGH----- 154
 DB 3154 WHVYSIRKTYIRIRIAD-----SFSNEVARKHADNDNPASFLSAFFGSGERT 3203
 QY 155 --FEGCISNVLVQRFSGSPVLDLASKSTKQASLGCCSLN 193
 DB 3204 PSFVGCIGDVTL-----NGKLDLPAN-SRIKEISLNGCSLS 3238

RESULT 13

T37316
 probable laminin alpha chain - Caenorhabditis elegans

C/Species: Caenorhabditis elegans
 C/Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
 C/Accession: T37316
 R/John, K.; Zhu, K.; Hedgecock, E.M.; Inoue, T.; Horii, K.
 A/Description: Laminin alpha chain gene in the nematode C. elegans.
 A/Reference number: Z21681

A/Accession: T37316
 A/Status: preliminary; translated from GB/EMBL/DBJ
 A/Molecule type: DNA
 A/Residues: 1-3704 <JOH>
 A/Cross-references: UNIPROT:P91904; EMBL:AB016806; PIDD:BAJ2347.1
 A/Experimental source: strain N2
 A/Genetic: epi-1

A/Map position: IV
 A/Insertions: 66/1; 284/3; 563/1; 1187/3; 1248/3; 1300/1; 1460/1; 1623/3; 2361/3; 2988/3; 3 C/Superfamily: laminin alpha-1 chain; laminin G repeat homology; laminin-type EGF-like

Query Match 8.9%; Score 99.5; DB 2; Length 3704;
 Best Local Similarity 27.1%; Pred. No. 5.1;
 Matches 60; Conservative 31; Mismatches 79; Indels 51; Gaps 12;

QY 1 MKNLKKTSGVRLND--TVGVTKKSEDMKLVRTASFGSGMSTFNDVSTDRFQSL 56
 DB 3041 IKSVKLGSDNVDLSSHASGVRGSC--PLHSVTVTFSLDRTTASFNMTRESFD--VSV 3097
 QY 57 SFGFQT---FQPSGTLNMQRTSSLVTL-EDGHIELSTRD--SNPIFKSPGTMDGL 110
 DB 3098 TFKFKTRISIRQPSLFTVNDDESVLVSINEDGILVTSGEDIATLELAASP----DEK 3153
 QY 111 LHHVSVISDPTSGRLIIDQVLRNRNQLPFSFNAQSLRGCGH----- 154
 DB 3154 WHVYSIRKTYIRIRIAD-----SFSNEVARKHADNDNPASFLSAFFGSGERT 3203
 QY 155 --FEGCISNVLVQRFSGSPVLDLASKSTKQASLGCCSLN 193
 DB 3204 PSFVGCIGDVTL-----NGKLDLPAN-SRIKEISLNGCSLS 3238

RESULT 14

E86327
 protein F1B014.19 [imported] - Arabidopsis thaliana

C/Species: Arabidopsis thaliana (mouse-ear cress)
 C/Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
 C/Accession: E86327
 R/Theologos, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso

Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K. ansen, N.P.; Hughes, B.; Hutzar, L.
 Nature 408, 816-820, 2000

A/Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luoro, J.S.; Maitl, R.; Marzalli Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
 A/Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.

A/Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
 A/Reference number: A86141; MIMD:21016719; PMID:11130712

A/Accession: E86327
 A/Status: preliminary
 A/Molecule type: DNA
 A/Residues: 1-1158 <STO>

A:Cross-references: UNIPROT:Q9LNS1, GB:AE005172, NID:g8778419, PID:AAF9427.1, GSPDB:GN
C:Genetics:
A:Gene: F18014.19
A:Map position: 1

Query Match 8.9%; Score 99; DB 2; Length 1158;
Best Local Similarity 26.1%; Pred. No. 1.2;
Matches 35; Conservative 22; Mismatches 51; Indels 26; Gaps 4;

QY 15 DTGVVTKKSGEDKLVRTASFSRGGMSFTNLDVPSDFQLSFGQTFQPSGTLNMQT 74
DB 135 DLVGISGLDDDKLQCHMLAEKKNK-----SIERSGKFFPESWIDTSSASNMT 185
QY 75 RT-----SSLVLTLEDGHIELSTRDSNIPFKSPGT---YMDGLLHH---VSVI 117
DB 186 GTLEFLDILHGMAPVLIKLPDGRFTTSTKRGVLMGSSLSLDVFFVDGLHCHLISVSQ 245
QY 118 SDTSGRLRLIDQV 131
DB 246 TRDSGYTFQITDKV 259

RESULT 15

KXEOS

plasma protein S precursor - bovine

N:Alternate names: vitamin K-dependent protein S

C:Species: Bos primigenius taurus (cattle)

C>Date: 08-Aug-1987 #sequence_revision 26-Jan-1996 #text_change 09-Jul-2004

C:Accession: A24759; A23888

R:Dahlback, B.; Lundwall, A.; Stenflo, J.

Proc. Natl. Acad. Sci. U.S.A. 83, 4199-4203, 1986

A:Title: Primary structure of bovine vitamin K-dependent protein S.

A:Reference number: A24759; PMID:86233400; PMID:2340598

A:Accession: A24759

A:Molecule type: mRNA

A:Residues: 1-675 <DNH>

A:Cross-references: UNIPROT:P07224; GB:M13044; NID:g163697; PID:AAA0757.1; PID:g163698

A>Note: parts of this sequence, including the amino end of the mature protein, were deter

R:Dahlback, B.; Lundwall, A.; Stenflo, J.

J. Biol. Chem. 261, 5111-5115, 1986

A:Title: Localization of thrombin cleavage sites in the amino-terminal region of bovine

A:Reference number: A23888; PMID:86168236; PMID:2337785

A:Accession: A23888

A:Molecule type: protein

A:Residues: 42-141 <DA2>

C:Complex: in plasma forms a complex with C4b binding protein

C:Function:

A>Description: a cofactor for activated protein C (EC 3.4.21.69); thrombin cleavage deact

C:Superfamily: plasma protein S; EGF homology; Gla domain homology; laminin G repeat hom

C:Keywords: beta-hydroxyasparagine; beta-hydroxyaspartic acid; blood coagulation; carbox

F:1-24/Domain: signal sequence #status predicted <SIG>

F:25-41/Domain: propeptide #status predicted <PRO>

F:26-85/Domain: Gla domain homology <GLA>

F:42-675/Product: plasma protein S #status experimental <MAT>

F:121-154/Domain: EGF homology <EG1>

F:161-199/Domain: EGF homology <EG2>

F:205-241/Domain: EGF homology <EG3>

F:247-282/Domain: EGF homology <EG4>

F:315-666/Domain: sex hormone-binding globulin homology <SHB>

F:325-478/Domain: laminin G repeat homology <LGR>

F:47-55,57,60,61,66,67,70,73,77/Modified site: gamma-carboxyglutamic acid (Glu) #stat

F:58-63,88-113,121-134,126-143,145-154,161-175,171-184,186-199,205-217,212-226,228-241,2

F:93-94/Cleavage site: Arg-Ala (thrombin) #status experimental

F:111-112/Cleavage site: Arg-Ser (thrombin) #status experimental

F:136/Modified site: erythro-beta-hydroxyaspartic acid (Asp) #status experimental

F:177,219,258/Modified site: erythro-beta-hydroxyasparagine (Asn) #status experimental

F:288-567,449-475,638-665/Diisulfide bonds: #status experimental

F:499/Binding site: carbohydrate (Asn) (covalent) #status experimental

F:509/Binding site: carbohydrate (Asn) (covalent) #status predicted

QY 39 GQMSFTNLDVPSDFQLSFGQTFQPSGTLNMQTRTS--LLVLTLEDGHIELSTRDSN 96
DB 308 GVVLLKFRRLPETTRFSAFPDFFRTYDSEGVLLVAESSDHSAMPILALAEKIEIQFNK 367
QY 97 IPFKSPGTYM-DGLLHVSV 116
DB 368 TTKMTYGGKVINIDGLMHVSV 388

Search completed: February 22, 2005, 08:19:40
Job time : 7.8166 secs

Query Match 8.5%; Score 94.5; DB 1; Length 675;
Best Local Similarity 29.6%; Pred. No. 1.4;
Matches 24; Conservative 15; Mismatches 39; Indels 3; Gaps 2;

DB 1129 MKRLKKTSGVRLNDTVGVTKKCSBDWKLVRTASFSRGQMFPTNLDPSTDFQLSPGF 1188
 QY QFPQPSGTLNHNQRTSSLVLTLEDGHIELSTDSNIPFKSPGTWMDGLHVVSYSDT 120
 DB 1189 QTFQPSGTLNHNQRTSSLVLTLEDGHIELSTDSNIPFKSPGTWMDGLHVVSYSDT 1248
 QY 121 SGIRLLIDQVLRNRRLPSFSNAQOSLRIGGHEGCIISNVLVQSPFSQPEVLDLASKS 180
 DB 1249 SGIRLLIDQVLRNRRLPSFSNAQOSLRIGGHEGCIISNVLVQSPFSQPEVLDLASKS 1308
 QY 181 TKKDAISLGGCSLNKPPFPLFKSPKPKNGKIRNNVQL 218
 DB 1309 TKKDAISLGGCSLNKPPFPLFKSPKPKNGKIRNNVQL 1346

RESULT 2
 LMA3_MOUSE
 ID LMA3_MOUSE STANDARD, PRT, 3333 AA.
 AC Q61789; Q08751; Q61788; Q61966; Q9UHQ7;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE laminin alpha-3 chain precursor (Nicein alpha subunit).
 GN Name=Lama3;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 [1]
 RN SEQUENCE OF 1-58 FROM N.A., AND SEQUENCE OF 32-38.
 RP MEDLINE=21818471; PubMed=11829758; DOI=10.1042/0264-6021:3620213;
 RA Garbe J.H., Gohring W., Mann K., Timpl R., Sasaki T.;
 RT "Complete sequence, recombinant analysis and binding to laminins and
 RT sulphated ligands of the N-terminal domains of laminin alpha3b and
 RT alpha5 chains.";
 RL Biochem. J. 362:213-221 (2002).
 RN [2]
 RP SEQUENCE OF 1-726 FROM N.A.
 RC STRAIN=ICR;
 RX MEDLINE=97296337; PubMed=9151674; DOI=10.1083/jcb.137.3.685;
 RA Miner J.H., Paton B.L., Lenz S.I., Gilbert D.J., Snider W.D.,
 RA Jenkins N.A., Copeland N.G., Sane J.R.;
 RT "The laminin alpha chains: expression, developmental transitions, and
 RT chromosomal locations of alpha1-5, identification of heterotrimeric
 RT laminin 8-11, and cloning of a novel alpha3 isoform.";
 RL J. Cell Biol. 137:685-701 (1997).
 RN [3]
 RP SEQUENCE FROM N.A. (ISOFORM A), AND SEQUENCE OF 716-3284 FROM N.A.
 RC (ISOFORM B).
 RX STRAIN=BALB/c; Tissue=Lung;
 MEDLINE=95394948; PubMed=7665604; DOI=10.1074/jbc.270.37.21820;
 RA Galliano M.-F., Aberdam D., Aguzzi A., Ortonne J.-P., Meneguzzi G.,
 RT "Cloning and complete primary structure of the mouse laminin alpha 3
 RT chain. Distinct expression pattern of the laminin alpha 3A and alpha
 RT 3B chain isoforms.";
 RL J. Biol. Chem. 270:21820-21826 (1995).
 RN [4]
 RP REVISIONS.
 RA Aberdam D.;
 RL Submitted (APR-1997) to the EMBL/GenBank/DBJ databases.
 RN [5]
 RP SEQUENCE OF 1767-2485 FROM N.A.
 RC TISSUE=Lung;
 RX MEDLINE=94261750; PubMed=8012114;
 RA Aberdam D., Galliano M.-F., Mattei M.-G., Pisaní-Spadafora A.,
 RA Ortonne J.-P., Meneguzzi G.;
 RT "Assignment of mouse nicein genes to chromosomes 1 and 18.";
 RL Mamm. Genome 5:229-233 (1994).
 RN [6]
 RP SEQUENCE OF 1767-2485 FROM N.A.
 RC TISSUE=Lung;
 RX MEDLINE=94353405; PubMed=8081888;
 RA Aberdam D., Aguzzi A., Baudoin C., Galliano M.-F., Ortonne J.-P.,

RA Meneguzzi G.;
 RT "Developmental expression of nicein adhesion protein (laminin-5)
 RT subunits suggests multiple morphogenic roles.";
 RL Cell Adhes. Commun. 2:115-129 (1994).
 CC -1- FUNCTION: Binding to cells via a high affinity receptor, laminin
 CC is thought to mediate the attachment, migration and organization
 CC of cells into tissues during embryonic development by interacting
 CC with other extracellular matrix components.
 CC -1- FUNCTION: Laminin-5 is thought to be involved in (1) cell adhesion
 CC via integrin alpha3/beta-1 in focal adhesion and integrin alpha-
 CC 6/beta-4 in hemidesmosomes, (2) signal transduction via tyrosine
 CC phosphorylation of p125-FAK and p80, (3) differentiation of
 CC keratinocytes (by similarity).
 CC -1- SUBUNIT: Laminin is a complex glycoprotein, consisting of three
 CC different polypeptide chains (alpha, beta, gamma), which are bound
 CC to each other by disulfide bonds into a cross-shaped molecule
 CC comprising one long and three short arms with globules at each
 CC end. The alpha-3 chain is a subunit of laminin-5
 CC (epiligrin/kalinin/nicein), and possibly also a component of
 CC laminin-6 (K-laminin) and laminin-7 (KS-laminin).
 CC -1- SUBCELLULAR LOCATION: Extracellular; found in the basement
 CC membranes (major component).
 CC -1- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=2;
 CC Name=B;
 CC Name=A;
 CC IsoId=Q61789-1; Sequence=Displayed;
 CC -1- ISOId=Q61789-2; Sequence=VSP_003038, VSP_003039;
 CC TISSUE SPECIFICITY: Basal membrane of the upper alimentary tract
 CC and urinary and nasal epithelia, salivary glands and teeth (both
 CC variants). Isoform A is predominantly expressed in skin, hair
 CC follicles and developing neurons of the trigeminal ganglion.
 CC Isoform B was found in bronchi, alveoli, stomach, intestinal
 CC crypts, whisker pads, CNS, telencephalic neuroectoderm, thalamus,
 CC Ratche's pouch and periventricular subependymal germinal layer.
 CC -1- DOMAIN: The alpha-helical domains I and II are thought to interact
 CC with other laminin chains to form a coiled coil structure.
 CC -1- DOMAIN: Domains IV and G are globular.
 CC -1- SIMILARITY: Contains 15 laminin BGF-like domains.
 CC -1- SIMILARITY: Contains 5 laminin G-like domains.
 CC -1- SIMILARITY: Contains 1 laminin IV domain.
 CC -1- SIMILARITY: Contains 1 laminin N-terminal domain.
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
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 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL; AJ293592; CAB99254.2; -;
 CC EMBL; U88353; AAC53179.1; -;
 CC EMBL; X84013; CAA58837.1; -;
 CC EMBL; X84013; CAA58836.1; ALT_FRAME.
 CC EMBL; L20478; AAA68091.1; -;
 CC HSSP; P02468; INPE.
 CC MGD; MGI:39909; Lama3.
 CC GO; GO:0005604; C:basement membrane, IDA.
 CC DR InterPro; IPR008985; Cona1ike_jec_g1.
 CC DR InterPro; IPR006209; EGF1ike.
 CC DR InterPro; IPR008979; Gal_bind1ike.
 CC DR InterPro; IPR009030; Grow_fac1recept.
 CC DR InterPro; IPR008212; Lam_N2.
 CC DR InterPro; IPR000034; Laminin_B.
 CC DR InterPro; IPR002049; Laminin_BGF.
 CC DR InterPro; IPR001791; Laminin_G.
 CC DR InterPro; IPR009254; Laminin_I.
 CC DR InterPro; IPR010307; Laminin_II.
 CC DR InterPro; IPR008211; Laminin_N.
 CC DR InterPro; IPR003129; TSP_N.
 CC DR Pfam; PF00052; Laminin_B_1.
 CC DR Pfam; PF00053; Laminin_EGF_10.

DR Pfam; PF00054; Laminin_G; 3.
 DR Pfam; PF06008; Laminin_I; 1.
 DR Pfam; PF06009; Laminin_II; 1.
 DR Pfam; PF00055; Laminin_N; 1.
 DR PRINTS; PR00011; EGF_LAMININ.
 DR PRODOM; PD003031; Laminin_B; 1.
 DR PROSITE; PS00022; EGF_1; 10.
 DR PROSITE; PS01186; EGF_2; 1.
 DR PROSITE; PSS0025; LAM_G_DOMAIN; 5.
 DR PROSITE; PS01248; LAMININ_TYPE_EGF; 10.
 KW Alternative splicing; Basement membrane; Cell adhesion; Coiled coil;
 KW Direct protein sequencing; Extracellular matrix; Glycoprotein;
 KW Laminin EGF-like domain; Repeat; Signal.
 FT STGNL 1 31
 FT CHAIN 32 333
 FT DOMAIN 32 294 Laminin alpha-3 chain.
 FT DOMAIN 295 725 Laminin N-terminal (domain VI).
 FT DOMAIN 296 350 Domain V.
 FT DOMAIN 353 420 Laminin EGF-like 1.
 FT DOMAIN 423 464 Laminin EGF-like 2.
 FT DOMAIN 488 530 Laminin EGF-like 3.
 FT DOMAIN 533 576 Laminin EGF-like 4.
 FT DOMAIN 582 625 Laminin EGF-like 5.
 FT DOMAIN 628 678 Laminin EGF-like 6.
 FT DOMAIN 681 725 Laminin EGF-like 7.
 FT DOMAIN 793 1262 Laminin EGF-like 8.
 FT DOMAIN 1263 1464 Laminin domain IV 1 (domain IV B).
 FT DOMAIN 1310 1353 Domain III B.
 FT DOMAIN 1354 1403 Laminin EGF-like 9.
 FT DOMAIN 1404 1454 Laminin EGF-like 10.
 FT DOMAIN 1455 1464 Laminin EGF-like 11.
 FT DOMAIN 1465 1653 Laminin EGF-like 12 (N-terminal).
 FT DOMAIN 1654 1821 Laminin domain IV (domain IV A).
 FT DOMAIN 1821 1821 Domain III A.
 FT DOMAIN 1686 1733 Laminin EGF-like 12 (C-terminal).
 FT DOMAIN 1734 1786 Laminin EGF-like 13.
 FT DOMAIN 1787 1821 Laminin EGF-like 14.
 FT DOMAIN 1822 2388 Laminin EGF-like 15 (incomplete).
 FT DOMAIN 2389 2590 Domain II and I.
 FT DOMAIN 2591 2759 Laminin G-like 1.
 FT DOMAIN 2766 2926 Laminin G-like 2.
 FT DOMAIN 2986 3150 Laminin G-like 3.
 FT DOMAIN 3157 3330 Laminin G-like 4.
 FT DOMAIN 1854 1983 Laminin G-like 5.
 FT DOMAIN 2015 2060 Coiled coil (potential).
 FT DOMAIN 2091 2168 Coiled coil (potential).
 FT DOMAIN 2214 2241 Coiled coil (potential).
 FT DOMAIN 2321 2386 Cell attachment site (potential).
 FT SITE 2277 2279
 FT DISULFID 1310 1317 By similarity.
 FT DISULFID 1312 1324 By similarity.
 FT DISULFID 1326 1335 By similarity.
 FT DISULFID 1338 1351 By similarity.
 FT DISULFID 1354 1369 By similarity.
 FT DISULFID 1356 1376 By similarity.
 FT DISULFID 1378 1387 By similarity.
 FT DISULFID 1390 1401 By similarity.
 FT DISULFID 1404 1416 By similarity.
 FT DISULFID 1406 1423 By similarity.
 FT DISULFID 1425 1434 By similarity.
 FT DISULFID 1437 1452 By similarity.
 FT DISULFID 1487 1496 By similarity.
 FT DISULFID 1689 1703 By similarity.
 FT DISULFID 1706 1715 By similarity.
 FT DISULFID 1718 1731 By similarity.
 FT DISULFID 1734 1746 By similarity.
 FT DISULFID 1736 1755 By similarity.
 FT DISULFID 1757 1766 By similarity.
 FT DISULFID 1769 1784 By similarity.
 FT DISULFID 1822 1822 Interchain (Probable).
 FT DISULFID 1825 1825 Interchain (Probable).

Query Match

92.4%; Score 1033; DB 1; Length 3333;

Best Local Similarity 92.7%; Pred. No. 1,1e-79;
 Matches 202; Conservative 5; Mismatches 11; Indels 0; Gaps 0;
 QY 1 MKRLKTSGVRLNDVGVTKKCESEDMKVRTPSPRGCGMSTPNDVPSDPSFQLSFGP 60
 DB 2737 MKRLKTSGVRLNDVGVTKKCESEDMKVRTPSPRGCGMSTPNDVPSDPSFQLSFGP 2796
 QY 61 QTFPSGTLNHTQRTSSLVLTLEDGHELESTDSNIPFSPQTYMDGLHHVSVISDT 120
 DB 2797 QTFPSGTLNHTQRTSSLVLTLEDGHELESTDSNIPFSPQTYMDGLHHVSVISDT 2856
 QY 121 SGRLRLIDQVLRNRQRLPSFNAQSLRGHGFEGCISNVLVGRFSQSPVLDLASKS 180
 DB 2857 SGRLRLIDQVLRNRQRLPSFNAQSLRGHGFEGCISNVLVGRFSQSPVLDLASKS 2916
 QY 181 TKRDASLGGCSLNKPPFLMFKSPKPKNGRIFFNVQL 218
 DB 2917 TKRDASLGGCSLNKPPFLMFKSPKPKNGRIFFNVQL 2954
 RESULT 3
 ID Q6VU69 PRELIMINARY; PRT; 1668 AA.
 AC Q6VU69;
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 DE Laminin alpha 3 splice variant a.
 GN Name=LAMA3;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OC NCBI_TaxID=9606;
 RN [1]
 RP MEDLINE=42833568; PubMed=12915477; DOI=10.1093/hmg/ddg234;
 RX McLean W.H., Irvine A.D., Hamill K.J., Whitlock N.V.,
 RA Coleman-Campbell C.M., Mellerio J.E., Ashton G.S.,
 RA Dopling-Hepnerstall P.U., Bady R.A., Jamil T., Phillips R.J.,
 RA Shabir S.G., Haroon T.S., Khurshid K., Moore J.B., Page B.,
 RA Darling J., Atherton D.J., Van Steensel M.A., Munro C.S., Smith F.J.,
 RA McGrath J.A.;
 RT "An unusual N-terminal deletion of the laminin (alpha)3a isoform leads
 to the chronic granulation tissue disorder laryngo-oncho-cutaneous
 syndrome.";
 RT Hum. Mol. Genet. 12:2395-2409(2003).
 RN [2]
 RP SEQUENCE FROM N.A.
 RU McLean W.H.I.;
 RU Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AY327114; AMQ72569.1; -;
 DR GO; GO:0005606; C:Laminin-1; IEA.
 DR GO; GO:0005102; F:receptor binding; IEA.
 DR GO; GO:0005198; F:structural molecule activity; IEA.
 DR GO; GO:0030155; P:regulation of cell adhesion; IEA.
 DR GO; GO:0030334; P:regulation of cell migration; IEA.
 DR GO; GO:0045995; P:regulation of embryonic development; IEA.
 DR InterPro; IPR001844; Chapterin_Cpn60.
 DR InterPro; IPR008985; Cona_like_1ec_g1.
 DR InterPro; IPR006209; EGF_like.
 DR InterPro; IPR002049; Laminin_EGF.
 DR InterPro; IPR001791; Laminin_G.
 DR InterPro; IPR009254; Laminin_I.
 DR InterPro; IPR010307; Laminin_II.
 DR InterPro; IPR003129; TSP_N.
 DR Pfam; PF00053; Laminin_EGF; 1.
 DR Pfam; PF02210; Laminin_G_2; 4.
 DR Pfam; PF06008; Laminin_I; 1.
 DR Pfam; PF06009; Laminin_II; 1.
 DR SMART; SM00180; EGF_Lam; 2.
 DR SMART; SM00282; LamG; 5.
 DR PROSITE; PS00296; CHAPERONINS_CPN60; UNKNOWN_1.
 DR PROSITE; PS00022; EGF_1; 1.

DR PROSITE, PS01186; EGF 2, 1.
 DR PROSITE, PS01248; LAMININ TYPE EGF, 2.
 DR PROSITE, PS50025; LAM G DOMAIN; 5.
 KW Laminin EGF-like domain.
 SQ SEQUENCE 1668 AA; 184053 MW; 98BF5FC45637645C CRC64;
 Query Match 76.2%; Score 852; DB 2; Length 1668;
 Best Local Similarity 76.6%; Pred. No. 1.9e-64;
 Matches 167; Conservative 18; Mismatches 33; Indels 0; Gaps 0;
 QY 1 MNKLKTSGVRLNDVGVTKKCSHDKLVRTASPSRGGMSFTNLDVSTDRFQLSPGF 60
 DB 1073 MNKLKTSGVRLNDVGVTKKCSHDKLVRSASPSRGGQLSTDLGLPTDHLQASFGF 1132
 QY 61 QTFQPSGTLNMQRTSSILVLTEDGHELESTRDSNIPFSPGTYMDGLHHSVISDT 120
 DB 1133 QTFQPSGTLNMQRTSSILVLTEDGHELESTRDSNIPFSPGTYMDGLHHSVISDTN 1192
 QY 121 SGLRLIIDQVLRNRQRLPSFSNAQSLRGSGHEGCGISNVLVGFOSQPEVLDAASKS 180
 DB 1193 SGLRLIIDQVLRNRQRLPSFSNAQSLRGSGHEGCGISNVLVGFQRLSLSPVLDLTNS 1252
 QY 181 TKKDAISGGCSLNKPPFLMLFKSPKPKGRIRFNNQL 218
 DB 1253 LKRDVSLGGCSLNKPPFLMLKSGTRFNKTKTFRINQL 1290
 RESULT 4
 Q6VU67 PRELIMINARY; PRT; 3277 AA.
 ID Q6VU67
 AC Q6VU67
 DT 05-JUL-2004 (TREMBlrel. 27, Created)
 DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
 DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)
 DE Laminin alpha 3 splice variant b2.
 GN Name=LAMA3;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 ON NCBI_Taxid=9606;
 RX MEDLINE=22833568; PubMed=12915477; DOI=10.1093/hmg/ddg234;
 RA McLean W.H., Irvine A.D., Hamill K.J., Whitlock N.V.,
 RA Coleman-Campbell C.M., Mellerio J.E., Ashton G.S.,
 RA Doppling-Hepensal P.J., Bady R.A., Jamil T., Phillips R.J.,
 RA Shabir S.G., Haroon T.S., Khurshid K., Moore J.E., Page B.,
 RA Darling J.A., Atherton D.J., Van Steensel M.A., Munro C.S., Smith F.J.,
 RA McGrath J.A.;
 RT "An unusual N-terminal deletion of the laminin (alpha)3a isoform leads
 RT to the chronic granulation tissue disorder laryngo-oncho-cutaneous
 RT syndrome";
 RT Hum. Mol. Genet. 12:2395-2409 (2003).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=22833568; PubMed=12915477; DOI=10.1093/hmg/ddg234;
 RA McLean W.H., Irvine A.D., Hamill K.J., Whitlock N.V.,
 RA Coleman-Campbell C.M., Mellerio J.E., Ashton G.S.,
 RA Doppling-Hepensal P.J., Bady R.A., Jamil T., Phillips R.J.,
 RA Shabir S.G., Haroon T.S., Khurshid K., Moore J.E., Page B.,
 RA Darling J.A., Atherton D.J., Van Steensel M.A., Munro C.S., Smith F.J.,
 RA McGrath J.A.;
 RT "An unusual N-terminal deletion of the laminin (alpha)3a isoform leads
 RT to the chronic granulation tissue disorder laryngo-oncho-cutaneous
 RT syndrome";
 RT Hum. Mol. Genet. 12:2395-2409 (2003).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=22833568; PubMed=12915477; DOI=10.1093/hmg/ddg234;
 RA McLean W.H., Irvine A.D., Hamill K.J., Whitlock N.V.,
 RA Coleman-Campbell C.M., Mellerio J.E., Ashton G.S.,
 RA Doppling-Hepensal P.J., Bady R.A., Jamil T., Phillips R.J.,
 RA Shabir S.G., Haroon T.S., Khurshid K., Moore J.E., Page B.,
 RA Darling J.A., Atherton D.J., Van Steensel M.A., Munro C.S., Smith F.J.,
 RA McGrath J.A.;
 RT "An unusual N-terminal deletion of the laminin (alpha)3a isoform leads
 RT to the chronic granulation tissue disorder laryngo-oncho-cutaneous
 RT syndrome";
 RT Hum. Mol. Genet. 12:2395-2409 (2003).
 RN [2]

DR InterPro; IPR009254; Laminin_I.
 DR InterPro; IPR010307; Laminin_II.
 DR InterPro; IPR008211; Laminin_N.
 DR InterPro; IPR003129; TSP_N.
 DR Pfam; PF00052; Laminin_B_1.
 DR Pfam; PF00053; Laminin_EGF_8.
 DR Pfam; PF02210; Laminin_G_2; 4.
 DR Pfam; PF06008; Laminin_I_1.
 DR Pfam; PF06009; Laminin_II_1.
 DR Pfam; PF00055; Laminin_N_1.
 DR PRINTS; PR00011; EGF_LAMININ.
 DR ProDom; PD003031; Laminin_B_1.
 DR SMART; SM00181; EGF; 8.
 DR SMART; SM00180; EGF_Lam; 14.
 DR SMART; SM00281; Lam3; 1.
 DR SMART; SM00282; Lam3; 5.
 DR SMART; SM00135; LamnT; 1.
 DR PROSITE; PS00296; CHAPERONINS_CPN60; UNKNOWN_1.
 DR PROSITE; PS00022; EGF_1; 12.
 DR PROSITE; PS01186; EGF_2; 1.
 DR PROSITE; PS01248; LAMININ TYPE EGF; 13.
 DR PROSITE; PS50025; LAM G DOMAIN; 5.
 KW Laminin EGF-like domain.
 SQ SEQUENCE 3277 AA; 360209 MW; 3ACFEB98357122B CRC64;
 Query Match 76.2%; Score 852; DB 2; Length 3277;
 Best Local Similarity 76.6%; Pred. No. 4.5e-64;
 Matches 167; Conservative 18; Mismatches 33; Indels 0; Gaps 0;
 QY 1 MNKLKTSGVRLNDVGVTKKCSHDKLVRTASPSRGGMSFTNLDVSTDRFQLSPGF 60
 DB 2682 MNKLKTSGVRLNDVGVTKKCSHDKLVRSASPSRGGQLSTDLGLPTDHLQASFGF 2741
 QY 61 QTFQPSGTLNMQRTSSILVLTEDGHELESTRDSNIPFSPGTYMDGLHHSVISDT 120
 DB 2742 QTFQPSGTLNMQRTSSILVLTEDGHELESTRDSNIPFSPGTYMDGLHHSVISDTN 2801
 QY 121 SGLRLIIDQVLRNRQRLPSFSNAQSLRGSGHEGCGISNVLVGFOSQPEVLDAASKS 180
 DB 2802 SGLRLIIDQVLRNRQRLPSFSNAQSLRGSGHEGCGISNVLVGFQRLSLSPVLDLTNS 2861
 QY 181 TKKDAISGGCSLNKPPFLMLFKSPKPKGRIRFNNQL 218
 DB 2862 LKRDVSLGGCSLNKPPFLMLKSGTRFNKTKTFRINQL 2899
 RESULT 5
 Q6VU68 PRELIMINARY; PRT; 3333 AA.
 ID Q6VU68
 AC Q6VU68
 DT 05-JUL-2004 (TREMBlrel. 27, Created)
 DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
 DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)
 DE Laminin alpha 3 splice variant b1.
 GN Name=LAMA3;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 ON NCBI_Taxid=9606;
 RX MEDLINE=22833568; PubMed=12915477; DOI=10.1093/hmg/ddg234;
 RA McLean W.H., Irvine A.D., Hamill K.J., Whitlock N.V.,
 RA Coleman-Campbell C.M., Mellerio J.E., Ashton G.S.,
 RA Doppling-Hepensal P.J., Bady R.A., Jamil T., Phillips R.J.,
 RA Shabir S.G., Haroon T.S., Khurshid K., Moore J.E., Page B.,
 RA Darling J.A., Atherton D.J., Van Steensel M.A., Munro C.S., Smith F.J.,
 RA McGrath J.A.;
 RT "An unusual N-terminal deletion of the laminin (alpha)3a isoform leads
 RT to the chronic granulation tissue disorder laryngo-oncho-cutaneous
 RT syndrome";
 RT Hum. Mol. Genet. 12:2395-2409 (2003).
 RN [2]

RP SEQUENCE FROM N.A.
 RL McLean W.H.I. to the EMBL/GenBank/DBJ databases.
 RA Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AY327115; AA072570.1; .
 DR GO: GO:0005578; C:extracellular matrix (sensu Metazoa); IEA.
 DR GO: GO:0005606; C:laminin-1; IEA.
 DR GO: GO:0005102; F:receptor binding; IEA.
 DR GO: GO:0005198; F:structural molecule activity; IEA.
 DR GO: GO:0030334; P:regulation of cell adhesion; IEA.
 DR GO: GO:0030355; P:regulation of cell migration; IEA.
 DR GO: GO:0045595; P:regulation of embryonic development; IEA.
 DR InterPro: IPR001844; Chaprin Cpn60.
 DR InterPro: IPR008985; Cona like_1ec_g1.
 DR InterPro: IPR006209; EGF like.
 DR InterPro: IPR008979; Gal_bind_like.
 DR InterPro: IPR006210; IEGF.
 DR InterPro: IPR000034; Laminin_B.
 DR InterPro: IPR002049; Laminin_EGF.
 DR InterPro: IPR001791; Laminin_G.
 DR InterPro: IPR009254; Laminin_I.
 DR InterPro: IPR010307; Laminin_II.
 DR InterPro: IPR008211; Laminin_N.
 DR InterPro: IPR003129; TSP_N.
 DR Pfam: PF00052; Laminin_B; 1.
 DR Pfam: PF00053; Laminin_EGF; 8.
 DR Pfam: PF02210; Laminin_G; 2; 4.
 DR Pfam: PF06008; Laminin_I; 1.
 DR Pfam: PF06009; Laminin_II; 1.
 DR Pfam: PF00055; Laminin_N; 1.
 DR PRINTS: PR00011; EGF_LAMININ.
 DR ProDom: PD003031; Laminin_B; 1.
 DR SMART: SM00181; EGF; 8.
 DR SMART: SM00180; EGF_Lam; 14.
 DR SMART: SM00281; LamB; 1.
 DR SMART: SM00282; LamG; 5.
 DR SMART: SM00136; LamT; 1.
 DR PROSITE: PS00296; CHAPERONINS_CPN60; UNKNOWN_1.
 DR PROSITE: PS00022; EGF_1; 12.
 DR PROSITE: PS01186; EGF_2; 1.
 DR PROSITE: PS01248; LAMININ_TYPE_EGF; 13.
 DR PROSITE: PS00025; LAM_G_DOMAIN; 5.
 DR KMW: Laminin_EGF-like domain.
 DR SEQUENCE 3333 AA; 36646 MW; 9F99AF49B8EF27DD CRC64;

Query Match 76.2%; Score 852; DB 2; Length 3333;
 Best Local Similarity 76.6%; Pred. No. 4.ee-64;
 Matches 167; Conservative 18; Mismatches 33; Indels 0; Gaps 0;

QY 1 MKRLKTSGVVRLNDVGVTKKSEDMKLVRTASFSFGQMSFTNLDVPESTRFQLSRGF 60
 DB 2738 MKRLKTSGVVRLNDVGVTKKSEDMKLVRSASFSFGQLSTFDGLPTDHLQASFGF 2797
 QY 61 QTFQPSGTLNHOVTRTSSLVLTLEDGHIETSDSNPIPKSPQTVWDGLLHVSVISDT 120
 DB 2798 QTFQPSGTLNHOVTRTSSLVLTLEDGHIETSDSNPIPKSPQTVWDGLLHVSVISDN 2857
 QY 121 SGLRLIDQVLRNORLPSPFSAQSLRGGFECISNVLVORPSQSEVYLDLASKS 180
 DB 2858 SGLRLIDQVLRNORLPSPFSAQSLRGGFECISNVLVORPSQSEVYLDLASKS 180
 QY 181 TKRDASLGGGSLNKKPPIAMFKSPKRVNKRIRVNDL 218
 DB 2918 LKRDVSLGGGSLNKKPPIAMFKSPKRVNKRIRVNDL 2955

DE (Nicein alpha subunit).
 GN Name=LAMA3;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OC NCBI_Taxid=9606;
 [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Keratinocytes;
 RX MEDLINE=94357926; PubMed=8077230;
 RA Ryan M.C., Tizard R., Vandevanter D.R., Carter W.G.,
 RT "Cloning of the LAMA3 gene encoding the alpha 3 chain of the adhesive
 RT ligand epiligrin. Expression in wound repair.";
 RL J. Biol. Chem. 269:22779-22787(1994).
 RN [2]
 RP SEQUENCE OF 1-1331 FROM N.A. (ISOFORMS A AND B).
 RX MEDLINE=96163880; PubMed=8586427;
 RA Vidal F., Baudouin C., Miguel C., Galliano M.-F., Christiano A.M.,
 RA Vltio J., Ortonne J.-P., Meneguzzi G.,
 RT "Cloning of the laminin alpha 3 chain gene (LAMA3) and identification
 RT of a homozygous deletion in a patient with Herlitz junctional
 RT epidermolysis bullosa.";
 RL Genomics 30:273-280(1995).
 RN [3]
 RP DISBASE.
 RX PubMed=12915477; DOI=10.1093/hmg/ddg224;
 RA Irwin McLean W.H., Irvine A.D., Hamill K.J., Whitlock N.V.,
 RA Coleman-Campbell C.M., Mellerio J.E., Ashton G.S.,
 RA Dopping-Hepenstall P.J.H., Eady R.A.J., Jamali T., Phillips R.J.,
 RA Shabbir S.G., Haroon T.S., Khurehd K., Moore J.E., Page B.,
 RA Darling J., Atherton D.J., Van Steensel M.A.M., Munro C.S.,
 RA Smith F.J.D., McGrath J.A.,
 RT "An unusual N-terminal deletion of the laminin alpha3 isoform leads
 RT to the chronic granulation tissue disorder laryngo-oncho-cutaneous
 RT syndrome.";
 RL Hum. Mol. Genet. 12:2395-2409(2003).
 CC -1- FUNCTION: Binding to cells via a high affinity receptor, laminin
 CC is thought to mediate the attachment, migration and organization
 CC of cells into tissues during embryonic development by interacting
 CC with other extracellular matrix components.
 CC -1- FUNCTION: Laminin-5 is thought to be involved in (1) cell adhesion
 CC via integrin alpha-3/beta-1 in focal adhesion and integrin alpha-
 CC 6/beta-4 in hemidesmosomes, (2) signal transduction via tyrosine
 CC phosphorylation of p125-FAK and p80, (3) differentiation of
 CC keratinocytes.
 CC -1- SUBUNIT: Laminin is a complex glycoprotein, consisting of three
 CC different polypeptide chains (alpha, beta, gamma), which are bound
 CC to each other by disulfide bonds into a cross-shaped molecule
 CC comprising one long and three short arms with globules at each
 CC end. The alpha-3 chain is a subunit of laminin-5
 CC (epiligrin/kalinin/nicein), and possibly also a component of
 CC laminin-6 (K-laminin) and laminin-7 (KS-laminin).
 CC -1- SUBCELLULAR LOCATION: Extracellular; found in the basement
 CC membranes (major component).
 CC -1- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=2;
 CC Name=A;
 CC IsoId=Q16787-1; Sequence=Displayed;
 CC Name=B;
 CC IsoId=Q16787-2; Sequence=VSP_003037;
 CC Note=Incomplete sequence;
 CC -1- TISSUE SPECIFICITY: Skin; respiratory, urinary, and digestive
 CC epithelia and in other specialized tissues with prominent
 CC secretory or protective functions. Epithelial basement membrane,
 CC and epithelial cell tongue that migrates into a wound bed. A
 CC differential and focal expression of the alpha-3 chain is observed
 CC in the CNS.
 CC -1- INDUCTION: Laminin-5 is up-regulated in wound sites of human skin.
 CC -1- DOMAIN: The alpha-helical domains I and II are thought to interact
 CC with other laminin chains to form a coiled coil structure.
 CC -1- DOMAIN: Domain G is globular.
 CC -1- DISEASE: Defects in LAMA3 are a cause of junctional epidermolysis
 CC bullosa gravis (JEB) [MIM:226700]; also known as junctional

CC	epidermolysis bullosa Herlitz-Pearson type,JBH is a blistering disorder in skin that is characterized by a separation of basal cells from the basement membrane due to a decreased number of hemidesmosomes. Laminin-5 is missing from the basement membrane of patients with the gravus form of epidermolysis bullosa.
CC	-1 DISEASE: Defects in LAMA3 are the cause of laryngoconjunctiveus syndrome (LOCS) [MIM:245660]. LOCS is an autosomal recessive epithelial disorder confined to the Punjabi Maslin population. The condition is characterized by cutaneous erosions, nail dystrophy and exuberant vascular granulation tissue in certain epithelia,
CC	especially conjunctiva and larynx.
CC	-1 SIMILARITY: Contains 3 laminin EGF-like domains.
CC	-1 SIMILARITY: Contains 5 laminin G-like domains.
CC	-----
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).
CC	-----
DR	EMBL, L34155; AAA59483.1; -.
DR	EMBL, X85107; CA559428.1; -.
DR	EMBL, X85108; CA559429.1; -.
DR	PIR, A55347; A55347.
DR	HSSP, P02468; INPE.
DR	GeneW, HGNC:6483; LAMA3.
DR	MIM, 600805; -.
DR	MIM, 226700; -.
DR	MIM, 245660; -.
DR	GO, GO:0005604; C:basement membrane, TMS.
DR	GO, GO:0008544; F:epidermal differentiation, TMS.
DR	InterPro, IPR008985; ConA_like_deg_gl.
DR	InterPro, IPR006209; EGF like.
DR	InterPro, IPR009030; Grow_fac_recept.
DR	InterPro, IPR002049; Laminin_EGF.
DR	InterPro, IPR001791; Laminin_G.
DR	InterPro, IPR009254; Laminin_I.
DR	InterPro, IPR010307; Laminin_II.
DR	InterPro, IPR003129; TSP_N.
DR	pfam, PF00053; Laminin_EGF; 2.
DR	pfam, PF00054; Laminin_G; 2.
DR	pfam, PF06008; Laminin_I; 1.
DR	pfam, PF06009; Laminin_II; 1.
DR	PROSITE, PS00022; EGF_1; 1.
DR	PROSITE, PS01186; EGF_2; 1.
DR	PROSITE, PS01248; LAMININ TYPE EGF; 2.
DR	PROSITE, PS50025; LAM_G_DOMAIN; 5.
KM	Alternative splicing; Basement membrane; Cell adhesion; Coiled coil; Epidermolysis bullosa; Extracellular matrix; Glycoprotein;
KW	Laminin EGF-like domain; Repeat; Signal.
FT	SIGNAL 1 20 Potential.
FT	CHAIN 21 1713 Laminin alpha-3 chain.
FT	DOMAIN 46 201 Domain III A.
FT	DOMAIN 67 113 Laminin EGF-like 1.
FT	DOMAIN 114 166 Laminin EGF-like 2.
FT	DOMAIN 167 185 Laminin EGF-like 3 (incomplete).
FT	DOMAIN 186 769 Domain II and I.
FT	DOMAIN 770 971 Laminin G-like 1.
FT	DOMAIN 978 1140 Laminin G-like 2.
FT	DOMAIN 1147 1307 Laminin G-like 3.
FT	DOMAIN 1366 1530 Laminin G-like 4.
FT	DOMAIN 1537 1710 Laminin G-like 5.
FT	DOMAIN 231 327 Coiled coil (Potential).
FT	DOMAIN 396 548 Coiled coil (Potential).
FT	DOMAIN 594 621 Coiled coil (Potential).
FT	DOMAIN 702 765 Coiled coil (Potential).
FT	DOMAIN 1686 1713 Coiled coil (Potential).
FT	DISULFID 67 76 By similarity.
FT	DISULFID 69 83 By similarity.
FT	DISULFID 86 95 By similarity.
FT	DISULFID 98 111 By similarity.

FT	DISULFID	114	126	By similarity.
FT <th>DISULFID</th> <td>116</td> <td>135</td> <td>By similarity.</td>	DISULFID	116	135	By similarity.
FT <th>DISULFID</th> <td>137</td> <td>146</td> <td>By similarity.</td>	DISULFID	137	146	By similarity.
FT <th>DISULFID</th> <td>149</td> <td>164</td> <td>By similarity.</td>	DISULFID	149	164	By similarity.
FT <th>DISULFID</th> <td>202</td> <td>202</td> <td>Interchain (Probable).</td>	DISULFID	202	202	Interchain (Probable).
FT <th>DISULFID</th> <td>205</td> <td>205</td> <td>Interchain (Probable).</td>	DISULFID	205	205	Interchain (Probable).
FT <th>SITE</th> <td>658</td> <td>660</td> <td>Cell attachment site (Potential).</td>	SITE	658	660	Cell attachment site (Potential).
FT <th>CARBOHYD</th> <td>542</td> <td>542</td> <td>N-linked (GLNAC. . .) (Potential).</td>	CARBOHYD	542	542	N-linked (GLNAC. . .) (Potential).
FT <th>CARBOHYD</th> <td>645</td> <td>645</td> <td>N-linked (GLNAC. . .) (Potential).</td>	CARBOHYD	645	645	N-linked (GLNAC. . .) (Potential).
FT <th>CARBOHYD</th> <td>745</td> <td>745</td> <td>N-linked (GLNAC. . .) (Potential).</td>	CARBOHYD	745	745	N-linked (GLNAC. . .) (Potential).
FT <th>CARBOHYD</th> <td>882</td> <td>882</td> <td>N-linked (GLNAC. . .) (Potential).</td>	CARBOHYD	882	882	N-linked (GLNAC. . .) (Potential).
FT <th>CARBOHYD</th> <td>964</td> <td>964</td> <td>N-linked (GLNAC. . .) (Potential).</td>	CARBOHYD	964	964	N-linked (GLNAC. . .) (Potential).
FT <th>CARBOHYD</th> <td>1108</td> <td>1108</td> <td>N-linked (GLNAC. . .) (Potential).</td>	CARBOHYD	1108	1108	N-linked (GLNAC. . .) (Potential).
FT <th>CARBOHYD</th> <td>1131</td> <td>1131</td> <td>N-linked (GLNAC. . .) (Potential).</td>	CARBOHYD	1131	1131	N-linked (GLNAC. . .) (Potential).
FT <th>CARBOHYD</th> <td>1325</td> <td>1325</td> <td>N-linked (GLNAC. . .) (Potential).</td>	CARBOHYD	1325	1325	N-linked (GLNAC. . .) (Potential).
FT <th>CARBOHYD</th> <td>1477</td> <td>1477</td> <td>N-linked (GLNAC. . .) (Potential).</td>	CARBOHYD	1477	1477	N-linked (GLNAC. . .) (Potential).
FT <th>CARBOHYD</th> <td>1667</td> <td>1667</td> <td>N-linked (GLNAC. . .) (Potential).</td>	CARBOHYD	1667	1667	N-linked (GLNAC. . .) (Potential).
FT <th>VARSPLIC</th> <td>1</td> <td>45</td> <td>MGMLIRGALGCGITGVSSQOORVPFLQPGQSOLASLYE FRPS -> KYVSQGYTVOAKSPALPDGMVLEKKPDVOL TCQHMSTIYEITNPPRDLRHGRVHYEENPRHASSRAY SREKMLTAVSLADVRIGSLPYETQRLTLYSEGLERAST GSGRIALVAIRICACPPAYVADSC (in isoform B).</td>	VARSPLIC	1	45	MGMLIRGALGCGITGVSSQOORVPFLQPGQSOLASLYE FRPS -> KYVSQGYTVOAKSPALPDGMVLEKKPDVOL TCQHMSTIYEITNPPRDLRHGRVHYEENPRHASSRAY SREKMLTAVSLADVRIGSLPYETQRLTLYSEGLERAST GSGRIALVAIRICACPPAYVADSC (in isoform B).
FT <th>CONFLICT</th> <td>5</td> <td>5</td> <td>/Ftd=VSP_003037.</td>	CONFLICT	5	5	/Ftd=VSP_003037.
FT <th>CONFLICT</th> <td>123</td> <td>125</td> <td>W -> R (in Ref. 2).</td>	CONFLICT	123	125	W -> R (in Ref. 2).
FT <th>CONFLICT</th> <td>481</td> <td>481</td> <td>ATG -> GGC (in Ref. 2).</td>	CONFLICT	481	481	ATG -> GGC (in Ref. 2).
FT <th>CONFLICT</th> <td>754</td> <td>754</td> <td>M -> K (in Ref. 2).</td>	CONFLICT	754	754	M -> K (in Ref. 2).
FT <th>CONFLICT</th> <td>969</td> <td>969</td> <td>R -> L (in Ref. 2).</td>	CONFLICT	969	969	R -> L (in Ref. 2).
FT <th>CONFLICT</th> <td>1052</td> <td>1052</td> <td>E -> Q (in Ref. 2).</td>	CONFLICT	1052	1052	E -> Q (in Ref. 2).
FT <th>CONFLICT</th> <td>1184</td> <td>1184</td> <td>D -> A (in Ref. 2).</td>	CONFLICT	1184	1184	D -> A (in Ref. 2).
FT <th>CONFLICT</th> <td>1184</td> <td>1184</td> <td>G -> A (in Ref. 2).</td>	CONFLICT	1184	1184	G -> A (in Ref. 2).
FT <th>SEQUENCE</th> <td>1713 AA;</td> <td>189304 MM;</td> <td>45A9BE1017B6D3 CRC64;</td>	SEQUENCE	1713 AA;	189304 MM;	45A9BE1017B6D3 CRC64;
Query Match		76.0%;	Score 850;	DB 1;
Best Local Similarity		76.6%;	Pred. 80;	Length 1713;
Matches 167;	Conservative 18;	Mismatches 33;	Indels 0;	Gaps 0;
OY	1	MKNLKTSSGVRLNDVTGVTKKSGEDMKVYRTASFSFGQMSPTNLDVPESTDTRFQLSFGF	60	
DB	1118	MKNLKTSSGVRLNDVTGVTKKSGEDMKVYRTASFSFGQMSPTNLDVPESTDTRFQLSFGF	1177	
OY	61	QTFQPSGLTNHQRSTSLVLTLEDGHEIESTDSNPIPKSPQTYWDGLLHYVSI	120	
DB	1178	QTFQPSGLTNHQRSTSLVLTLEDGHEIESTDSNPIPKSPQTYWDGLLHYVSI	1237	
OY	121	SGRLRLIDDOVLRNRQRLPFSNAOQSLRGGHFEGCISNVLVQRFSSQSPVYLDA	180	
DB	1238	SGRLRLIDDOVLRNRQRLPFSNAOQSLRGGHFEGCISNVLVQRFSSQSPVYLDA	1297	
OY	181	TKDQASLGGGSLNPPFLMLFKSKPKRNRKGRINRVNOL	218	
DB	1298	LKRQVSLGGGSLNPPFLMLFKSKPKRNRKGRINRVNOL	1335	
RESULT 7				
096TGO	PRELIMINARY;	PRT;	1806 AA.	
AC	096TGO;			
DT	01-DEC-2001 (TREMBLREL_19, Created)			
DT	01-DEC-2001 (TREMBLREL_19, Last sequence update)			
DT	01-MAR-2004 (TREMBLREL_26, Last annotation update)			
DE	Alpha 3B chain of laminin-5 (fragment).			
GN	Name=LAMA3;			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	SEQUENCE FROM N.A.			
RA	Aberdam D., Vidal, Baudoin, Miguel, Ortonne, Mengusz;			
RL	Submitted (FEB-1995) to the EMBL/GenBank/DBJ databases.			
DR	EMBL; X84900; CA55925.1; -.			
DR	HSSP; P02468; INPE.			
DR	GO; GO:0005606; C:laminin-1; IEA.			

DR GO; GO:0005102; F:receptor binding; IEA.
 DR GO; GO:0005198; F:structural molecule activity; IEA.
 DR GO; GO:0005195; P:regulation of cell adhesion; IEA.
 DR GO; GO:0030334; P:regulation of cell migration; IEA.
 DR GO; GO:0045995; P:regulation of embryonic development; IEA.
 DR InterPro; IPR001844; Chaprin Cpn60.
 DR InterPro; IPR008985; Cona 1like_1ec_g1.
 DR InterPro; IPR006209; EGF like_1ec_g1.
 DR InterPro; IPR000034; laminin B.
 DR InterPro; IPR002049; laminin_EGF.
 DR InterPro; IPR001791; laminin_G.
 DR InterPro; IPR009254; laminin_I.
 DR InterPro; IPR010307; laminin_II.
 DR InterPro; IPR003129; TSP N.
 DR Pfam; PF00052; laminin_B_1.
 DR Pfam; PF00053; laminin_EGF_2.
 DR Pfam; PF02210; laminin_G_2; 4.
 DR Pfam; PF06008; laminin_I_1.
 DR Pfam; PF06009; laminin_II_1.
 DR ProDom; PD003031; laminin_B; 1.
 DR SMART; SM00180; EGF_Lam; 2.
 DR SMART; SM00281; EGF_Lam; 1.
 DR SMART; SM00282; LamG; 5.
 DR PROSITE; PS00296; CHAPERONINS_CPN60; UNKNOWN_1.
 DR PROSITE; PS00022; EGF_1; 2.
 DR PROSITE; PS01186; EGF_2; 1.
 DR PROSITE; PS01248; LAMININ_TYPE_EGF; 3.
 DR PROSITE; PS50025; LAM_G_DOMAIN; 5.
 DR Laminin EGF-like domain.
 FT NON TER 1 1
 SQ SEQUENCE 1806 AA; 199411 MW; 8P94CDE2A5A52B93 CRC64;

Query Match 76.0%; Score 850; DB 2; Length 1806;
 Best Local Similarity 76.6%; Pred. No. 3.2e-64;
 Matches 167; Conservative 18; Mismatches 33; Indels 0; Gaps 0;

QY 1 MKKLKTSGVVRLNDVTGVTKKCEDMKLVRTASFSRGGQMSFTNLDPSTDRFQLSFGF 60
 DB 1211 MKKLKTSGVVRLNDVTGVTKKCEDMKLVRSASFSGQUSFTDGLPPTDHLQASFGF 1270
 QY 61 QTFQPSGTLINHOQRTSSLVLTLEDGHIELSTRDSNIPFKSPQTYMDGLLHVSVISDT 120
 DB 1271 QTFQPSGTLINHOQRTSSLVLTLEDGHIELSTRDSNIPFKSPQTYMDGLLHVSVISDN 1330
 QY 121 SGLRLIDQVLRNRQRLBSFSAOQSLRLGGHFGECISNVLVQRFSSPEVLDLASKS 180
 DB 1331 SGLRLIDQVLRNRQRLBSFSAOQSLRLGGHFGECISNVLVQRFSSPEVLDLASKS 1390
 QY 181 TKKDAISGGCSLNKPPFLMFKSPKRFNKGRIPNVNOL 218
 DB 1391 LKRDVSLGGCSLNKPPFLMFKSPKRFNKGRIPNVNOL 1428

RESULT 8

ID Q76E14 PRELIMINARY; PRT; 3333 AA.
 AC Q76E14;
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 DE Laminin alpha 3b chain.
 GN Name=LAM3;
 OS Homo sapiens (human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
 OC NCBI_Taxid=9606;
 RN 1)
 RP SEQUENCE FROM N.A.
 RA Kariya Y., Yasuda C., Nakashima Y., Ishida K., Tsubota Y.,
 RA Miyazaki K.;
 RT "Characterization of laminin 5B and NH2-terminal proteolytic fragment
 of its alpha3b chain: promotion of cellular adhesion, migration, and
 proliferation.";

RL J. Biol. Chem. 279:24774-24784(2004).
 DR EMBL; AB107369; BAD13428.1; -
 DR GO; GO:0005578; C:extracellular matrix (sensu Metazoa); IEA.
 DR GO; GO:0005606; C:laminin-1; IEA.
 DR GO; GO:0005102; F:receptor binding; IEA.
 DR GO; GO:0005198; F:structural molecule activity; IEA.
 DR GO; GO:0030334; P:regulation of cell adhesion; IEA.
 DR GO; GO:0045995; P:regulation of embryonic development; IEA.
 DR InterPro; IPR001844; Chaprin Cpn60.
 DR InterPro; IPR008985; Cona 1like_1ec_g1.
 DR InterPro; IPR006209; EGF like.
 DR InterPro; IPR008979; Gal bind_1like.
 DR InterPro; IPR006210; IEGF.
 DR InterPro; IPR000034; laminin B.
 DR InterPro; IPR002049; laminin_EGF.
 DR InterPro; IPR001791; laminin_G.
 DR InterPro; IPR009254; laminin_I.
 DR InterPro; IPR010307; laminin_II.
 DR InterPro; IPR008211; laminin_N.
 DR InterPro; IPR003129; TSP N.
 DR Pfam; PF00052; laminin_B_1.
 DR Pfam; PF00053; laminin_EGF_8.
 DR Pfam; PF02210; laminin_G_2; 4.
 DR Pfam; PF06008; laminin_I_1.
 DR Pfam; PF06009; laminin_II_1.
 DR PRINTS; PR00011; EGF_LAMININ.
 DR ProDom; PD003031; laminin_B; 1.
 DR SMART; SM00181; EGF; 8.
 DR SMART; SM00180; EGF_Lam; 14.
 DR SMART; SM00281; LamE; 1.
 DR SMART; SM00282; LamG; 5.
 DR SMART; SM00136; LamNT; 1.
 DR PROSITE; PS00296; CHAPERONINS_CPN60; UNKNOWN_1.
 DR PROSITE; PS00022; EGF_1; 12.
 DR PROSITE; PS01186; EGF_2; 1.
 DR PROSITE; PS01248; LAMININ_TYPE_EGF; 13.
 DR PROSITE; PS50025; LAM_G_DOMAIN; 5.
 DR Laminin EGF-like domain.
 KW SEQUENCE 3333 AA; 366616 MW; 6F99A4D4B99FCB0 CRC64;

Query Match 76.0%; Score 850; DB 2; Length 3333;
 Best Local Similarity 76.6%; Pred. No. 6.9e-64;
 Matches 167; Conservative 18; Mismatches 33; Indels 0; Gaps 0;

QY 1 MKKLKTSGVVRLNDVTGVTKKCEDMKLVRTASFSRGGQMSFTNLDPSTDRFQLSFGF 60
 DB 2738 MKKLKTSGVVRLNDVTGVTKKCEDMKLVRSASFSGQUSFTDGLPPTDHLQASFGF 2797
 QY 61 QTFQPSGTLINHOQRTSSLVLTLEDGHIELSTRDSNIPFKSPQTYMDGLLHVSVISDT 120
 DB 2798 QTFQPSGTLINHOQRTSSLVLTLEDGHIELSTRDSNIPFKSPQTYMDGLLHVSVISDN 2857
 QY 121 SGLRLIDQVLRNRQRLBSFSAOQSLRLGGHFGECISNVLVQRFSSPEVLDLASKS 180
 DB 2858 SGLRLIDQVLRNRQRLBSFSAOQSLRLGGHFGECISNVLVQRFSSPEVLDLASKS 2917
 QY 181 TKKDAISGGCSLNKPPFLMFKSPKRFNKGRIPNVNOL 218
 DB 2918 LKRDVSLGGCSLNKPPFLMFKSPKRFNKGRIPNVNOL 2955

RESULT 9

ID Q867A1 PRELIMINARY; PRT; 1725 AA.
 AC Q867A1;
 DT 01-JUN-2003 (TrEMBLrel. 24, Created)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE Laminin alpha 3 (Fragment).
 OS Canis familiaris (Dog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

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OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OX NCB1_TaxID=9615;
RP SEQUENCE FROM N.A.
RA Spitzito F., Capt A., Guagnere F., Ortonne J.-P., Meneguzzi G.;
RL Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF236865; AAL54876.1; -.
DR HSSP; P11209; IG2C.
DR GO; GO:0005606; C:lamnin-1; IEA.
DR GO; GO:0005102; P:receptor binding; IEA.
DR GO; GO:0005198; P:structural molecule activity; IEA.
DR GO; GO:0030155; P:regulation of cell adhesion; IEA.
DR GO; GO:0030334; P:regulation of cell migration; IEA.
DR GO; GO:0045395; P:regulation of embryonic development; IEA.
DR InterPro; IPR008985; Cons like _lec_g1.
DR InterPro; IPR006209; EGF like.
DR InterPro; IPR002049; Laminin_EGF.
DR InterPro; IPR001791; Laminin_G.
DR InterPro; IPR009254; Laminin_I.
DR InterPro; IPR010307; Laminin_II.
DR InterPro; IPR003129; TSP N.
DR Pfam; PF00053; Laminin_EGF; 2.
DR Pfam; PF02210; Laminin_G_2; 4.
DR Pfam; PF06008; Laminin_I; 1.
DR Pfam; PF06009; Laminin_II; 1.
DR SMART; SM00282; LamG; 2.
DR SMART; SM00180; EGF; 5.
DR PROSITE; PS00022; EGF_1; 1.
DR PROSITE; PS01186; EGF_2; 1.
DR PROSITE; PS01248; LAMININ_TYPE_EGF; 2.
DR PROSITE; PS50025; LAM_G_DOMAIN; 5.
KW Laminin EGF-like domain.
FT NON_TER 1725 1725
SQ SEQUENCE 1725 AA; 191053 MW; DF71EB0E1FB5134C CRC64;

Query Match 68.0%; Score 760.5; DB 2; Length 1725;
Best Local Similarity 69.1%; Pred. No. 1.6e-56;
Matches 150; Conservative 20; Mismatches 46; Indels 1; Gaps 1;

QY 1 MKNLKTSGVRLNDVGVYTKKSEBWKLVRTASFSRGQMSFTNLDVSTDRFQLSFGF 60
DB 1129 MKNLKTTGVRLNDVGVYTKKSEBWKLVRSASFSDGQLRTGLDLPSEFQASFGG 1188

QY 61 QTFQPSGTLNHQRTSSLVLTLEDGHIELSTRDSNPIFKSPGTYMDGLLHHVYSIPT 120
DB 1189 QTFQPSGTLNHQRTSSLVLTLEDGHIELSTRDSNPIFKSPGTYMDGLLHHVYSIPT 1247

QY 121 SGRLIIDQVLRNRQLPSFSNAQOSLRIGGHPGECISNVLVQRPSPSEVLDLASKS 180
DB 1248 SGRLIIDQVLRNRQLPSFSNAQOSLRIGGHPGECISNVLVQRPSPSEVLDLASKS 1307

QY 181 TKKDALIGGCSLNKPPLMLFKSPKPKNGKIRFNVNO 217
DB 1308 FKRDVSLGGCSLNKPPLMLRKGSTRLNKSHFTNINO 1344

RESULT 10
Q91VVO PRELIMINARY; PRT; 1254 AA.
AC Q91VVO;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DB Lama4 protein (Fragment).
GN Name=Lama4;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCB1_TaxID=10090;
RN [1]
RC SEQUENCE FROM N.A.
MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
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RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins S.F., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diachenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares W.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Uebli T.B., Toshiyuki S., Carrinci P., Prange C.,
RA Raha S.S., Loquejano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulik S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Ramey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Gilmour J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzyminski M.I., Skalska U., Smallos D.E., Scherch A., Schein J.E.,
RA Jones S.J., Marra M.A.,
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=mix FVB/N; TISSUE=Mammary tumor;
RA Strausberg R.;
RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC008533; AA08533.1; -.
DR HSSP; O60675; IQUO.
DR MGJ; MGJ:109321; Lama4.
DR GO; GO:0005605; C:basal lamina; IDA.
DR GO; GO:0005615; C:extracellular space; TAS.
DR GO; GO:0001568; P:blood vessel development; IMP.
DR Pfam; PF02210; Laminin_G_2; 5.
DR Pfam; PF06009; Laminin_I; 1.
DR SMART; SM00282; LamG; 5.
DR PROSITE; PS50025; LAM_G_DOMAIN; 5.
FT NON_TER 1 1
SQ SEQUENCE 1254 AA; 139723 MW; 54D49EF76D37CD9 CRC64;

Query Match 18.2%; Score 204; DB 2; Length 1254;
Best Local Similarity 29.1%; Pred. No. 1.3e-08;
Matches 64; Conservative 35; Mismatches 99; Indels 22; Gaps 8;

QY 5 KKTSGVRLNDVGVYTKKSEBWKLVRTASFSRGQMSFTNLDVSTDRFQLSFGF 63
DB 642 KDFNLLEQTERLGVYGGCPEDSLISRAYFN--GQSFASIQKISFGDGFEGGNFRL 699

QY 64 QPSGTLNHQRTSSLVLTLEDGHIELSTRDSNPIFKSPGTYMDGLLHHVYSIPT 122
DB 700 QPSGTLNHQRTSSLVLTLEDGHIELSTRDSNPIFKSPGTYMDGLLHHVYSIPT 756

QY 123 LRLIIDQVLRNRQLPSFSNAQOS-----LRLGG-----GHPEGCISNVLVQRPSPQ 169
DB 757 YELVNDKSRLRKGN--PTKGRABQOTTEKKFPGSGSPISQYANFTGCISNAYFTRLDR 814

QY 170 SPEVLDLASKSTKKDALIGGCSLNKPPLMLFKSPKPKNGKIRFNVNO 209
DB 815 DVEVEDPQRYSEKVTSTLYECPIESSPLFLHKKGKNSK 854

RESULT 11
LMA4 MOUSE STANDARD; PRT; 1816 AA.
ID LMA4 MOUSE
AC P97927; O88785; P70409;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DB Laminin alpha-4 chain precursor.
GN Name=Lama4;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCB1_TaxID=10090;
RN [1]
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RP SEQUENCE FROM N.A., AND SEQUENCE OF 462-469; 478-483; 776-782 AND
 RP 940-945.
 RC SRRAIN-BALB/C; TISSUE=Endothelial cells;
 RX MEDLINE=97363207; PubMed=9219532;
 RA Frieber M., Noeckel H., Pausch F., Roeder C., Hahn A., Deutzmann R.,
 Sorokin L.M.;
 RT "Cloning of the mouse laminin alpha 4 cDNA. Expression in a subset of
 endothelium";
 RL Eur. J. Biochem. 246:727-735(1997).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Heart;
 RX MEDLINE=97202462; PubMed=9049981; DOI=10.1016/S0945-053X(96)90162-6;
 RA Liu J., Mayne R.;
 RT "The complete cDNA coding sequence and tissue-specific expression of
 the mouse laminin alpha 4 chain";
 RL Matrix Biol. 15:433-437(1996).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC SRRAIN-BALB/C;
 RX MEDLINE=98010627; PubMed=9346933; DOI=10.1074/jbc.272.44.27862;
 RA Iivanainen A., Korasmaa J., Sahberg C., Morita T., Bergmann U.,
 Thegeleif I., Trygvaeson K.;
 RT "Primary structure, developmental expression, and immunolocalization
 of the murine laminin alpha4 chain";
 RL J. Biol. Chem. 272:27862-27868(1997).
 RN [4]
 RP SEQUENCE OF 836-1106 FROM N.A.
 RC SRRAIN=ICR; TISSUE=Placenta;
 RX MEDLINE=97296337; PubMed=9151674; DOI=10.1083/jcb.137.3.685;
 RA Miner J.H., Patton B.L., Lentz S.I., Gilbert D.J., Snider W.D.,
 Jenkins N.A., Copeland N.G., Sane J.R.;
 RT "The laminin alpha chains: expression, developmental transitions, and
 chromosomal locations of alpha1-5, identification of heterotimeric
 laminins 8-11, and cloning of a novel alpha3 isoform";
 RL J. Cell Biol. 137:685-702(1997).
 RN [5]
 RP SEQUENCE OF 1467-1691 FROM N.A.
 RC TISSUE=Placenta;
 RX MEDLINE=97187457; PubMed=9034910;
 RA DOI=10.1002/(SICI)1096-9861(19970224)378:4<547::AID-CNE9>3.0.CO;2-2;
 RL Lentz S.I., Miner J.H., Sane J.R., Snider W.D.;
 RT "Distribution of the ten known laminin chains in the pathways and
 targets of developing sensory axons";
 RL J. Comp. Neurol. 378:547-561(1997).
 CC -1- FUNCTION: Binding to cells via a high affinity receptor, laminin
 is thought to mediate the attachment, migration and organization
 of cells into tissues during embryonic development by interacting
 with other extracellular matrix components.
 CC -1- SUBUNIT: Laminin is a complex glycoprotein, consisting of three
 different polypeptide chains (alpha, beta, gamma), which are bound
 to each other by disulfide bonds into a cross-shaped molecule
 comprising one long and three short arms with globules at each
 end.
 CC -1- SUBCELLULAR LOCATION: Extracellular; found in the basement
 membranes (major component).
 CC -1- TISSUE SPECIFICITY: Strongly expressed in peripheral nerves,
 cardiac muscle, fat, dermis, lung stroma, aortic endothelium,
 endocardium and endothelium of blood vessels in skin and brain.
 CC -1- DOMAIN: The alpha-helical domains I and II are thought to interact
 with other laminin chains to form a coiled coil structure.
 CC -1- DOMAIN: Domain G is globular.
 CC -1- SIMILARITY: Contains 4 laminin G-like domains.
 CC -1- SIMILARITY: Contains 5 laminin G-like domains.
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 entities requires a license agreement (See <http://www.ebi.ac.uk/announcements>
 or send an email to license@ebi.ac.uk).

DR EMBL; U58950; ABA41840.1; -
 DR EMBL; Y09827; CAA70970.1; -
 DR EMBL; U59865; AAC24725.1; -
 DR EMBL; U86352; AAC3178.1; -
 DR HSSB; U69176; AAC52982.1; -
 DR HSSB; P02468; INPE.
 DR MGI; MGI:109321; Lama4.
 DR GO; GO:0005604; C:basement membrane; IDA.
 DR InterPro; IPR008985; CoIL_1like_rec_1.
 DR InterPro; IPR006209; EGF-like.
 DR InterPro; IPR009030; Grow_fac_recept.
 DR InterPro; IPR002049; Laminin_EGF.
 DR InterPro; IPR001791; Laminin_G.
 DR InterPro; IPR009254; Laminin_I.
 DR InterPro; IPR010307; Laminin_II.
 DR InterPro; IPR003129; TSP_N.
 DR Pfam; PF00054; Laminin_EGF_3.
 DR Pfam; PF00053; Laminin_G_4.
 DR Pfam; PF06008; Laminin_I_1.
 DR Pfam; PF06009; Laminin_II_1.
 DR PROSITE; PS00022; EGF_1; UNKNOWN 1.
 DR PROSITE; PS01248; LAMININ_TYPE_EGF_3.
 DR PROSITE; PS50025; LAM G DOMAIN; 5.
 KW Basement membrane; Cell adhesion; Coiled coil;
 KW Direct protein sequencing; Extracellular matrix; Glycoprotein;
 KW Laminin EGF-like domain; Repeat; Signal.
 KM Laminin EGF-like domain; Repeat; Signal.
 FT SIGNAL 1 24
 FT CHAIN 1 1816
 FT DOMAIN 82 131 Laminin alpha-4 chain.
 FT DOMAIN 132 186 Laminin EGF-like 1.
 FT DOMAIN 187 240 Laminin EGF-like 2.
 FT DOMAIN 241 255 Laminin EGF-like 3.
 FT DOMAIN 256 825 Laminin EGF-like 4 (incomplete).
 FT DOMAIN 826 1030 Domain II and I.
 FT DOMAIN 1042 1222 Laminin G-like 1.
 FT DOMAIN 1229 1397 Laminin G-like 2.
 FT DOMAIN 1462 1633 Laminin G-like 3.
 FT DOMAIN 1640 1813 Laminin G-like 4.
 FT DOMAIN 431 523 Laminin G-like 5.
 FT DOMAIN 556 604 Coiled coil (Potential).
 FT DOMAIN 655 717 Coiled coil (Potential).
 FT DOMAIN 770 799 Coiled coil (Potential).
 FT SITE 717 719 Cell attachment site (Potential).
 FT DISULFID 82 91 By similarity.
 FT DISULFID 84 98 By similarity.
 FT DISULFID 101 110 By similarity.
 FT DISULFID 113 129 By similarity.
 FT DISULFID 132 146 By similarity.
 FT DISULFID 134 155 By similarity.
 FT DISULFID 157 166 By similarity.
 FT DISULFID 169 184 By similarity.
 FT DISULFID 187 202 By similarity.
 FT DISULFID 189 209 By similarity.
 FT DISULFID 212 221 By similarity.
 FT DISULFID 224 236 By similarity.
 FT DISULFID 266 266 Interchain (Probable).
 FT DISULFID 269 269 Interchain (Probable).
 FT CARBOHYD 104 104 N-linked (GlcNAc...)
 FT CARBOHYD 104 104 N-linked (GlcNAc...)
 FT CARBOHYD 215 215 N-linked (GlcNAc...)
 FT CARBOHYD 308 308 N-linked (GlcNAc...)
 FT CARBOHYD 333 333 N-linked (GlcNAc...)
 FT CARBOHYD 458 458 N-linked (GlcNAc...)
 FT CARBOHYD 550 550 N-linked (GlcNAc...)
 FT CARBOHYD 571 571 N-linked (GlcNAc...)
 FT CARBOHYD 574 574 N-linked (GlcNAc...)
 FT CARBOHYD 631 631 N-linked (GlcNAc...)
 FT CARBOHYD 639 639 N-linked (GlcNAc...)
 FT CARBOHYD 735 735 N-linked (GlcNAc...)
 FT CARBOHYD 751 751 N-linked (GlcNAc...)
 FT CARBOHYD 754 754 N-linked (GlcNAc...)
 FT CARBOHYD 780 780 N-linked (GlcNAc...)
 FT CARBOHYD 803 803 N-linked (GlcNAc...)
 FT CARBOHYD 1086 1086 N-linked (GlcNAc...)


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FT CARBOHYD 1283 1283 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 1361 1361 N-linked (GlcNAc...) (Potential).
FT CONFLICT 8 8 C->S (in Ref. 2).
FT CONFLICT 18 18 C->Y (in Ref. 2).
FT CONFLICT 248 248 C->R (in Ref. 3).
FT CONFLICT 297 297 G->A (in Ref. 3).
FT CONFLICT 431 431 THR->HIS (in Ref. 2).
FT CONFLICT 679 679 S->C (in Ref. 3).
FT CONFLICT 703 703 D->G (in Ref. 2).
FT CONFLICT 706 706 N->H (in Ref. 2).
FT CONFLICT 728 728 K->R (in Ref. 2).
FT CONFLICT 730 730 F->I (in Ref. 2).
FT CONFLICT 779 779 R->G (in Ref. 1; AA sequence).
FT CONFLICT 810 810 R->S (in Ref. 3).
FT CONFLICT 865 865 AEP->QT (in Ref. 2).
FT CONFLICT 936 936 K->E (in Ref. 3).
FT CONFLICT 970 970 L->V (in Ref. 3).
FT CONFLICT 1132 1132 H->R (in Ref. 3).
FT CONFLICT 1200 1200 F->I (in Ref. 2).
FT CONFLICT 1382 1382 D->A (in Ref. 2).
FT CONFLICT 1413 1414 NS->EF (in Ref. 1).
FT CONFLICT 1489 1489 A->S (in Ref. 2).
SO SEQUENCE 1816 AA; 201818 MW; B49C45F3A45999D8 CRC64;

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Query Match 18.2%; Score 204; DB 1; Length 1816;
Best Local Similarity 29.1%; Pred. No. 2e-08;
Matches 64; Conservative 35; Mismatches 99; Indels 22; Gaps 8;

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QY 5 KKTSGVRLNDVYGVKCKSEDKLVRTASFSRGCGMSPFND-VSTDRFQSLSPQRF 63
DB 1204 KQFNLEBOTETLVGVGCEBLSIRRYFN--GQSFLASIQKISFFGEGGFNRTL 1261
QY 64 QPSGTLNQTSTSLVTLDEGHIELSPDSNIPFKSPGTMDGLHH-VSVIDSTSG 122
DB 1262 QPVGGLFYTSSGSDVSIENCTVMDYK--GIKMSIDKQVHDLPHRYVTSIDTR- 1318
QY 123 LRLIIDQVLRNRNRLPSFNSNAQS-----LRLGG-----GHREGCISNVLVQRF 169
DB 1319 YELVVKSLRGRGN--PTKGRKAEQOTTEKKFYFGSGSPISQYANFTGCSINAYFTRLDR 1376
QY 170 SPVPLDLASKSTYKCKASLGCCSLNKPPLMLPKSPKRFK 209
DB 1377 DVEVEDPQRYSEKVTSLYCEPLSSPLFLHKKGNSSK 1416

```

RESULT 12

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ID LAMA4_HUMAN STANDARD; PRT; 1816 AA.
AC Q16363; Q14735; Q15335; Q9UB18; Q9UJN9;
DT 01-NOV-1997 (Rel. 35, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Laminin alpha-4 chain precursor.
GN Name=LAMA4;
OS Homo sapiens (human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Fetal Lung;
RX MEDLINE=95300971; PubMed=7781776; DOI=10.1016/0014-5793(95)00462-1;
RA Iivanainen A., Sainio K., Sariola H., Tryggvason K.;
RT "Primary structure and expression of a novel human laminin alpha 4
chain.";
RL FEBS Lett. 365:183-188(1995).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Heart;
RX MEDLINE=97454279; PubMed=9310354;
RA Richards A.J., Lucatini C., Pope F.M.;
RT "The structural organisation of LAMA4, the gene encoding laminin
alpha4.";

```

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RL Eur. J. Biochem. 248:15-23(1997).
RN [3]
RP SEQUENCE OF 236-1816 FROM N.A.
RC TISSUE=Heart;
RX MEDLINE=95048381; PubMed=7959779;
RA Richards A.J., Al-Imara L., Carter N.P., Lloyd J.C., Leversha M.A.,
RA Pope F.M.;
RT "Localization of the gene (LAMA4) to chromosome 6q21 and isolation of
a partial cDNA encoding a variant laminin A chain.";
RL Genomics 22:237-239(1994).
RN [4]
RP SEQUENCE OF 66-1816 FROM N.A.
RL Tubby B.;
CC Submitted (MAR-1998) to the EMBL/Genbank/DBJ databases.
CC -1- FUNCTION: Binding to cells via a high affinity receptor, laminin
is thought to mediate the attachment, migration and organization
of cells into tissues during embryonic development by interacting
with other extracellular matrix components.
CC -1- SUBUNIT: Laminin is a complex glycoprotein, consisting of three
different polypeptide chains (alpha, beta, gamma), which are bound
to each other by disulfide bonds into a cross-shaped molecule
comprising one long and three short arms with globules at each
end.
CC -1- SUBCELLULAR LOCATION: Extracellular; found in the basement
membranes (major component).
CC -1- TISSUE SPECIFICITY: In adult, strong expression in heart, lung,
ovary small and large intestines, placenta, liver; weak or no
expression in skeletal muscle, kidney, pancreas, testis, prostate,
brain. High expression in fetal lung and kidney. Expression in
fetal and newborn tissues is observed in certain mesenchymal cells
in tissues such as smooth muscle and dermis.
CC -1- DOMAIN: The alpha-helical domains I and II are thought to interact
with other laminin chains to form a coiled coil structure.
CC -1- DOMAIN: Domain G is globular.
CC -1- SIMILARITY: Contains 4 laminin EGF-like domains.
CC -1- SIMILARITY: Contains 5 laminin G-like domains.
CC -1- CAUTION: Gene LAMA4 was formerly called LAMA3.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
between the Swiss Institute of Bioinformatics and the EMBL outstation -
the European Bioinformatics Institute. There are no restrictions on its
use by non-profit institutions as long as its content is in no way
modified and this statement is not removed. Usage by and for commercial
entities requires a license agreement (see http://www.isb-sib.ch/announce/
or send an email to license@sib-sib.ch).
CC -----
DR EMBL, S78569; AA334635.1; -.
DR EMBL, X91171; CA62596.1; -.
DR EMBL, Y14240; CA74636.1; -.
DR EMBL, X76939; CA54258.1; -.
DR EMBL, Z99289; NOT_ANNOTATED_CDS.
DR PIR, S68960; S68960.
DR HSPF, P02468; INPE.
DR Genew; HGNC:6484; LAMA4.
DR MIM; 600133; -.
DR GO; GO:0005605; C:basal lamina; TAS.
DR GO; GO:0005201; F:extracellular matrix structural constituent; TAS.
DR InterPro; IPR008985; CoLA-like_1ec_g1.
DR InterPro; IPR006209; EGF-like.
DR InterPro; IPR002049; Laminin_BGF.
DR InterPro; IPR001791; Laminin_G.
DR InterPro; IPR009254; Laminin_I.
DR InterPro; IPR010307; Laminin_II.
DR InterPro; IPR003129; TSP_N.
DR Pfam; PF00053; Laminin_EGF; 3.
DR Pfam; PF00054; Laminin_G; 3.
DR Pfam; PF06008; Laminin_I; 1.
DR Pfam; PF06009; Laminin_II; 1.
DR PROSITE; PS00022; EGF_1; UNKNOWN 1.
DR PROSITE; PS50025; LAM_G_DOMAIN; 5.
DR PROSITE; PS01248; LAMININ_TYRP_EGF; 3.
KW Basement membrane; Cell adhesion; Coiled coil; Extracellular matrix;
KW Glycoprotein; Laminin EGF-like domain; Repeat; Signal.

```


FT SIGNAL 1 24 Potential.
 FT CHAIN 25 1816 laminin alpha-4 chain.
 FT DOMAIN 82 131 laminin EGF-like 1.
 FT DOMAIN 132 186 laminin EGF-like 2.
 FT DOMAIN 187 240 laminin EGF-like 3.
 FT DOMAIN 241 255 laminin EGF-like 4 (incomplete).
 FT DOMAIN 256 825 Domain II and I.
 FT DOMAIN 826 1028 laminin G-like 1.
 FT DOMAIN 1040 1220 laminin G-like 2.
 FT DOMAIN 1227 1395 laminin G-like 3.
 FT DOMAIN 1462 1633 laminin G-like 4.
 FT DOMAIN 1640 1813 laminin G-like 5.
 FT DOMAIN 1813 396 Coiled coil (Potential).
 FT DOMAIN 396 521 Coiled coil (Potential).
 FT DOMAIN 521 607 Coiled coil (Potential).
 FT DOMAIN 607 717 Coiled coil (Potential).
 FT DOMAIN 717 799 Coiled coil (Potential).
 FT DOMAIN 799 91 Cell attachment site (Potential).
 FT SITE 717 719 By similarity.
 FT DISULFID 82 98 By similarity.
 FT DISULFID 84 98 By similarity.
 FT DISULFID 101 110 By similarity.
 FT DISULFID 113 129 By similarity.
 FT DISULFID 132 146 By similarity.
 FT DISULFID 134 155 By similarity.
 FT DISULFID 157 166 By similarity.
 FT DISULFID 169 184 By similarity.
 FT DISULFID 187 202 By similarity.
 FT DISULFID 189 209 By similarity.
 FT DISULFID 212 221 By similarity.
 FT DISULFID 224 238 By similarity.
 FT DISULFID 266 266 Interchain (Probable).
 FT DISULFID 269 269 Interchain (Probable).
 FT CARBOHYD 104 104 N-linked (GlcNAc).
 FT CARBOHYD 104 104 N-linked (GlcNAc).
 FT CARBOHYD 215 215 N-linked (GlcNAc).
 FT CARBOHYD 308 308 N-linked (GlcNAc).
 FT CARBOHYD 458 458 N-linked (GlcNAc).
 FT CARBOHYD 524 524 N-linked (GlcNAc).
 FT CARBOHYD 550 550 N-linked (GlcNAc).
 FT CARBOHYD 571 571 N-linked (GlcNAc).
 FT CARBOHYD 574 574 N-linked (GlcNAc).
 FT CARBOHYD 631 631 N-linked (GlcNAc).
 FT CARBOHYD 639 639 N-linked (GlcNAc).
 FT CARBOHYD 735 735 N-linked (GlcNAc).
 FT CARBOHYD 751 751 N-linked (GlcNAc).
 FT CARBOHYD 754 754 N-linked (GlcNAc).
 FT CARBOHYD 780 780 N-linked (GlcNAc).
 FT CARBOHYD 803 803 N-linked (GlcNAc).
 FT CARBOHYD 1086 1086 N-linked (GlcNAc).
 FT CARBOHYD 1281 1281 N-linked (GlcNAc).
 FT CARBOHYD 1359 1359 N-linked (GlcNAc).
 FT CARBOHYD 1411 1411 N-linked (GlcNAc).
 FT CARBOHYD 1411 1411 A -> P (in Ref. 1).
 FT CARBOHYD 143 143 L -> F (in Ref. 1).
 FT CARBOHYD 178 178 G -> GMDCTIS (in Ref. 4).
 FT CARBOHYD 265 265 D -> A (in Ref. 4).
 FT CARBOHYD 276 276 Y -> H (in Ref. 2 and 3).
 FT CARBOHYD 491 491 T -> P (in Ref. 1).
 FT CARBOHYD 1057 1057 SGR -> GGP (in Ref. 4).
 FT CARBOHYD 1110 1112
 FT CARBOHYD 1816 AA, 201908 MW, 04E9AF379A0FAAD CRC64;
 SQ SEQUENCE

Query Match 16.7%; Score 187, DB 1, Length 1816;
 Best Local Similarity 28.3%; Pred. No. 6e-07;
 Matches 62, Conservative 34, Mismatches 103, Indels 20, Gaps 8;

QY 5 KKTSGVRLNDYVTGKSGEDWLVTAFAFRGQGSFTNLD-VPTDRFQSLFQFQTF 63
 DB 1202 KQPNLEQETETGVGCEPDSLSIRAFYN--GQFISISIQKISFDFEGGFNRTL 1259
 QY 64 QPSGTLNHTQRTSLVLTEDGHILSTRDSNIPFKSGFTYMDGLHHVSVISDTGSL 123
 DB 1260 QPNGLLFFYVAGSDVFSISLDNGTVIMDK--GIKIVQSVDKQVNDGISHF--VYSSVSPT 1315
 QY 124 R--LLLD-DQVLRNQLPFSNAQSLR---LGG-----GHFECISNVLVQRSSQS 170

DB 1316 RYELIYDKSKVSGKNFTKGIETQASSEKFFYRGSPISAOYANFPGCISNAVFYVDRD 1375
 QY 171 PEVLDAKSTKQASLGGCSLKPPLMLFKSPKPKFNK 209
 DB 1376 VEVEDFORVTEKVTSLYECPRISSPLFLHKKKNLSK 1414

RESULT 13
 ID QBR3Y7 PRELIMINARY; PRT; 794 AA.
 AC QBR3Y7;
 DT 01-JUN-2002 (TrEMBLrel. 21, Created)
 DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Lama5 protein (Fragment).
 GN Name=Lama5;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CZECH II; TISSUE=Mammary tumor;
 RX MEDLINE=2238257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Bueltow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marsina K., Farmer A.A., Rubin G.W., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Schetz T.E.,
 RA Brownstein M.J., Ueda T.B., Tomihata S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Muliyil S.J.,
 RA Bosak S.A., McMan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hultk S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Raey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
 RA Krzywinski M.I., Skalek U., Smaluk D.E., Schnerch A., Schein J.E.,
 RA Jones S.J., Matra M.A.;
 RT "generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CZECH II; TISSUE=Mammary tumor;
 RA Strausberg R.,
 RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC020313; AAH20313.1; -.
 DR HSSP; Q14393; IH30.
 DR MGD; MGI:105382; Lama5.
 DR GO; GO:0005604; C:basement membrane; IDA.
 DR GO; GO:0005615; C:extracellular space; TMS.
 DR GO; GO:0005178; F:protein binding; IDA.
 DR GO; GO:0005515; F:protein binding; IPI.
 DR GO; GO:0001763; P:branching morphogenesis; IDA.
 DR GO; GO:0030324; P:lung development; IMP.
 DR GO; GO:0007517; P:muscle development; IMP.
 DR InterPro; IPR008965; Cona_like_1ec_91.
 DR InterPro; IPR001791; Laminin_G.
 DR InterPro; IPR003129; TSP_N.
 DR Pfam; PF02210; Laminin_G_2; 4.
 DR SMART; SM00282; LamG; 4.
 DR PROSITE; PSS0025; LamG_DOMAIN; 4.
 FT NON_TER 1
 SQ SEQUENCE 794 AA; 86936 MW; 5316391F38E5662C CRC64;

Query Match 16.6%; Score 186, DB 2, Length 794;
 Best Local Similarity 29.2%; Pred. No. 2.6e-07;
 Matches 59, Conservative 34, Mismatches 91, Indels 18, Gaps 6;

Oy		MKLLKTSQSVRLNDVGVGLKKCSBWKLVFTASRSRGGSFNTLDV-PSTDRFQLSFG	59
Dd	174	IKALGKYVDLKRLLN-TTGISFGCTADLLGRMTTFHGHEFLPALPDVAPTTEVTYSFGF	233
Oy	60	FOTFOBSGTLINHQRTSSILVLTLEDGHTELSTRDSNIPIFKSPGYMDGLAHVSVID	119
Dd	233	FRGTQDNMLLYRTPSDPGFYQSIRAGHTLAFPMGEV---ETQVFPADGA PHYA PYSN	289
Oy	120	TSGRLRLIID--QVLRRNQRLPSFSNAQ-----OSLRLG-----GHPEGCISNVLYOR	166
Dd	290	VTVGMVLVYDDQDLQVLVSHERTPEMLOLQEERPSRLILGGLPVSYGFNFHNSGCISNVFOR	349
Oy	167	FQSOSPEYLDIASKTSKKDASIG	188
Dd	350	LREGPQRFVEDLHNMGSVNVSVG	371
 RESULT 14 O6ZOAI PRELIMINARY; PRT; 1524 AA.			
ID	O6ZOAI		
AC	O6ZOAI;		
DT	05-JUL-2004 (TrEMBLrel. 27, Created)		
DT	05-JUL-2004 (TrEMBLrel. 27, Last sequence update)		
DT	05-JUL-2004 (TrEMBLrel. 27, last annotation update)		
DE	MKIAA0533 protein (Fragment).		
CN	Name=MKIAA0533;		
OS	Mus musculus (Mouse).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
CC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.		
OX	NCBI_TaxId=10099;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RC	TISSUE=Embryonic tail;		
RX	PubMed=14621295;		
RA	Okazaki N., Kikuno R., Ohara R., Inamoto S., Koseki H., Hiraoaka S.,		
SA	Saga Y., Nagase T., Ohara O., Koga H.;		
RT	"Prediction of the coding sequences of mouse homologues of KIA gene:		
RT	III, the complete nucleotide sequences of 500 mouse KIAA-homologous		
RT	cDNAs identified by screening of terminal sequences of cDNA clones		
RL	randomly sampled from size-fractionated libraries.";		
RNA	Seq. 10:167-180(2003).		
DR	EMBL: AK129157; BAC97967.2; -		
DR	GO: GO:0005604; C:bassment membrane; IDA.		
DR	GO: GO:0005615; C:extracellular space; TAS.		
DR	GO: GO:0005178; F:integrin binding; IDA.		
DR	GO: GO:0005515; F:protein binding; IPI.		
DR	GO: GO:0001763; P:branching morphogenesis; IDA.		
DR	GO: GO:0030324; P:lung development; IMP.		
DR	GO: GO:007517; P:muscle development; IMP.		
DR	InterPro: IPRO06985; Cona like_1ec_g1.		
DR	InterPro: IPRO06209; EGF like.		
DR	InterPro: IPRO09303; Grow fac recept.		
DR	InterPro: IPRO02049; Laminin_EGF.		
DR	InterPro: IPRO01791; laminin_G.		
DR	InterPro: IPRO09254; laminin_I.		
DR	InterPro: IPRO10307; laminin_II.		
DR	InterPro: IPRO01368; TNFR_c6-		
DR	InterPro: IPRO03129; TSP_N.		
DR	Pfam: PF00053; Laminin_EGF; 2.		
DR	Pfam: PF02210; Laminin_G_2; 4.		
DR	Pfam: PF06008; Laminin_I; 1.		
DR	Pfam: PF06009; Laminin_II; 1.		
DR	PRINTS: PR00011; EGF_LAMININ.		
DR	SMART: SMO0180; EGF_Lam; 2.		
DR	SMART: SMO0282; LamG; 5.		
DR	PROSITE: PS00022; EGF_1; UNKNOWN_3.		
DR	PROSITE: PS01248; LAMININ_TYRE_EGF; UNKNOWN_1.		
DR	PROSITE: PSS0025; LAM G DOMAIN; 5.		
DR	PROSITE: PS00652; TNFR_NGFR_1; UNKNOWN_1.		
KW	Laminin EGF-like domain.		
PT	NON_TER	1	
FT	NON_TER	1524	1524
SEQ	SEQUENCE	1524 AA; 166516 MW; FA3411828FF0E691 CRC64;	

	Query March	16.6%	Score 186;	DB 2:	Length 1524;
	Best Similarity	29.2%	Pred. No. 5.8e-07;		
	Match Local	59;	Conservative 34;	Mismatches 91;	Indels 18; Gaps 6;
OY	1 MKNLKTSGVRLNDVTGVTKKCSBDMKLVTAASFSRQGMSPFNLDV-PSTDRFOLSPG	59			
Dd	IKALGGKYDLKRNL-TGISIFGCTADLLVGRTWTFHGHGFPLPLPDPVAPITBVVYSSEFG	989			
OY	60 FQTQPSSGTLANHQTRRSSLLVTEEDGHIETSDSNIPRKSPGTWDGLIHHVSVD	119			
Dd	990 FRGTQDNNLTLYRRSPGPVCVSRREGIVTLRFNMOEV---ETORVPADGAPHYAFAYSN	1046			
OY	120 TSGRLILDD--GYLRNRQLPSPSMNQ-----QSRLRG-----GHFECCISNVLCOR	166			
Dd	1047 VTGWVLVDDQQLGVLSHERTTPEMLQLCPPEPSRIILGGLEFVSGTFFNFSGCISNVFOR	1106			
OY	167 FSQSPENVLDLASKSTKKDASIG	188			
Dd	1107 LRGPQVFDFLHQNMGSVVAVSIVG	1128			
	RESULT 15				
ID	LMA5_MOUSE	STANDARD;	PRF,	3718 AA.	
AC	061001; O3JHO6;				
DT	01-NOV-1997 (Rel. 35, Created)				
DT	28-FEB-2003 (Rel. 41, Last sequence update)				
DT	05-JUL-2004 (Rel. 44, Last annotation update)				
DE	Laminin alpha-5 chain precursor.				
GN	Name=Lama5;				
OS	Mus musculus (Mouse).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC	Mammalia; Butheraia; Rodentia; Sciurognathi; Muridae; Murinae; Mus.				
OX	NCBI_TaxID=10090;				
RN	[1]				
RP	SEQUENCE OF 1-92 FROM N.A., AND SEQUENCE OF 41-46.				
RX	MEDLINE=21816471; PubMed=11829758; DOI=10.1042/0264-6021.3620213;				
RA	Garbe J.H., Gehring W., Mann K., Timml R., Sasaki T.;				
RT	"Complete sequence, recombinant analysis and binding to laminins and				
RT	sulphated ligands of the N-terminal domains of laminin alpha3b and				
RL	alphas chains.";				
RN	Biochem. J. 362:213-221(2002).				
RN	[2]				
RP	SEQUENCE OF 84-3718 FROM N.A.				
RX	STRAIN=C57BL/6 X CBA; TISSUE=lung;				
RC	MEDLINE=96081906; PubMed=749364; DOI=10.1074/jbc.270.48.28523;				
RA	Miner J.H., Lewis R.M., Sanes J.R.;				
RT	"Molecular cloning of a novel laminin chain, alpha 5, and widespread				
RT	expression in adult mouse tissues.";				
RL	J Biol. Chem. 270:28523-28526(1995).				
RN	[3]				
RP	REVATIONS.				
RP	Miner J.H., Lewis R.M., Sanes J.R.;				
RL	Submitted (NOV-1997) to the EMBL/Genebank/DBJ databases.				
CC	-1- FUNCTION: Binding to cells via a high affinity receptor, laminin				
CC	is thought to mediate the attachment, migration and organization				
CC	of cells into tissues during embryonic development by interacting				
CC	with other extracellular matrix components. Alpha-5 chain may be				
CC	the major laminin alpha chain of adult epithelial and/or				
CC	endothelial basal laminae.				
CC	-1- SUBUNIT: Laminin is a complex glycoprotein, consisting of three				
CC	different polypeptide chains (alpha, beta, gamma), which are bound				
CC	to each other by disulfide bonds into a cross-shaped molecule				
CC	comprising one long and three short arms with globules at each				
CC	end.				
CC	-1- SUBCELLULAR LOCATION: Extracellular; found in the basement				
CC	membranes (major component).				
CC	-1- TISSUE SPECIFICITY: In adult, high levels in heart, lung, and				
CC	kidney; lower in brain, muscle and testis; very low in liver, gut				
CC	and skin. Expressed in many tissues in embryonic day 11.				
CC	-1- DOMAIN: The alpha-helical domains I and II are thought to interact				
CC	with other laminin chains to form a coiled coil structure.				

```
CC -1- DOMAIN: Domains VI, IV and G are globular.
CC -1- SIMILARITY: Contains 22 laminin EGF-like domains.
CC -1- SIMILARITY: Contains 5 laminin G-like domains.
CC -1- SIMILARITY: Contains 2 laminin IV domains.
CC -1- SIMILARITY: Contains 1 laminin N-terminal domain.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.1sb-sib.ch/announce/
CC or send an email to license@1sb-sib.ch).
CC -----
CC EMBL, AJ293593; CAB9255.1; -.
CC EMBL, U37501; AAC3430.1; -.
CC PIR, T10053; T10053.
CC HSSP, P02468; 1NPE.
CC MGD, MGI:105382; Lama5.
CC GO, GO:0005604; C:basement membrane; IDA.
CC GO, GO:0005178; F:integrin binding; IDA.
CC GO, GO:000515; F:protein binding; IPT.
CC GO, GO:0001763; P:branching morphogenesis; IDA.
CC GO, GO:0030324; P:lung development; IMP.
CC GO, GO:007517; P:muscle development; IMP.
CC InterPro, IPR008985; Cona_like_1ec_g1.
CC InterPro, IPR006209; EGF_like.
CC InterPro, IPR008979; Gal_bind_like.
CC InterPro, IPR009030; Grow_fac_recept.
CC InterPro, IPR000034; Laminin_B.
CC InterPro, IPR001791; Laminin_G.
CC InterPro, IPR009254; Laminin_I.
CC InterPro, IPR010307; Laminin_II.
CC InterPro, IPR008211; Laminin_N.
CC InterPro, IPR008212; Lam_N2.
CC InterPro, IPR003129; TSP_N.
CC Pfam, PF00052; Laminin_B_1.
CC Pfam, PF00053; Laminin_B_17.
CC Pfam, PF00054; Laminin_G_2.
CC Pfam, PF06008; Laminin_I_1.
CC Pfam, PF06009; Laminin_II_1.
CC Pfam, PF00055; Laminin_N_1.
CC PRINTS, PRO0011; EGF_LAMININ.
CC ProDom, PD003031; Laminin_B_1.
CC PROSITE, PS00022; EGF_1; 19.
CC PROSITE, PS01186; EGF_2; 3.
CC PROSITE, PS01248; LAMININ_TYPE_EGF_19.
CC PROSITE, PS50025; LAM_G_DOMAIN_5.
CC Basement membrane, Cell adhesion, Coiled coil,
CC Direct protein sequencing, Extracellular matrix, Glycoprotein,
CC Laminin EGF-like domain; Repeat; Signal.
CC -----
FT CHAIN 1 3718 laminin alpha-5 chain.
FT SIGNAL 41 40 laminin N-terminal (domain VI).
FT DOMAIN 305 363 laminin EGF-like 1.
FT DOMAIN 364 433 laminin EGF-like 2.
FT DOMAIN 434 479 laminin EGF-like 3.
FT DOMAIN 500 546 laminin EGF-like 4.
FT DOMAIN 547 592 laminin EGF-like 5.
FT DOMAIN 593 637 laminin EGF-like 6.
FT DOMAIN 638 682 laminin EGF-like 7.
FT DOMAIN 683 728 laminin EGF-like 8.
FT DOMAIN 729 781 laminin EGF-like 9.
FT DOMAIN 782 833 laminin EGF-like 10.
FT DOMAIN 834 855 laminin EGF-like 11.
FT DOMAIN 856 1442 laminin EGF-like 12. (incomplete).
FT DOMAIN 1443 1488 laminin EGF-like 13.
FT DOMAIN 1489 1532 laminin EGF-like 14.
FT DOMAIN 1533 1581 laminin EGF-like 15.
FT DOMAIN 1582 1632 laminin EGF-like 16.
FT DOMAIN 1633 1642 laminin EGF-like 16 (N-terminal).
FT DOMAIN 1643 1631 laminin domain IV 2 (domain IV A).
FT DOMAIN 1832 1864 laminin EGF-like 16 (C-terminal).
FT DOMAIN 1865 1914 laminin EGF-like 17.
FT DOMAIN 1915 1970 laminin EGF-like 18.
FT DOMAIN 1971 2024 laminin EGF-like 19.
FT DOMAIN 2025 2071 laminin EGF-like 20.
FT DOMAIN 2072 2118 laminin EGF-like 21.
FT DOMAIN 2119 2168 laminin EGF-like 22.
FT DOMAIN 2169 2735 Domain II and I.
FT DOMAIN 2736 2933 laminin G-like 1.
FT DOMAIN 2947 3119 laminin G-like 2.
FT DOMAIN 3128 3296 laminin G-like 3.
FT DOMAIN 3337 3511 laminin G-like 4.
FT DOMAIN 3518 3689 laminin G-like 5.
FT DOMAIN 2205 2257 Coiled coil (Potential).
FT DOMAIN 2330 2464 Coiled coil (Potential).
FT DOMAIN 2604 2621 Coiled coil (Potential).
FT DOMAIN 2639 2705 Coiled coil (Potential).
FT DOMAIN 1723 1725 Cell attachment site (Potential).
FT SITE 1839 1841 Cell attachment site (Potential).
FT SITE 305 314 By similarity.
FT DISUPID 307 327 By similarity.
FT DISUPID 329 338 By similarity.
FT DISUPID 341 361 By similarity.
FT DISUPID 364 373 By similarity.
FT DISUPID 366 398 By similarity.
FT DISUPID 401 410 By similarity.
FT DISUPID 413 431 By similarity.
FT DISUPID 434 445 By similarity.
FT DISUPID 436 452 By similarity.
FT DISUPID 454 463 By similarity.
FT DISUPID 466 476 By similarity.
FT DISUPID 500 512 By similarity.
FT DISUPID 502 521 By similarity.
FT DISUPID 523 532 By similarity.
FT DISUPID 535 544 By similarity.
FT DISUPID 547 559 By similarity.
FT DISUPID 549 566 By similarity.
FT DISUPID 568 577 By similarity.
FT DISUPID 580 590 By similarity.
FT DISUPID 593 605 By similarity.
FT DISUPID 595 611 By similarity.
FT DISUPID 613 622 By similarity.
FT DISUPID 625 635 By similarity.
FT DISUPID 638 650 By similarity.
FT DISUPID 640 656 By similarity.
FT DISUPID 658 667 By similarity.
FT DISUPID 670 680 By similarity.
FT DISUPID 683 695 By similarity.
FT DISUPID 685 702 By similarity.
FT DISUPID 704 713 By similarity.
FT DISUPID 716 726 By similarity.
FT DISUPID 1443 1455 By similarity.
FT DISUPID 1445 1462 By similarity.
FT DISUPID 1464 1473 By similarity.
FT DISUPID 1476 1486 By similarity.
FT DISUPID 1533 1548 By similarity.
FT DISUPID 1535 1555 By similarity.
FT DISUPID 1557 1566 By similarity.
FT DISUPID 1569 1579 By similarity.
FT DISUPID 1582 1594 By similarity.
FT DISUPID 1584 1601 By similarity.
FT DISUPID 1603 1612 By similarity.
FT DISUPID 1615 1630 By similarity.
FT DISUPID 1865 1874 By similarity.
FT DISUPID 1867 1891 By similarity.
FT DISUPID 1884 1893 By similarity.
FT DISUPID 1896 1912 By similarity.
FT DISUPID 1915 1930 By similarity.
FT DISUPID 1917 1939 By similarity.
FT DISUPID 1941 1950 By similarity.
FT DISUPID 1953 1968 By similarity.
FT DISUPID 1971 1986 By similarity.
FT DISUPID 1973 1993 By similarity.
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FT	DISULFID	1996	2005	By similarity.
FT	DISULFID	2008	2022	By similarity.
FT	DISULFID	2072	2083	By similarity.
FT	DISULFID	2074	2090	By similarity.
FT	DISULFID	2092	2101	By similarity.

Query Match 16.6%; Score 186; DB 1; Length 3718;
 Best Local Similarity 29.2%; Pred. No. 1.8e-06;
 Matches 59; Conservative 34; Mismatches 91; Indels 18; Gaps 6;

Qy	1	MKNLKKTSGVRLNDVGVTKKCEMDKLVRTAFSRGGQMSFTNLDV-PSTDRFQLSPG	59
Db	3098	IKRLGKYVDLKRIN-TTGISFGCTADLVGRITFHGHGFLPALPDVAPITEVVTSGFG	3156
Qy	60	PQTFQPSGTLNQHRTSSILVTLBDGHIELSTRDSNIPFKSPGTMDGLHHVSVISD	119
Db	3157	FRGTQNNLLYRTSPDPYQVSLRSGHTLRFMNGEV---ETQRYFADGAPHYVAFYFN	3213
Qy	120	TSGLRLLID--QVLRNQRLPSFSNAQ---QSLRLG-----GHFEGCISNVLVOR	166
Db	3214	VTGVMLYVDQQLVKSHERITPMLQLQPEEPSRLILGGILPVSGTFHNFSGCISNVEYOR	3273
Qy	167	FSQSPFVLDLASKSTKQASIG	188
Db	3274	LRGPRVFPDLHQMGSVNVSVG	3295

Search completed: February 22, 2005, 08:24:24
 Job time : 37.8842 secs

CC line produces and secretes recombinant heterotrimeric laminin, whereas

CC prior art cell lines have been created that produce but do not secrete
CC only one or two chain laminins
XX
SQ Sequence 1694 AA;

Query Match 100.0%; Score 1118; DB 3; Length 1694;
Best Local Similarity 100.0%; Pred. No. 2.1e-123;
Matches 218; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MNLLKKTSGVRLNDVGVTKKCEEDMKLVRTASFSRGQMSFTNLDPSTDRFOLSGF 60
DB 1098 MNLLKKTSGVRLNDVGVTKKCEEDMKLVRTASFSRGQMSFTNLDPSTDRFOLSGF 1157
QY 61 QTFQPSGTLNMQRTSSILVTLDEGHIELSTRDSNIPFSPGTYMDGLHRSV1SDT 120
DB 1158 QTFQPSGTLNMQRTSSILVTLDEGHIELSTRDSNIPFSPGTYMDGLHRSV1SDT 1217
QY 121 SGLRLIIDQVLRNRQLPFSFNAQOSLRIGGHEGCIISNVLVGRFSQSPVLDLASKS 180
DB 1218 SGLRLIIDQVLRNRQLPFSFNAQOSLRIGGHEGCIISNVLVGRFSQSPVLDLASKS 1277
QY 181 TKKDAISLGCSLNKPPFLMLFKSPKRFNKGRIFFNNOL 218
DB 1278 TKKDAISLGCSLNKPPFLMLFKSPKRFNKGRIFFNNOL 1315

RESULT 2

AAB48460
ID AAB48460 standard; protein; 1725 AA.

AC AAB48460;

DT 02-MAR-2001 (first entry)

DE Rat laminin 5 polypeptide, SEQ ID NO: 10.

XX Rat; laminin 5; vulnery; antilucer; antinflammatory; antidiabetic;
XX cell adhesion promoter; wound healing; ulcers; burn; skin graft;
XX periodontitis; gingivitis; Type I diabetes; angiogenesis regulation.
OS Rattus norvegicus.

PN WO200066731-A2.

PD 09-NOV-2000.

PF 28-APR-2000; 2000MO-US011459.

PR 30-APR-1999; 99US-0131720P.

PR 21-AUG-1999; 99US-0149738P.

PR 24-SEP-1999; 99US-0155945P.

PA (BIOS-) BIOSTATUM INC.

PI Boutaud A;

DR WPI; 2000-687538/67.

DR N-PSDB; AAC83721.

PT Laminin 5-expressing cells, used to accelerate wound healing associated
PT with diabetic foot ulcers, venous ulcers, pressure sores, skin surgery,
PT burns, acute wounds and skin grafts.
XX
XX
PS Claim 3; Page 104-109; 232pp; English.

CC The present sequence is a laminin 5 chain polypeptide. Recombinant
CC laminin 5-expressing cells are used to accelerate wound healing,
CC especially diabetic foot ulcers, venous ulcers, pressure sores, skin
CC surgery, burns, acute wounds, skin grafts, corneal ulcerations, gastro-
CC intestinal ulcers, periodontitis, and gingivitis. They are also used to
CC improve the biocompatibility of medical devices, and to promote cell
CC adhesion to a surface. They can be used for the ex vivo treatment of Type
CC I diabetes. Laminin can also be used to regulate angiogenesis. The cell

CC line produces and secretes recombinant heterotrimeric laminin, whereas
CC prior art cell lines have been created that produce but do not secrete
CC only one or two chain laminins
XX

SQ Sequence 1725 AA;

Query Match 100.0%; Score 1118; DB 3; Length 1725;
Best Local Similarity 100.0%; Pred. No. 2.1e-123;
Matches 218; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MNLLKKTSGVRLNDVGVTKKCEEDMKLVRTASFSRGQMSFTNLDPSTDRFOLSGF 60
DB 1129 MNLLKKTSGVRLNDVGVTKKCEEDMKLVRTASFSRGQMSFTNLDPSTDRFOLSGF 1188
QY 61 QTFQPSGTLNMQRTSSILVTLDEGHIELSTRDSNIPFSPGTYMDGLHRSV1SDT 120
DB 1189 QTFQPSGTLNMQRTSSILVTLDEGHIELSTRDSNIPFSPGTYMDGLHRSV1SDT 1248
QY 121 SGLRLIIDQVLRNRQLPFSFNAQOSLRIGGHEGCIISNVLVGRFSQSPVLDLASKS 180
DB 1249 SGLRLIIDQVLRNRQLPFSFNAQOSLRIGGHEGCIISNVLVGRFSQSPVLDLASKS 1308
QY 181 TKKDAISLGCSLNKPPFLMLFKSPKRFNKGRIFFNNOL 218
DB 1309 TKKDAISLGCSLNKPPFLMLFKSPKRFNKGRIFFNNOL 1346

RESULT 3

AAB48459
ID AAB48459 standard; protein; 1693 AA.

AC AAB48459;

DT 02-MAR-2001 (first entry)

DE Human laminin 5 polypeptide, SEQ ID NO: 8.

XX Human; laminin 5; vulnery; antilucer; antinflammatory; antidiabetic;
XX cell adhesion promoter; wound healing; ulcers; burn; skin graft;
XX periodontitis; gingivitis; Type I diabetes; angiogenesis regulation.
OS Homo sapiens.

PN WO200066731-A2.

PD 09-NOV-2000.

PF 28-APR-2000; 2000MO-US011459.

PR 30-APR-1999; 99US-0131720P.

PR 21-AUG-1999; 99US-0149738P.

PR 24-SEP-1999; 99US-0155945P.

PA (BIOS-) BIOSTATUM INC.

PI Boutaud A;

DR WPI; 2000-687538/67.

DR N-PSDB; AAC83720.

PT Laminin 5-expressing cells, used to accelerate wound healing associated
PT with diabetic foot ulcers, venous ulcers, pressure sores, skin surgery,
PT burns, acute wounds and skin grafts.
XX
XX
PS Claim 3; Page 91-97; 232pp; English.

CC The present sequence is a laminin 5 chain polypeptide. Recombinant
CC laminin 5-expressing cells are used to accelerate wound healing,
CC especially diabetic foot ulcers, venous ulcers, pressure sores, skin
CC surgery, burns, acute wounds, skin grafts, corneal ulcerations, gastro-
CC intestinal ulcers, periodontitis, and gingivitis. They are also used to
CC improve the biocompatibility of medical devices, and to promote cell
CC adhesion to a surface. They can be used for the ex vivo treatment of Type

CC I diabetes. Laminin can also be used to regulate angiogenesis. The cell
 CC line produces and secretes recombinant heterotrimeric laminin, whereas
 CC prior art cell lines have been created that produce but do not secrete
 CC only one or two chain laminins
 XX
 SQ Sequence 1693 AA;

Query Match 76.0%; Score 850; DB 3; Length 1693;
 Best Local Similarity 76.6%; Pred. No. 2.6e-91;
 Matches 167; Conservative 18; Mismatches 33; Indels 0; Gaps 0;

QY 1 MKNLKTSQVRLNDVGVTKKCEDEKLVRTASFSRGGOMSPFTNLDVSTDFQSLSGF 60
 DB 1098 MKNLKTSQVRLNDVGVTKKCEDEKLVRSASFSRGGOLSTFDGLPPTDHLQASFGF 1157
 QY 61 QTFQPSGTLNHQTRTSSLVLTLEDGHIETLSTDSNIPFKSPGTMDGLLHVSVISDT 120
 DB 1158 QTFQPSGTLNHQTRTSSLVLTLEDGHIETLSTDSNIPFKSPGTMDGLLHVSVISDN 1217
 QY 121 SGRLILDDQVLRNRQLRPSNAQSLRLGGHFECCISNVLYORFQSPFVLDLASKS 180
 DB 1218 SGRLILDDQVLRNRQLRPSNAQSLRLGGHFECCISNVLYORFQSPFVLDLASKS 1277
 QY 181 TKKDAISLGGCSLNKPPFLMLFKSPKRFNKGRIFNVNQL 218
 DB 1278 LKRDVSLGGCSLNKPPFLMLFKSPKRFNKGRIFNVNQL 1315

RESULT 4

AAB48457
 ID AAB48457 standard; protein; 1693 AA.

AC AAB48457;

DT 02-MAR-2001 (first entry)

DE Human laminin 5 polypeptide, SEQ ID NO: 4.

KW Human; laminin 5; vulneryary; antiulcer; antiinflammatory; antidiabetic;
 cell adhesion promoter; wound healing; ulcers; burn; skin graft;

KM periodontitis; gingivitis; Type I diabetes; angiogenesis regulation.

OS Homo sapiens.

PN WO200066731-A2.

PD 09-NOV-2000.

PF 28-APR-2000; 2000MO-US011459.

PR 30-APR-1999; 99US-0131720P.

PR 21-AUG-1999; 99US-0149738P.

PR 24-SEP-1999; 99US-0155945P.

PA (BIOS-) BIOSTATUM INC.

PI Boutaud A;

DR WPI; 2000-687538/67.

DR N-PSDB; AAC83718.

PT Laminin 5-expressing cells, used to accelerate wound healing associated
 with diabetic foot ulcers, venous ulcers, pressure sores, skin surgery,
 burn, acute wounds and skin grafts.

PS Claim 3; Page 66-71; 232pp; English.

CC The present sequence is a laminin 5 chain polypeptide. Recombinant
 CC laminin 5-expressing cells are used to accelerate wound healing,
 CC especially diabetic foot ulcers, venous ulcers, pressure sores, skin
 CC surgery, burns, acute wounds, skin grafts, corneal ulcerations, gastro-
 CC intestinal ulcers, periodontitis, and gingivitis. They are also used to
 CC improve the biocompatibility of medical devices, and to promote cell

CC adhesion to a surface. They can be used for the ex vivo treatment of Type
 CC I diabetes. Laminin can also be used to regulate angiogenesis. The cell
 CC line produces and secretes recombinant heterotrimeric laminin, whereas
 CC prior art cell lines have been created that produce but do not secrete
 CC only one or two chain laminins
 XX
 SQ Sequence 1693 AA;

Query Match 76.0%; Score 850; DB 3; Length 1693;
 Best Local Similarity 76.6%; Pred. No. 2.6e-91;
 Matches 167; Conservative 18; Mismatches 33; Indels 0; Gaps 0;

QY 1 MKNLKTSQVRLNDVGVTKKCEDEKLVRTASFSRGGOMSPFTNLDVSTDFQSLSGF 60
 DB 1098 MKNLKTSQVRLNDVGVTKKCEDEKLVRSASFSRGGOLSTFDGLPPTDHLQASFGF 1157
 QY 61 QTFQPSGTLNHQTRTSSLVLTLEDGHIETLSTDSNIPFKSPGTMDGLLHVSVISDT 120
 DB 1158 QTFQPSGTLNHQTRTSSLVLTLEDGHIETLSTDSNIPFKSPGTMDGLLHVSVISDN 1217
 QY 121 SGRLILDDQVLRNRQLRPSNAQSLRLGGHFECCISNVLYORFQSPFVLDLASKS 180
 DB 1218 SGRLILDDQVLRNRQLRPSNAQSLRLGGHFECCISNVLYORFQSPFVLDLASKS 1277
 QY 181 TKKDAISLGGCSLNKPPFLMLFKSPKRFNKGRIFNVNQL 218
 DB 1278 LKRDVSLGGCSLNKPPFLMLFKSPKRFNKGRIFNVNQL 1315

RESULT 5

AAR70148
 ID AAR70148 standard; protein; 1713 AA.

AC AAR70148;

DT 25-MAR-2003 (revised)

DT 05-OCT-1995 (first entry)

DE Deduced sequence of cDNA corresp. to the alpha-3BPA transcript.

KW E170; epithelial ligand glycoprotein; epiligrin complex;
 epithelial cell binding.

KM Homo sapiens.

PN WO9506660-A1.

PD 09-MAR-1995.

PF 02-SEP-1994; 94MO-US010261.

PR 02-SEP-1993; 93US-00115918.

PA (HUTC-) HUTCHINSON CANCER RES CENT FRID.

PI Carter WG, Gil SG, Ryan MC;

DR WPI; 1995-115398/15.

DR N-PSDB; AAQ83236.

PT New nucleic acid encoding epiligrin, an epithelial ligand complex - also
 PT related vectors, transformed cells, proteins and antibodies, useful
 PT therapeutically and diagnostically, e.g., in cases of inflammation and to
 PT induce cancer cell differentiation.

PS Claim 12; Fig 15A-F; 187pp; English.

CC AAQ83235 depicts the nt. sequence compiled from sequencing cDNA clones
 CC corresp. to the alpha-3 BPA transcript. The invention includes nt
 CC sequences in the gp. comprising the nt sequence shown in AAQ83235, the
 CC cDNA clone Bp-1 (ATCC No. 75540) shown in AAQ83234, the cDNA clone 1-1
 CC (ATCC No. 75539), and the cDNA clone 8-6 (ATCC No. 75538), or the nt.
 CC sequences shown in AAQ83236. The entire nt region encoding E170 is

CC depicted in AA083236, and corresp. to the SQ of alpha-3. AA083236
CC consists of a composite sequence derived from several overlapping clones.
CC A synthetic polypeptide of at least 5 AAs that corresp. to part or all of
CC the nt. sequence shown in AA083236 is claimed. (Updated on 25-MAR-2003 to
CC correct PN field.)
XX
SQ Sequence 1713 AA;

Query Match 76.0%; Score 850; DB 2; Length 1713;
Best Local Similarity 76.6%; Pred. No. 2.6e-91;
Matches 167; Conservative 18; Mismatches 33; Indels 0; Gaps 0;

QY 1 MKNLKTSGVRLNDVTGVTKKCSDEWKLVRNLSFRGGQMSFTNLDVSTDRFQLSFGF 60
DB 1118 MKNLKTSGVRLNDVTGVTKKCSDEWKLVRNLSFRGGQMSFTNLDVSTDRFQLSFGF 1177
QY 61 QTFQPSGTLNHTQRTSSLLVTLDEGHIELSTDSNIPFKSGPTMDGLHNVSVISDT 120
DB 1178 QTFQPSGTLNHTQRTSSLLVTLDEGHIELSTDSNIPFKSGPTMDGLHNVSVISDN 1237
QY 121 SGLRLIDQVLRNRQLPSFSNAQSLRLGGHREGCISNVLYORFSGSPREVLDAASKS 180
DB 1238 SGLRLIDQVLRNRQLPSFSNAQSLRLGGHREGCISNVLYORFSGSPREVLDAASKS 1297
QY 181 TKQDASLGCGSLNKPPLMLFKSPKRPNGRIFFNVNQL 218
DB 1298 LKRDVSLGGCSLNKPPLMLFKSGTRFNTKTFRINQL 1335

RESULT 6
AAB48458
ID AAB48458 standard; protein; 1713 AA.
XX
AC AAB48458;
XX

DT 02-MAR-2001 (first entry)
XX

DE Human laminin 5 polypeptide, SEQ ID NO: 6.
XX

KM Human; laminin 5; vulnereary; antiulcer; antiinflammatory; antidiabetic;
cell adhesion promoter; wound healing; ulcer; burn; skin graft;
KM periodontitis; gingivitis; type I diabetes; angiogenesis regulation.
XX

OS Homo sapiens.
XX

PN WO200066731-A2.
XX

PD 09-NOV-2000.
XX

PF 28-APR-2000; 2000WO-US011459.
XX

PR 30-APR-1999; 99US-0131720P.
XX

PR 21-AUG-1999; 99US-0149738P.
XX

PR 24-SEP-1999; 99US-0155945P.
XX

PA (BIO-) BIOSTARTUM INC.
XX

PI Boutaud A;
XX

PI WPI; 2000-687538/67.
XX

DR N-PSDB; AAC83719.
XX

XX Laminin 5-expressing cells, used to accelerate wound healing associated
PT with diabetic foot ulcers, venous ulcers, pressure sores, skin surgery,
PT burns, acute wounds and skin grafts.
XX

PS Claim 3; Page 79-84; 232pp; English.
XX

CC The present sequence is a laminin 5 chain polypeptide. Recombinant
CC laminin 5-expressing cells are used to accelerate wound healing,
CC especially diabetic foot ulcers, venous ulcers, pressure sores, skin
CC surgery, burns, acute wounds, skin grafts, corneal ulcerations, gastro-
CC intestinal ulcers, periodontitis, and gingivitis. They are also used to

CC Improve the biocompatibility of medical devices, and to promote cell
CC adhesion to a surface. They can be used for the ex vivo treatment of Type
CC I diabetes. Laminin can also be used to regulate angiogenesis. The cell
CC line produces and secretes recombinant heterotimeric laminin, whereas
CC prior art cell lines have been created that produce but do not secrete
CC only one or two chain laminins
XX
SQ Sequence 1713 AA;

Query Match 76.0%; Score 850; DB 3; Length 1713;
Best Local Similarity 76.6%; Pred. No. 2.6e-91;
Matches 167; Conservative 18; Mismatches 33; Indels 0; Gaps 0;

QY 1 MKNLKTSGVRLNDVTGVTKKCSDEWKLVRNLSFRGGQMSFTNLDVSTDRFQLSFGF 60
DB 1118 MKNLKTSGVRLNDVTGVTKKCSDEWKLVRNLSFRGGQMSFTNLDVSTDRFQLSFGF 1177
QY 61 QTFQPSGTLNHTQRTSSLLVTLDEGHIELSTDSNIPFKSGPTMDGLHNVSVISDT 120
DB 1178 QTFQPSGTLNHTQRTSSLLVTLDEGHIELSTDSNIPFKSGPTMDGLHNVSVISDN 1237
QY 121 SGLRLIDQVLRNRQLPSFSNAQSLRLGGHREGCISNVLYORFSGSPREVLDAASKS 180
DB 1238 SGLRLIDQVLRNRQLPSFSNAQSLRLGGHREGCISNVLYORFSGSPREVLDAASKS 1297
QY 181 TKQDASLGCGSLNKPPLMLFKSPKRPNGRIFFNVNQL 218
DB 1298 LKRDVSLGGCSLNKPPLMLFKSGTRFNTKTFRINQL 1335

RESULT 7
ABR92102
ID ABR92102 standard; protein; 1713 AA.
XX
AC ABR92102;
XX

DT 10-SEP-2003 (first entry)
XX

DE Human cervical cancer cell marker encoding cDNA SEQ ID NO:113.
XX

KM Human; cervical cancer; cervical cancer marker; cancer therapy;
KM detection; gene therapy; vaccine.
XX

OS Homo sapiens.
XX

PN WO2002101075-A2.
XX

PD 19-DEC-2002.
XX

PF 12-JUN-2002; 2002WO-US018638.
XX

PR 13-JUN-2001; 2001US-0298155P.
XX

PR 13-JUN-2001; 2001US-0298155P.
XX

PR 14-NOV-2001; 2001US-0335936P.
XX

PA (MILL-) MILLENNIUM PHARM INC.
XX

PI Schlegel R, Chen Y, Zhao X, Monahan JB, Kamatkar S;
XX

PI Gamavara M, Glatt K, Hoersch S;
XX

DR WPI; 2003-156967/15.
XX

DR N-PSDB; ACF12884.
XX

XX New isolated nucleic acid molecule useful for detecting, characterizing,
PT preventing and treating human cervical cancers, in various prognostic and
PT diagnostic assays, in pharmacogenomics and in monitoring clinical trials.
XX

PS Claim 4; Page 269-273; 386pp; English.
XX

CC ACF12884 to ACF1947 encode the human cervical cancer marker proteins (I)
CC given in ABR92047 to ABR92164. A higher level of expression of (I) than
CC normal indicates the presence of cervical cancer. Also described: (1) a
CC vector (II) containing (I); (2) a host cell (III) containing (I); and (3)

CC assessing (M1) whether a patient is afflicted with cervical cancer,
CC comprising comparing the level of expression of a marker in a patient's
CC sample, and the normal level of expression of the marker in a control non
CC cervical cancer sample, where a significant increase in the level of
CC expression of the marker in the patient's sample relative to that in the
CC control sample is an indication that the patient is afflicted with
CC cervical cancer. (1) has cytostatic activity, and can be used in gene
CC therapy and in vaccines. (1) is useful in detecting, characterizing,
CC preventing and treating human cervical cancers. (1) may also be used in
CC various prognostic and diagnostic assays, pharmacogenomics and in
CC monitoring clinical trials

SQ Sequence 1713 AA;

Query Match 76.0%; Score 850; DB 6; Length 1713;

Best Local Similarity 76.6%; Pred. No. 2.6e-91;

Matches 167; Conservative 18; Mismatches 33; Indels 0; Gaps 0;

QY 1 MKNLKKTSGVRLNDVGVTKKSEBWKLVRTASFSFGQMSFTNLDVSTDFPQLSFGF 60
DB 1118 MKNLKKTSGVRLNDVGVTKKSEBWKLVRSASFSFGQLSTFDGLPPTDHLQASFGF 1177
QY 61 QTFPSGTLNHQTRTSLSLVTLEDGHIELSTRDSNIPFKSPQTYMDGLHHVSVISPT 120
DB 1178 QTFPSGTLNHQTRTSLSLVTLEDGHIELSTRDSNIPFKSPQTYMDGLHHVSVISDN 1237
QY 121 SGRLRIDQVLRNRQLPSFSAQSLRIGGHEGECISNVLVORFSQSPFVLDLASKS 180
DB 1238 SGRLRIDQVLRNRQLPSFSAQSLRIGGHEGECISNVLVORFSQSPFVLDLTSNS 1297
QY 181 TKKDAALGGCSLNKPPFLMFKSPKRNKRIFNVNOL 218
DB 1298 LKRDVSLGGCSLNKPPFLMFKSTRFNKTFRINOL 1335

RESULT 8

ADD29904 standard; protein; 1713 AA.

ID ADD29904

AC ADD29904;

DE 15-JAN-2004 (first entry)

XX Human laminin alpha 3 seq id 2.

XX ophthalmological; dermatological; laminin alpha 3; G3 domain;
XX cell adhesion function; cell movement effect; epithelial tissue function;
XX retinal detachment; cosmetic surgery; skin graft; human.

OS Homo sapiens.

PN JP2003093064-A.

PD 02-APR-2003.

PF 20-SEP-2001; 2001JP-00287519.

PR 20-SEP-2001; 2001JP-00287519.

PA (KAGA-) KAGAKU GIUTTSU SHINKO JIGYODAN.

DR (KIHA-) ZH KIHARA KINEN YOKOHAMA SEIMEI KAGAKU.

XX WPI, 2003-817304/77.

XX N-PSDB; ADD29903.

XX Novel modified G3 domain of laminin alpha 3 chain useful for controlling
XX cell adhesion and cell movement.

PS Claim 1; SEQ ID NO 2; 49pp; Japanese.

CC The invention describes a modified laminin alpha3 chain comprising one or
CC more amino acid deletions, substitutions or additions at region
CC corresponding to a region of G3 domain having amino acids 1214-1324 of

CC laminin alpha3 chain having a fully defined sequence of 1713 amino acids
CC as given in the specification. (1) can control cell adhesion function and
CC cell movement effect. A composition comprising laminin is useful for
CC maintaining or treating the function of epithelial tissue and for
CC treatment or prevention of retinal detachment and in cosmetic surgery and
CC skin graft. The modified region of laminin alpha3 chain can control cell
CC adhesion function and cell movement effect. This is the amino acid
CC sequence of human laminin alpha 3.

SQ Sequence 1713 AA;

Query Match 76.0%; Score 850; DB 7; Length 1713;

Best Local Similarity 76.6%; Pred. No. 2.6e-91;

Matches 167; Conservative 18; Mismatches 33; Indels 0; Gaps 0;

QY 1 MKNLKKTSGVRLNDVGVTKKSEBWKLVRTASFSFGQMSFTNLDVSTDFPQLSFGF 60
DB 1118 MKNLKKTSGVRLNDVGVTKKSEBWKLVRSASFSFGQLSTFDGLPPTDHLQASFGF 1177
QY 61 QTFPSGTLNHQTRTSLSLVTLEDGHIELSTRDSNIPFKSPQTYMDGLHHVSVISPT 120
DB 1178 QTFPSGTLNHQTRTSLSLVTLEDGHIELSTRDSNIPFKSPQTYMDGLHHVSVISDN 1237
QY 121 SGRLRIDQVLRNRQLPSFSAQSLRIGGHEGECISNVLVORFSQSPFVLDLASKS 180
DB 1238 SGRLRIDQVLRNRQLPSFSAQSLRIGGHEGECISNVLVORFSQSPFVLDLTSNS 1297
QY 181 TKKDAALGGCSLNKPPFLMFKSPKRNKRIFNVNOL 218
DB 1298 LKRDVSLGGCSLNKPPFLMFKSTRFNKTFRINOL 1335

RESULT 9

ADG37225 standard; protein; 1713 AA.

ID ADG37225

AC ADG37225;

DE 26-FEB-2004 (first entry)

XX Human laminin-6 alpha 3 subunit.

XX human; laminin-6; alpha 3; B1 subunit; B2 subunit; cell-movement;
XX cell-adhesion; dermatological; neuroprotective; muscular;
XX epithelial tissue; nervous tissue; varicella disease.

OS Homo sapiens.

PN JP2003212791-A.

PD 30-JUL-2003.

PF 17-JAN-2002; 2002JP-00009227.

PR 17-JAN-2002; 2002JP-00009227.

PA (KAGA-) KAGAKU GIUTTSU SHINKO JIGYODAN.

DR WPI, 2003-819867/77.

XX N-PSDB; ADG37224.

XX Composition comprising laminin-6 for regulation of cell-movement activity
XX and/or cell-adhesion activity, useful for treating or maintaining
XX function of epithelial tissue, nervous tissue and muscles.

PS Claim 2; SEQ ID NO 2; 55pp; Japanese.

CC This invention describes a novel composition comprising the human laminin
CC -6 alpha 3; B1 or B2 subunits for regulation of cell-movement activity
CC and/or cell-adhesion activity. The products of the invention have
CC dermatological, neuroprotective and muscular activity. The composition of
CC the invention is useful for treating or maintaining the function of the
CC epithelial tissue, the nervous tissue and muscles and is also useful for

CC treatment or prevention of varicella disease.
 XX Sequence 1713 AA;
 SQ Query Match 76.0%; Score 850; DB 7; Length 1713;
 Best Local Similarity 76.6%; Pred. No. 2.6e-91; Indels 0; Gaps 0;
 Matches 167; Conservative 18; Mismatches 33; Indels 0; Gaps 0;
 QY 1 MNLLKKTSGVRLNDVTGVTKKCSSEDMKLVRTASFSRGGQMSFTNLDVSTDRFQLSFGF 60
 DB 1118 MNLLKKTSGVRLNDVTGVTKKCSSEDMKLVRSASFSRGGQLSTDLGLPTDHLQASFGF 1177
 QY 61 QTFQPSGTLNMQRTSSILVLTEDGHIELSTRDSNIPFKSPGYMDGLAHVSVISDT 120
 DB 1178 QTFQPSGTLNMQRTSSILVLTEDGHIELSTRDSNIPFKSPGYMDGLAHVSVISDN 1237
 QY 121 SGLRLIIDDOVLRRNORLPSFSNAOQSLRLGGHFGECISNVLVORFSGSPRYLDLASKS 180
 DB 1238 SGLRLIIDDOVLRRNORLPSFSNAOQSLRLGGHFGECISNVLVORFSGSPRYLDLASKS 1297
 QY 181 TKKDSILGGCSLNKPEPFLMLFKSPKRNKGRIFNNQL 218
 DB 1298 LKRDVSLGGCSLNKPEPFLMLFKSTRFNKTKTRINQL 1335
 RESULT 10
 AEM81957
 ID AEM81957 standard; protein; 1713 AA.
 XX
 AC AEM81957;
 DT 18-NOV-2004 (first entry)
 DE Tumour-associated antigenic target (TAT) polypeptide PRO2799, SEQ:5041.
 XX
 KM Tumour-associated antigenic target; TAT; human; overexpression; cancer;
 KM tumour; diagnosis; cell proliferative disorder; breast cancer;
 KM colorectal cancer; lung cancer; ovarian cancer; liver cancer;
 KM central nervous system cancer; bladder cancer; pancreatic cancer;
 KM cervical cancer; melanoma; leukemia; hybridisation probe;
 KM chromosome identification; chromosome mapping; gene mapping;
 KM gene therapy; cytostatic.
 XX
 OS Homo sapiens.
 PN WO2004030615-A2.
 XX
 PD 15-APR-2004.
 XX
 PF 29-SEP-2003; 2003WO-US028547.
 XX
 PR 02-OCT-2002; 2002US-0414971P.
 XX
 PA (GETH) GENENTECH INC.
 PI Wu TD, Zhang Z, Zhou Y;
 DR WPI; 2004-347921/32.
 DR N-PSDB; ACN40327.
 XX
 PT New tumor-associated antigenic target polypeptides and nucleic acids,
 PT useful in preparing a medicament for treating or detecting a
 PT proliferative disorder, e.g. breast, lung, colorectal, ovarian or
 PT prostate cancer or tumor.
 XX
 PS Claim 12; SEQ ID NO 5041; 7273bp; English.
 XX
 CC The invention relates to human tumour-associated antigenic target (TAT)
 CC polypeptides, and their related nucleic acids. The TAT polypeptides are
 CC overexpressed in cancer tissues compared to normal tissues, and may thus
 CC serve as effective targets for the diagnosis and treatment of cancer in
 CC mammals. The invention also relates to the TAT nucleic acid and polypeptide
 CC sequences at least 80% identical to the TAT nucleic acids and

CC polypeptides; expression vectors and host cells comprising a TAT nucleic
 CC acid; an antibody specific for a TAT polypeptide; a peptide or organic
 CC molecule which binds to a TAT polypeptide; fusion proteins comprising a
 CC TAT polypeptide; and methods and compositions for the treatment or
 CC diagnosis of cancer in mammals. TAT polypeptides, nucleic acids,
 CC antibodies, antagonists, binding molecules and compositions are useful
 CC for diagnosing or treating a cell proliferative disorder associated with
 CC increased TAT expression, particularly cancers such as breast cancer,
 CC colorectal cancer, lung cancer, ovarian cancer, liver cancer, bladder
 CC cancer, pancreatic cancer, cervical cancer, cancers of the central
 CC nervous system, melanoma and leukemia. TAT nucleic acids may further be
 CC used as hybridisation probes, in chromosome and gene mapping, in
 CC chromosome identification and in gene therapy. The present sequence
 CC represents a TAT polypeptide of the invention
 XX
 SQ Sequence 1713 AA;
 Query Match 76.0%; Score 850; DB 8; Length 1713;
 Best Local Similarity 76.6%; Pred. No. 2.6e-91; Indels 0; Gaps 0;
 Matches 167; Conservative 18; Mismatches 33; Indels 0; Gaps 0;
 QY 1 MNLLKKTSGVRLNDVTGVTKKCSSEDMKLVRTASFSRGGQMSFTNLDVSTDRFQLSFGF 60
 DB 1118 MNLLKKTSGVRLNDVTGVTKKCSSEDMKLVRSASFSRGGQLSTDLGLPTDHLQASFGF 1177
 QY 61 QTFQPSGTLNMQRTSSILVLTEDGHIELSTRDSNIPFKSPGYMDGLAHVSVISDT 120
 DB 1178 QTFQPSGTLNMQRTSSILVLTEDGHIELSTRDSNIPFKSPGYMDGLAHVSVISDN 1237
 QY 121 SGLRLIIDDOVLRRNORLPSFSNAOQSLRLGGHFGECISNVLVORFSGSPRYLDLASKS 180
 DB 1238 SGLRLIIDDOVLRRNORLPSFSNAOQSLRLGGHFGECISNVLVORFSGSPRYLDLASKS 1297
 QY 181 TKKDSILGGCSLNKPEPFLMLFKSPKRNKGRIFNNQL 218
 DB 1298 LKRDVSLGGCSLNKPEPFLMLFKSTRFNKTKTRINQL 1335
 RESULT 11
 ADR87606
 ID ADR87606 standard; protein; 1713 AA.
 XX
 AC ADR87606;
 DT 02-DEC-2004 (first entry)
 DE Human laminin alpha 3 (nicein), SEQ ID 10.
 XX
 KM Cytostatic; Gene Therapy; renal cell carcinoma; Wilms tumour; human;
 KM laminin alpha 3; nicein.
 XX
 OS Homo sapiens.
 PN WO2004075835-A2.
 XX
 PD 10-SEP-2004.
 XX
 PF 20-FEB-2004; 2004WO-US005042.
 XX
 PR 21-FEB-2003; 2003US-00372683.
 XX
 PA (GETH) GENENTECH INC.
 PI Gerltzen ME, Peale FV, Wu TD;
 DR WPI; 2004-676901/66.
 DR N-PSDB; ADR87605.
 XX
 PT New anti-EDNRA antibody, useful in preparing a composition for diagnosing
 PT or inhibiting the growth of renal cell carcinoma or Wilms tumor.
 XX
 PS Example 1; SEQ ID NO 10; 257pp; English.
 XX

CC The present invention relates to novel antibodies which bind to proteins
CC which are overexpressed in renal cell carcinomas or Wilms tumour. The
CC antibody can bind to a protein comprising CCKR4 (ADR87598), laminin alpha
CC 4 (ADR87600), TIMP1 (ADR87602), Type IV collagen alpha 1 (ADR87604),
CC laminin alpha 3 (mucin) (ADR87606), Adrenomedullin (ADR87608), Type IV
CC collagen alpha 2 (ADR87610), Thrombospondin 2 (ADR87612), Type I collagen
CC alpha 2 (ADR87614), Type VI collagen alpha 3 (ADR87616), Latent TGFbeta
CC binding protein 2 (LTBP2) (ADR87618), Serine or cysteine protease
CC inhibitor heat shock protein 47 (HSP47) (ADR87620), Procollagen-lysine, 2
CC -oxoglutarate 5-dioxygenase (ADR87622), connexin 43 (ADR87624), Type IV
CC collagen alpha 2 (ADR87626), Connexin 37 (ADR87628), Ephrin A1
CC (ADR87630), Laminin beta 2 (ADR87632), Integrin alpha 1, hevin
CC (ADR87635), Stemlocalcin 1 (ADR87637), Thrombospondin 4 (ADR87639), CD36
CC polypeptide (ADR87641), Endothelin receptor A (EDNRA, ADR87643) or
CC Endothelin receptor B (EDNRB, ADR87645). The proteins of ADR87598-ADR87641
CC and ADR87645 are all overexpressed in renal cell carcinoma, and ADR87643
CC (EDNRA) is overexpressed in Wilms tumour. The antibodies are useful in
CC preparing a composition for diagnosing or inhibiting the growth of renal
CC cell carcinoma or Wilms tumour. The present sequence is one such protein
CC of the invention.

XX SQ Sequence 1713 AA;

Query Match 76.0%; Score 850; DB 8; Length 1713;
Best Local Similarity 76.6%; Pred. No. 2.6e-91;
Matches 167; Conservative 18; Mismatches 33; Indels 0; Gaps 0;

QY 1 MKNLKKTSGVRLNDVTVGTVKCCSEDMKLVRTASFSRGGQMSFTNLDVPSDFRQSLFGF 60
DB 1118 MKNLKKTSGVRLNDVTVGTVKCCSEDMKLVRTASFSRGGQSLSTDLGLPTDHLQASFGF 1177
QY 61 QTFQPSGTLNHOQTRTSSLVLTEDGHIEISTDSNIPFKSPGTMDGLLHVSVISDT 120
DB 1178 QTFQPSGTLNHOQTRTSSLVLTEDGHIEISTDSNIPFKSPGTMDGLLHVSVISDN 1237
QY 121 SGRLILIDQVLRNORLPSFSNAQSLRLGGHFEFGCTSNVLYORPSOSPEVLDLTSNS 180
DB 1238 SGRLILIDQVLRNORLPSFSNAQSLRLGGHFEFGCTSNVLYORPSOSPEVLDLTSNS 1297
QY 181 TKDASLGGCSLNKPPFLMLFKSPKRNKRIFFNVNOL 218
DB 1298 LKRDVSLGGCSLNKPPFLMLFKSGSTRFNKTKTRINQL 1335

RESULT 12

ID AAB48456 standard; protein; 1724 AA.

XX AAB48456;
XX
XX 02-MAR-2001 (first entry)
XX
XX Human laminin 5 polypeptide, SEQ ID NO: 2.
XX
XX Human; laminin 5; vulnery; antiulcer; antiinflammatory; antidiabetic;
XX cell adhesion promoter; wound healing; ulcers; burn; skin graft;
XX periodontitis; gingivitis; Type I diabetes; angiogenesis regulation.
XX
XX Homo sapiens.
XX
XX WO200066731-A2.
XX
XX 09-NOV-2000.
XX
XX 28-APR-2000; 2000MO-US011459.
XX
XX 30-APR-1999; 99US-0131738P.
XX 21-AUG-1999; 99US-0149738P.
XX 24-SEP-1999; 99US-0155945P.
XX
XX (BIOS-) BIOSTATUM INC.
XX
XX Boutaud A;
XX
XX

XX
DR WPI: 2000-687538/67.
DR N-PSDB; AAC83717.
PT Laminin 5-expressing cells, used to accelerate wound healing associated
PT with diabetic foot ulcers, venous ulcers, pressure sores, skin surgery,
PT burns, acute wounds and skin grafts.
XX
PS Claim 3; Page 53-59; 232pp; English.

XX
XX The present sequence is a laminin 5 chain polypeptide. Recombinant
XX laminin 5-expressing cells are used to accelerate wound healing,
XX especially diabetic foot ulcers, venous ulcers, pressure sores, skin
XX surgery, burns, acute wounds, skin grafts, corneal ulcerations, gastro-
XX intestinal ulcers, periodontitis, and gingivitis. They are also used to
XX improve the biocompatibility of medical devices, and to promote cell
XX adhesion to a surface. They can be used for the ex vivo treatment of Type
XX I diabetes. Laminin can also be used to regulate angiogenesis. The cell
XX line produces and secretes recombinant heterotrimeric laminin, whereas
XX prior art cell lines have been created that produce but do not secrete
XX only one or two chain laminins

XX SQ Sequence 1724 AA;

Query Match 76.0%; Score 850; DB 3; Length 1724;
Best Local Similarity 76.6%; Pred. No. 2.7e-91;
Matches 167; Conservative 18; Mismatches 33; Indels 0; Gaps 0;

QY 1 MKNLKKTSGVRLNDVTVGTVKCCSEDMKLVRTASFSRGGQMSFTNLDVPSDFRQSLFGF 60
DB 1129 MKNLKKTSGVRLNDVTVGTVKCCSEDMKLVRTASFSRGGQSLSTDLGLPTDHLQASFGF 1188
QY 61 QTFQPSGTLNHOQTRTSSLVLTEDGHIEISTDSNIPFKSPGTMDGLLHVSVISDT 120
DB 1189 QTFQPSGTLNHOQTRTSSLVLTEDGHIEISTDSNIPFKSPGTMDGLLHVSVISDN 1248
QY 121 SGRLILIDQVLRNORLPSFSNAQSLRLGGHFEFGCTSNVLYORPSOSPEVLDLTSNS 180
DB 1249 SGRLILIDQVLRNORLPSFSNAQSLRLGGHFEFGCTSNVLYORPSOSPEVLDLTSNS 1308
QY 181 TKDASLGGCSLNKPPFLMLFKSPKRNKRIFFNVNOL 218
DB 1309 LKRDVSLGGCSLNKPPFLMLFKSGSTRFNKTKTRINQL 1346

RESULT 13

ID ADE08094 standard; protein; 3332 AA.

XX ADE08094;
XX
XX 29-JAN-2004 (first entry)
XX
XX Novel protein (useful for identifying genetic disorders) #249.
XX
XX novel gene; novel protein; tissue marker; molecular weight marker;
XX chromosome marker; genetic disorder.
XX
XX Unidentified.
XX
XX WO2003054152-A2.
XX
XX 03-JUL-2003.
XX
XX 10-DEC-2002; 2002MO-US039555.
XX
XX 10-DEC-2001; 2001US-0339739P.
XX 11-DEC-2001; 2001US-0339453P.
XX 14-MAR-2002; 2002US-0365091P.
XX 14-MAR-2002; 2002US-0365844P.
XX 12-APR-2002; 2002US-0372381P.
XX 12-APR-2002; 2002US-0372615P.
XX 22-APR-2002; 2002US-00128558.
XX
XX

	P	(HUMA-) HUMAN GENOME SCI INC.
XX	PI	Ruben SM, Barash SC, Birse CE, Rosen CA;
XX	DR	N-PSDB; AAH34508.
PT	XX	Nucleic acids encoding 4277 human colon cancer-associated polypeptides,
XX	XX	ClaIm 11; Page 7395-7387; 9803pp; English.
CC	AAH32943	to AAH37195 and AAG73514 to AAG77788 represent human colon
CC	cancer-associated nucleic acid molecules (N) and proteins (P), where the	
CC	proteins are collectively known as colon cancer antigens. The colon	
CC	cancer antigens have cytostatic activity and can be used in gene therapy	
CC	and vaccine production. N and P may be used in the prevention, diagnosis	
CC	and treatment of diseases associated with inappropriate P expression. For	
CC	example, N and P may be used to treat disorders associated with decreased	
CC	expression by rectifying mutations or deletions in a patient's genome	
CC	that affect the activity of P by expressing inactive proteins or to	
CC	suppress the patients own production of P. Additionally, N may be used	
CC	to produce the colon cancer-associated Ps, by inserting the nucleic acids	
CC	into a host cell and culturing the cell to express the proteins. N and P	
CC	can be used in the prevention, diagnosis and treatment of colorectal	
CC	carcinomas and cancers. AAH37196 to AAH37204 and AAB77789 represent	
CC	sequences used in the exemplification of the present invention. N.B.	
CC	Pages 666 to 682 and page 7053 of the sequence listing were missing at	
CC	time of publication, meaning no sequences are present for SEQ ID NO:1027	
SQ	Sequence 469 AA:	
	Query Match 60.8%; Score 680; DB 4; Length 469; Best Local Similarity 72.2%; Pred. No. 8e-72; Matches 135; Conservative 17; Mismatches 35; Indels 0; Gaps 0 DY 32 TASFSGGGMSTNTIDVPSTRFQLSRFGQTFRPGSGLTNHQRTSSLVLTEDGHIEIS 91 :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: : Db 1 SASFSKXQLSTFDLGPLPTHLOASFFQTFPPSPGGILLDHQWTRXLQVTEDEGYIELS 60 DY 92 TDNSNPTRFKSGTMDGLAHNVSVISTSLRLIDDYLRNRNQPLPRSNNAQSIRLG 151 : :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: : Db 61 TSXSXPFPKSKPYTMGDILHYVSIDSNGELRIIDLRRSKRKHIISSRSGLRG 120 DY 152 GGHEFCISNLTVORFOSPEVLDLASKSTKGDAISGCISLNKPFLMLFKSPKRFNKGR 211 :::: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: : Db 121 GSIFBECINAVVGRLISPREVDLTLSLKRDVSILOGCSLINRPFLMLAKGSTRNKKR 180 DY 212 IFNNVQL 218 : Db 181 TFRRINQL 187 RESULT 15 AAB48447 ID AAB48447 standard; protein; 1792 AA. XX XX AAB48447? DT 02-MAR-2001 (first entry) DE Mouse laminin 8 polypeptide, SEQ ID NO: 12. KM Mouse; laminin 8; neuroprotective; angiogenic; osteopathic; KW antiarteriosclerotic; glycoprotein; mesenchymal tissue injury; XM vascular tissue injury; neural injury; angiogenesis regulation. XX OS Mus musculus. PN DN WO2000066732-A2. DD 09-NOV-2000.	

XX 28-APR-2000; 2000WO-US011543.
 PF
 XX
 PR 30-APR-1999; 99US-0131720P.
 PR 21-AUG-1999; 99US-0149738P.
 PR 24-SEP-1999; 99US-0155945P.
 PR 11-FEB-2000; 2000US-0182012P.
 XX
 PA (BIOS-) BIOSTRATUM INC.
 XX
 PI Kortessmaa J, Tryggvason K;
 XX
 DR MPI; 2000-687539/67.
 DR N-PSDB; AAC83708.
 XX
 PT Purified laminin 8 protein, useful for research and therapeutic purposes
 PT including peripheral nerve regeneration, treatment of degenerative muscle
 PT disorders, angiogenesis regulation, and ex vivo cell therapy.
 XX
 PS Claim 5; Page 136-142; 245pp; English.
 XX
 CC The present sequence is a laminin 8 polypeptide chain. Laminins are a
 CC family of heterotrimeric glycoproteins that function via binding
 CC interactions with neighbouring cell receptors and by forming laminin
 CC networks. They are signalling molecules which influence cellular
 CC function. Laminin 8 is useful for treating injuries to tissue of
 CC mesenchymal origin, such as bone, cartilage, tendon, and ligament,
 CC treating injuries to vascular tissue, promoting cell attachment and
 CC migration, ex vivo cell therapy, improving the biocompatibility of
 CC medical devices, and preparing improved cell culture devices and media.
 CC Laminin 8 is also useful for promoting re-endothelialisation at the site
 CC of vascular injuries, improving the take of grafts, improving the
 CC biocompatibility of medical devices, treating neural injuries (neural
 CC regeneration), regulating angiogenesis, and promoting cell attachment and
 CC migration
 XX
 SQ Sequence 1792 AA;

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Db 1278 TKKDAISLGCCSLNKPPFLMLFKSPKRFNKGRIFFNVNQL 1315

RESULT 2

US-10-603-725-10
; Sequence 10, Application US/10603725
; Publication No. US20040014665A1
; GENERAL INFORMATION:
; APPLICANT: Bouland, Arjel
; TITLE OF INVENTION: Recombinant Laminin 5
; FILE REFERENCE: 99-274-C
; CURRENT FILING DATE: 2003-06-25
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 10
; LENGTH: 1725
; TYPE: PRT
; ORGANISM: Rattus norvegicus
US-10-603-725-10

Query Match 100.0%; Score 1118; DB 15; Length 1725;
Best Local Similarity 100.0%; Pred. No. 7.2e-109;
Matches 218; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKNLKKTSGVRLNDTVGVTKKCSBDMKLVRTASFSRGQMSFTNLDVSTDRFQLSFGF 60
DB 1129 MKNLKKTSGVRLNDTVGVTKKCSBDMKLVRTASFSRGQMSFTNLDVSTDRFQLSFGF 1188
QY 61 QTFQPSGTLNHQRTSSLLVLTLEDGHIELSTDSNIPFKSPGTYMDGLHHVSVISDT 120
DB 1189 QTFQPSGTLNHQRTSSLLVLTLEDGHIELSTDSNIPFKSPGTYMDGLHHVSVISDT 1248
QY 121 SGLRLIIDQVLRNRQRLPSFSNAOQSLRLGGGHFPGCISNVLVORFSQSPFVLDAASKS 180
DB 1249 SGLRLIIDQVLRNRQRLPSFSNAOQSLRLGGGHFPGCISNVLVORFSQSPFVLDAASKS 1308
QY 181 TKKDAISLGCCSLNKPPFLMLFKSPKRFNKGRIFFNVNQL 218
DB 1309 TKKDAISLGCCSLNKPPFLMLFKSPKRFNKGRIFFNVNQL 1346

RESULT 3

US-10-603-725-4
; Sequence 4, Application US/10603725
; Publication No. US20040014665A1
; GENERAL INFORMATION:
; APPLICANT: Bouland, Arjel
; TITLE OF INVENTION: Recombinant Laminin 5
; FILE REFERENCE: 99-274-C
; CURRENT APPLICATION NUMBER: US/10/603,725
; CURRENT FILING DATE: 2003-06-25
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 1693
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-603-725-4

Query Match 76.0%; Score 850; DB 15; Length 1693;
Best Local Similarity 76.6%; Pred. No. 2e-80;
Matches 167; Conservative 18; Mismatches 33; Indels 0; Gaps 0;

QY 1 MKNLKKTSGVRLNDTVGVTKKCSBDMKLVRTASFSRGQMSFTNLDVSTDRFQLSFGF 60
DB 1098 MKNLKKTSGVRLNDTVGVTKKCSBDMKLVRTASFSRGQMSFTNLDVSTDRFQLSFGF 1157
QY 61 QTFQPSGTLNHQRTSSLLVLTLEDGHIELSTDSNIPFKSPGTYMDGLHHVSVISDT 120
DB 1158 QTFQPSGTLNHQRTSSLLVLTLEDGHIELSTDSNIPFKSPGTYMDGLHHVSVISDT 1217
QY 121 SGLRLIIDQVLRNRQRLPSFSNAOQSLRLGGGHFPGCISNVLVORFSQSPFVLDAASKS 180

Db 1218 SGLRLIIDQVLRNRQRLPSFSNAOQSLRLGGGHFPGCISNVLVORFSQSPFVLDAASKS 1277

QY 181 TKKDAISLGCCSLNKPPFLMLFKSPKRFNKGRIFFNVNQL 218

Db 1278 LKRDVSLGGCSLNKPPFLMLFKSPTFRNKTFFRINQL 1315

RESULT 4

US-10-603-725-8
; Sequence 8, Application US/10603725
; Publication No. US20040014665A1
; GENERAL INFORMATION:
; APPLICANT: Bouland, Arjel
; TITLE OF INVENTION: Recombinant Laminin 5
; FILE REFERENCE: 99-274-C
; CURRENT APPLICATION NUMBER: US/10/603,725
; CURRENT FILING DATE: 2003-06-25
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 8
; LENGTH: 1693
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-603-725-8

Query Match 76.0%; Score 850; DB 15; Length 1693;
Best Local Similarity 76.6%; Pred. No. 2e-80;
Matches 167; Conservative 18; Mismatches 33; Indels 0; Gaps 0;

QY 1 MKNLKKTSGVRLNDTVGVTKKCSBDMKLVRTASFSRGQMSFTNLDVSTDRFQLSFGF 60
DB 1098 MKNLKKTSGVRLNDTVGVTKKCSBDMKLVRTASFSRGQMSFTNLDVSTDRFQLSFGF 1157
QY 61 QTFQPSGTLNHQRTSSLLVLTLEDGHIELSTDSNIPFKSPGTYMDGLHHVSVISDT 120
DB 1158 QTFQPSGTLNHQRTSSLLVLTLEDGHIELSTDSNIPFKSPGTYMDGLHHVSVISDT 1217
QY 121 SGLRLIIDQVLRNRQRLPSFSNAOQSLRLGGGHFPGCISNVLVORFSQSPFVLDAASKS 180
DB 1218 SGLRLIIDQVLRNRQRLPSFSNAOQSLRLGGGHFPGCISNVLVORFSQSPFVLDAASKS 1277
QY 181 TKKDAISLGCCSLNKPPFLMLFKSPKRFNKGRIFFNVNQL 218
DB 1278 LKRDVSLGGCSLNKPPFLMLFKSPTFRNKTFFRINQL 1315

RESULT 5

US-10-171-311-113
; Sequence 113, Application US/10171311
; Publication No. US20030087270A1
; GENERAL INFORMATION:
; APPLICANT: Schlegel, Robert
; APPLICANT: Chen, Yan
; APPLICANT: Zhao, Xumei
; APPLICANT: Monahan, John
; APPLICANT: Kamackar, Shubhangi
; APPLICANT: Glatt, Karen
; APPLICANT: Gamavarapu, Manjula
; APPLICANT: Hoerish, Sebastian
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
; TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND THERAPY
; FILE REFERENCE: MRI-035
; CURRENT APPLICATION NUMBER: US/10/171,311
; CURRENT FILING DATE: 2002-06-12
; PRIOR APPLICATION NUMBER: US 60/298,159
; PRIOR FILING DATE: 2001-06-13
; PRIOR APPLICATION NUMBER: US 60/298,155
; PRIOR FILING DATE: 2001-06-13
; PRIOR APPLICATION NUMBER: US 60/335,936
; PRIOR FILING DATE: 2001-11-14
; NUMBER OF SEQ ID NOS: 238

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 113
LENGTH: 1713
TYPE: PRT
ORGANISM: Homo sapiens
US-10-171-311-113

Query Match 76.0%; Score 850; DB 14; Length 1713;
Best Local Similarity 76.6%; Pred. No. 2e-80;
Matches 167; Conservative 18; Mismatches 33; Indels 0; Gaps 0;

QY 1 MKNLKKTSGVRLNDVGVTKKSEBWKLVRTASFSRGGQMSFTNLDVPTDRFQLSFGF 60
DB 1118 MKNLKKTSGVRLNDVGVTKKSEBWKLVRTASFSRGGQLSFTDGLPTDHLQASFGF 1177
QY 61 QTFQPSGTLNHOQRTSSLLVTLDEGHIELSTDSNIPFKSPGTVMGGLHHVSVISDT 120
DB 1178 QTFQPSGTLNHOQRTSSLLVTLDEGHIELSTDSGSGPIFKSPGTVMGGLHHVSVISDN 1237
QY 121 SGLRLIIDQVLRNORLPFSNAOQSLRLGGHFEFCISNVLVORFOSPEVLDLASKS 180
DB 1238 SGLRLIIDQVLRNORLPFSNAOQSLRLGGHFEFCISNVFVQRLSLSPVLDLTSNS 1297
QY 181 TKDASLGGCSLNKPPFLMLFKSPKRNKGRIFNVNQL 218
DB 1298 LKRDVSLGGCSLNKPPFLMLKSGTRFNKTKTRINQL 1335

RESULT 6

US-10-372-683-10
Sequence 10, Application US/10372683
Publication No. US20040009171A1
GENERAL INFORMATION:
APPLICANT: GERRITSEN, MARY E.
APPLICANT: WU, THOMAS D.
TITLE OF INVENTION: METHODS FOR THE TREATMENT OF CARCINOMA
FILE REFERENCE: P1928R1P1
CURRENT APPLICATION NUMBER: US/10/372,683
PRIOR FILING DATE: 2003-02-21
PRIOR APPLICATION NUMBER: US 10/271,690
PRIOR FILING DATE: 2002-10-16
PRIOR APPLICATION NUMBER: US 60/344,534
PRIOR FILING DATE: 2001-10-18
NUMBER OF SEQ ID NOS: 49
SEQ ID NO 10
LENGTH: 1713
TYPE: PRT
ORGANISM: Homo sapiens
US-10-372-683-10

Query Match 76.0%; Score 850; DB 15; Length 1713;
Best Local Similarity 76.6%; Pred. No. 2e-80;
Matches 167; Conservative 18; Mismatches 33; Indels 0; Gaps 0;

QY 1 MKNLKKTSGVRLNDVGVTKKSEBWKLVRTASFSRGGQMSFTNLDVPTDRFQLSFGF 60
DB 1118 MKNLKKTSGVRLNDVGVTKKSEBWKLVRTASFSRGGQLSFTDGLPTDHLQASFGF 1177
QY 61 QTFQPSGTLNHOQRTSSLLVTLDEGHIELSTDSNIPFKSPGTVMGGLHHVSVISDT 120
DB 1178 QTFQPSGTLNHOQRTSSLLVTLDEGHIELSTDSGSGPIFKSPGTVMGGLHHVSVISDN 1237
QY 121 SGLRLIIDQVLRNORLPFSNAOQSLRLGGHFEFCISNVLVORFOSPEVLDLASKS 180
DB 1238 SGLRLIIDQVLRNORLPFSNAOQSLRLGGHFEFCISNVFVQRLSLSPVLDLTSNS 1297
QY 181 TKDASLGGCSLNKPPFLMLFKSPKRNKGRIFNVNQL 218
DB 1298 LKRDVSLGGCSLNKPPFLMLKSGTRFNKTKTRINQL 1335

RESULT 7

US-10-603-725-6
Sequence 6, Application US/10603725
Publication No. US20040014665A1
GENERAL INFORMATION:
APPLICANT: BOUTLAND, Arlet
TITLE OF INVENTION: Recombinant Laminin 5
FILE REFERENCE: 99-274-C
CURRENT APPLICATION NUMBER: US/10/603,725
PRIOR FILING DATE: 2003-06-25
NUMBER OF SEQ ID NOS: 36
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 6
LENGTH: 1713
TYPE: PRT
ORGANISM: Homo sapiens
US-10-603-725-6

Query Match 76.0%; Score 850; DB 15; Length 1713;
Best Local Similarity 76.6%; Pred. No. 2e-80;
Matches 167; Conservative 18; Mismatches 33; Indels 0; Gaps 0;

QY 1 MKNLKKTSGVRLNDVGVTKKSEBWKLVRTASFSRGGQMSFTNLDVPTDRFQLSFGF 60
DB 1118 MKNLKKTSGVRLNDVGVTKKSEBWKLVRTASFSRGGQLSFTDGLPTDHLQASFGF 1177
QY 61 QTFQPSGTLNHOQRTSSLLVTLDEGHIELSTDSNIPFKSPGTVMGGLHHVSVISDT 120
DB 1178 QTFQPSGTLNHOQRTSSLLVTLDEGHIELSTDSGSGPIFKSPGTVMGGLHHVSVISDN 1237
QY 121 SGLRLIIDQVLRNORLPFSNAOQSLRLGGHFEFCISNVLVORFOSPEVLDLASKS 180
DB 1238 SGLRLIIDQVLRNORLPFSNAOQSLRLGGHFEFCISNVFVQRLSLSPVLDLTSNS 1297
QY 181 TKDASLGGCSLNKPPFLMLFKSPKRNKGRIFNVNQL 218
DB 1298 LKRDVSLGGCSLNKPPFLMLKSGTRFNKTKTRINQL 1335

RESULT 8

US-10-603-725-2
Sequence 2, Application US/10603725
Publication No. US20040014665A1
GENERAL INFORMATION:
APPLICANT: BOUTLAND, Arlet
TITLE OF INVENTION: Recombinant Laminin 5
FILE REFERENCE: 99-274-C
CURRENT APPLICATION NUMBER: US/10/603,725
PRIOR FILING DATE: 2003-06-25
NUMBER OF SEQ ID NOS: 36
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 2
LENGTH: 1724
TYPE: PRT
ORGANISM: Homo sapiens
US-10-603-725-2

Query Match 76.0%; Score 850; DB 15; Length 1724;
Best Local Similarity 76.6%; Pred. No. 2e-80;
Matches 167; Conservative 18; Mismatches 33; Indels 0; Gaps 0;

QY 1 MKNLKKTSGVRLNDVGVTKKSEBWKLVRTASFSRGGQMSFTNLDVPTDRFQLSFGF 60
DB 1129 MKNLKKTSGVRLNDVGVTKKSEBWKLVRTASFSRGGQLSFTDGLPTDHLQASFGF 1188
QY 61 QTFQPSGTLNHOQRTSSLLVTLDEGHIELSTDSNIPFKSPGTVMGGLHHVSVISDT 120
DB 1189 QTFQPSGTLNHOQRTSSLLVTLDEGHIELSTDSGSGPIFKSPGTVMGGLHHVSVISDN 1248
QY 121 SGLRLIIDQVLRNORLPFSNAOQSLRLGGHFEFCISNVLVORFOSPEVLDLASKS 180
DB 1249 SGLRLIIDQVLRNORLPFSNAOQSLRLGGHFEFCISNVFVQRLSLSPVLDLTSNS 1308
QY 181 TKDASLGGCSLNKPPFLMLFKSPKRNKGRIFNVNQL 218

Db 1309 LKRDVSLGGCSLNKPPFLMLKSGTSTFKTKPRINQL 1346

RESULT 9

US-10-106-698-5877
Sequence 5877, Application US/10106698
Publication No. US20030109690A1
GENERAL INFORMATION:
APPLICANT: Ruben et al.
TITLE OF INVENTION: Colon and Colon Cancer Associated Polynucleotides and Polypeptide
FILE REFERENCE: PA005P1
CURRENT APPLICATION NUMBER: US/10/106,698
CURRENT FILING DATE: 2002-03-27
PRIOR APPLICATION NUMBER: PCT/US00/26524
PRIOR FILING DATE: 2000-09-28
PRIOR APPLICATION NUMBER: US 60/157,137
PRIOR FILING DATE: 1999-09-29
PRIOR APPLICATION NUMBER: US 60/163,280
PRIOR FILING DATE: 1999-11-03
NUMBER OF SEQ ID NOS: 8564
SOFTWARE: PatentIn Ver. 3.0
SEQ ID NO 5877
LENGTH: 469
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: MISC_FEATURE
LOCATION: (8)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
NAME/KEY: MISC_FEATURE
LOCATION: (47)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
NAME/KEY: MISC_FEATURE
LOCATION: (65)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
NAME/KEY: MISC_FEATURE
LOCATION: (436)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-10-106-698-5877

Query Match 60.8%; Score 680; DB 14; Length 469;
Best Local Similarity 72.2%; Pred. No. 3.6e-63;
Matches 135; Conservative 17; Mismatches 35; Indels 0; Gaps 0;

QY 32 TASFSRGQMSFTNLVPSIDRQLSFGQTPQPSGTLNHOVRTSSLVLTEDGHIEIS 91
DB 1 SASFSRGQMSFTNLVPSIDRQLSFGQTPQPSGTLNHOVRTSSLVLTEDGHIEIS 60
QY 92 TRDSNIPFESPGTYNDGLAHVSVISDTSGRLRLIDDQVLRNRQRLPFSNAQSLRLG 151
DB 61 TSDSXPGRFSPQTYNDGLAHVSVISDTSGRLRLIDDQVLRNRQRLPFSNAQSLRLG 120
QY 152 GHEGECISNVLVORPSQSEVVDLASKSTYKQASLGGCSLNKPPFLMLFKSPRRNK 211
DB 121 GSNFEGCISNVLVORPSQSEVVDLASKSTYKQASLGGCSLNKPPFLMLFKSPRRNK 180
QY 212 IFNVNQL 218
DB 181 TFRINQL 187

RESULT 10

US-10-408-765A-154
Sequence 154, Application US/10408765A
Publication No. US20040101874A1
GENERAL INFORMATION:
APPLICANT: Ghosh, Soumitra S.
APPLICANT: Fahy, Bojin D.
APPLICANT: Zhang, Bing
APPLICANT: Gibson, Bradford W.
APPLICANT: Taylor, Steven W.
APPLICANT: Glenn, Gary M.

APPLICANT: Warnock, Dale E.
TITLE OF INVENTION: TARGETS FOR THERAPEUTIC INTERVENTION
TITLE OF INVENTION: IDENTIFIED IN THE MITOCHONDRIAL PROTEOME
FILE REFERENCE: 660088.465
CURRENT APPLICATION NUMBER: US/10/408,765A
CURRENT FILING DATE: 2003-04-04
NUMBER OF SEQ ID NOS: 3077
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 154
LENGTH: 1581
TYPE: PRT
ORGANISM: Homo sapiens
US-10-408-765A-154

Query Match 16.7%; Score 187; DB 16; Length 1581;
Best Local Similarity 28.3%; Pred. No. 4.3e-10;
Matches 62; Conservative 34; Mismatches 103; Indels 20; Gaps 8;

QY 5 KKTSGVRLNDTVGYTKKCSBDWKLVRTPASFRGQMSFTNLD-VPSIDRQLSFGQTP 63
DB 967 KDFNLBQETETLVGYGCPEDSLISRAYFN--GQSFIAISIQKISFDFGFGGFTNRL 1024
QY 64 QPSGTLNHOVRTSSLVLTEDGHIEISLSTRSNIPFESPGTYNDGLAHVSVISDTSG 123
DB 1025 QPNSGLLFYASGSDVFSISLNDGTVMQV--GIRVQSVNDKQYNDGLSHF--VSSVSPT 1080
QY 124 R--LLID-DQVLRNRQRLPFSNAQSLR---LGG-----GHEGECISNVLVORPSQS 170
DB 1081 RYELIVDSRVSQSKPTGKLEQDQASRKPFPGSPISAGYANVTGCSINAYFRVRD 1140
QY 171 PEVLDAKSTYKQASLGGCSLNKPPFLMLFKSPRRNK 209
DB 1141 VEVEDFORTEKVRHTSLVECPLESSPLFLHKKGNLSK 1179

RESULT 11

US-10-299-058-2
Sequence 2, Application US/10299058
Publication No. US20030103975A1
GENERAL INFORMATION:
APPLICANT: JONES, JONATHAN C.R.
APPLICANT: GONZALES, MEREDITH
TITLE OF INVENTION: MODULATION OF ANGIOGENESIS AND ENDOTHELIALIZATION
FILE REFERENCE: 1720-1-002 CIP
CURRENT APPLICATION NUMBER: US/10/299,058
CURRENT FILING DATE: 2002-11-18
PRIOR APPLICATION NUMBER: 09/706,235
PRIOR FILING DATE: 2000-11-03
PRIOR APPLICATION NUMBER: 60/163,199
PRIOR FILING DATE: 1999-11-03
NUMBER OF SEQ ID NOS: 13
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 2
LENGTH: 1816
TYPE: PRT
ORGANISM: Homo sapiens
OTHER INFORMATION: X in position 1112 = Arg/Pro
US-10-299-058-2

Query Match 16.7%; Score 187; DB 14; Length 1816;
Best Local Similarity 28.3%; Pred. No. 5.3e-10;
Matches 62; Conservative 34; Mismatches 103; Indels 20; Gaps 8;

QY 5 KKTSGVRLNDTVGYTKKCSBDWKLVRTPASFRGQMSFTNLD-VPSIDRQLSFGQTP 63
DB 1202 KDFNLBQETETLVGYGCPEDSLISRAYFN--GQSFIAISIQKISFDFGFGGFTNRL 1259
QY 64 QPSGTLNHOVRTSSLVLTEDGHIEISLSTRSNIPFESPGTYNDGLAHVSVISDTSG 123
DB 1260 QPNSGLLFYASGSDVFSISLNDGTVMQV--GIRVQSVNDKQYNDGLSHF--VSSVSPT 1315
QY 124 R--LLID-DQVLRNRQRLPFSNAQSLR---LGG-----GHEGECISNVLVORPSQS 170

Db 1316 RYELIYDKSRVSGKNPTKGIETQASSEKFFYFGSGSPISAQYANFTGCISNAFYTRVDRD 1375
QY 171 PEVLDLASKSTKQDASLGCSLNKPPFLMLFKSPKRFNK 209
Db 1376 VEVEDFORYTEKVTSLYECPISSPFLHKKGNLSK 1414

RESULT 12

US-10-299-058-4
; Sequence 4, Application US/10299058
; Publication No. US20030103975A1
; GENERAL INFORMATION:
; APPLICANT: JONES, JONATHAN C.R.
; APPLICANT: GONZALES, MEREDITH
; TITLE OF INVENTION: MODULATION OF ANGIOGENESIS AND ENDOTHELIALIZATION
; FILE REFERENCE: 1720-1-002 CIP
; CURRENT APPLICATION NUMBER: US/10/299,058
; CURRENT FILING DATE: 2002-11-18
; PRIOR APPLICATION NUMBER: 09/706,235
; PRIOR FILING DATE: 2000-11-03
; PRIOR APPLICATION NUMBER: 60/163,199
; PRIOR FILING DATE: 1999-11-03
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 1816
; TYPE: PRT
; ORGANISM: Homo sapien
; FEATURE:
; OTHER INFORMATION: X in position 1112 = R/P
US-10-299-058-4

Query Match 16.7%; Score 187; DB 14; Length 1816;
Best Local Similarity 28.3%; Pred. No. 5.3e-10;
Matches 62; Conservative 34; Mismatches 103; Indels 20; Gaps 8;

QY 5 KKTSGVRLNDYGVYTKKSEBDMKLVRTASFSRGGMSFTNLD-VSTDRFOLSFGQTF 63
Db 1202 KQFNLEETETLVGVYGCPEBLSIRRAYFN--GQSFASIOKISFPDGFEGGFNRTL 1259
QY 64 QPSTLLNHQTRTSLVTLLEDGHIETSDSNIPFKSGTYMDGLHNVYSIDTSGL 123
Db 1260 QPGLLFTYASGSDVSIISDNGTVIMDK--GIKQSVKQXNDLSHF--VISSVSP 1315
QY 124 R--LLID-DQVLRNRQLPSPSNAQSLR--LGG-----GHFECISNVLVQRPQS 170
Db 1316 RYELIYDKSRVSGKNPTKGIETQASSEKFFYFGSGSPISAQYANFTGCISNAFYTRVDRD 1375
QY 171 PEVLDLASKSTKQDASLGCSLNKPPFLMLFKSPKRFNK 209
Db 1376 VEVEDFORYTEKVTSLYECPISSPFLHKKGNLSK 1414

RESULT 13

US-10-372-683-4
; Sequence 4, Application US/10372683
; Publication No. US20040009171A1
; GENERAL INFORMATION:
; APPLICANT: GERRITSEN, MARY E.
; APPLICANT: PEARL JR., FRANKLIN V.
; APPLICANT: WU, THOMAS D.
; TITLE OF INVENTION: METHODS FOR THE TREATMENT OF CARCINOMA
; FILE REFERENCE: P1928R1P1
; CURRENT APPLICATION NUMBER: US/10/372,683
; CURRENT FILING DATE: 2003-02-21
; PRIOR APPLICATION NUMBER: US 10/271,690
; PRIOR FILING DATE: 2002-10-16
; PRIOR APPLICATION NUMBER: US 60/344,534
; PRIOR FILING DATE: 2001-10-18
; NUMBER OF SEQ ID NOS: 49
; SEQ ID NO 4
; LENGTH: 1816

; TYPE: PRT
; ORGANISM: Homo sapien
US-10-372-683-4

Query Match 16.7%; Score 187; DB 15; Length 1816;
Best Local Similarity 28.3%; Pred. No. 5.3e-10;
Matches 62; Conservative 34; Mismatches 103; Indels 20; Gaps 8;

QY 5 KKTSGVRLNDYGVYTKKSEBDMKLVRTASFSRGGMSFTNLD-VSTDRFOLSFGQTF 63
Db 1202 KQFNLEETETLVGVYGCPEBLSIRRAYFN--GQSFASIOKISFPDGFEGGFNRTL 1259
QY 64 QPSTLLNHQTRTSLVTLLEDGHIETSDSNIPFKSGTYMDGLHNVYSIDTSGL 123
Db 1260 QPGLLFTYASGSDVSIISDNGTVIMDK--GIKQSVKQXNDLSHF--VISSVSP 1315
QY 124 R--LLID-DQVLRNRQLPSPSNAQSLR--LGG-----GHFECISNVLVQRPQS 170
Db 1316 RYELIYDKSRVSGKNPTKGIETQASSEKFFYFGSGSPISAQYANFTGCISNAFYTRVDRD 1375
QY 171 PEVLDLASKSTKQDASLGCSLNKPPFLMLFKSPKRFNK 209
Db 1376 VEVEDFORYTEKVTSLYECPISSPFLHKKGNLSK 1414

RESULT 14

US-10-363-616-457
; Sequence 457, Application US/10363616
; Publication No. US20040044181A1
; GENERAL INFORMATION:
; APPLICANT: Hyseg, Inc
; TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
; FILE REFERENCE: 21272-113 (793)
; CURRENT APPLICATION NUMBER: US/10/363,616
; CURRENT FILING DATE: 2003-03-03
; PRIOR APPLICATION NUMBER: 09/654,935
; PRIOR FILING DATE: 2000-09-01
; NUMBER OF SEQ ID NOS: 490
; SEQ ID NO 457
; LENGTH: 1823
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-363-616-457

Query Match 16.7%; Score 187; DB 15; Length 1823;
Best Local Similarity 28.3%; Pred. No. 5.3e-10;
Matches 62; Conservative 34; Mismatches 103; Indels 20; Gaps 8;

QY 5 KKTSGVRLNDYGVYTKKSEBDMKLVRTASFSRGGMSFTNLD-VSTDRFOLSFGQTF 63
Db 1209 KQFNLEETETLVGVYGCPEBLSIRRAYFN--GQSFASIOKISFPDGFEGGFNRTL 1266
QY 64 QPSTLLNHQTRTSLVTLLEDGHIETSDSNIPFKSGTYMDGLHNVYSIDTSGL 123
Db 1267 QPGLLFTYASGSDVSIISDNGTVIMDK--GIKQSVKQXNDLSHF--VISSVSP 1322
QY 124 R--LLID-DQVLRNRQLPSPSNAQSLR--LGG-----GHFECISNVLVQRPQS 170
Db 1323 RYELIYDKSRVSGKNPTKGIETQASSEKFFYFGSGSPISAQYANFTGCISNAFYTRVDRD 1382
QY 171 PEVLDLASKSTKQDASLGCSLNKPPFLMLFKSPKRFNK 209
Db 1383 VEVEDFORYTEKVTSLYECPISSPFLHKKGNLSK 1421

RESULT 15

US-09-845-583-2
; Sequence 2, Application US/09845583
; Patent No. US20020142934A1
; GENERAL INFORMATION:
; APPLICANT: Burgeson, Robert
; APPLICANT: Brunklen, William Joseph
; APPLICANT: Champliand, Marie-France

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: February 22, 2005, 08:13:40 ; Search time 10.1795 Seconds
(without alignments)
1598.653 Million cell updates/sec

Title: US-10-817-423-6

Perfect score: 1118
Sequence: 1 MNKLKKTSGVRLNDTVGVTVT.....MLEKSPKRFNKGRIFFVNVQL 218

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA:
1: /cgn2_6/prodata/1/iaa/5A COMB.pep.*
2: /cgn2_6/prodata/1/iaa/5E COMB.pep.*
3: /cgn2_6/prodata/1/iaa/5A COMB.pep.*
4: /cgn2_6/prodata/1/iaa/5B COMB.pep.*
5: /cgn2_6/prodata/1/iaa/5C COMB.pep.*
6: /cgn2_6/prodata/1/iaa/5D COMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1118	100.0	1694	US-09-560-385A-12	Sequence 12, Appl
2	1118	100.0	1725	US-09-560-385A-10	Sequence 10, Appl
3	850	76.0	1693	US-09-560-385A-4	Sequence 4, Appl
4	850	76.0	1693	US-09-560-385A-8	Sequence 8, Appl
5	850	76.0	1713	US-08-600-382-24	Sequence 24, Appl
6	850	76.0	1713	US-09-560-385A-6	Sequence 6, Appl
7	850	76.0	1713	US-09-538-092-1359	Sequence 1359, Ap
8	850	76.0	1713	PCT-US94-10261A-24	Sequence 24, Appl
9	850	76.0	1724	US-09-560-385A-2	Sequence 2, Appl
10	204	18.2	1792	US-09-561-818A-12	Sequence 12, Appl
11	204	18.2	1816	US-09-561-818A-10	Sequence 10, Appl
12	187	16.7	1792	US-09-561-818A-4	Sequence 4, Appl
13	187	16.7	1800	US-09-561-818A-8	Sequence 8, Appl
14	187	16.7	1816	US-09-561-818A-2	Sequence 2, Appl
15	187	16.7	1824	US-09-561-818A-6	Sequence 6, Appl
16	186	16.6	3635	US-09-845-583A-2	Sequence 2, Appl
17	174	15.6	953	US-09-845-583A-4	Sequence 4, Appl
18	174	15.6	3647	US-09-949-016-10932	Sequence 10932, A
19	144.5	12.9	3084	US-09-562-702A-12	Sequence 12, Appl
20	144.5	12.9	3106	US-09-562-702A-10	Sequence 10, Appl
21	137.5	12.3	1130	5444158-2	Patent No. 5444158
22	137.5	12.3	1130	5444158-2	Patent No. 5444158
23	137.5	12.0	1130	US-08-460-309-2	Sequence 2, Appl
24	134.5	12.0	1130	US-08-125-077-2	Sequence 2, Appl
25	134.5	12.0	3070	US-09-961-403-7	Sequence 7, Appl
26	134.5	12.0	3088	US-09-562-702A-8	Sequence 8, Appl
27	134.5	12.0	3089	US-09-562-702A-4	Sequence 4, Appl

28	134.5	12.0	3110	US-09-562-702A-2	Sequence 2, Appl
29	134.5	12.0	3110	US-09-562-702A-6	Sequence 6, Appl
30	134.5	12.0	3110	US-09-561-7098-7	Sequence 7, Appl
31	134.5	12.0	3110	US-09-917-254-86	Sequence 86, Appl
32	134.5	12.0	3110	US-09-917-254-86	Sequence 5937, Ap
33	134.5	12.0	3111	US-08-460-309-4	Sequence 4, Appl
34	134.5	12.0	3111	US-08-125-077-4	Sequence 4, Appl
35	101.5	9.1	3075	US-08-460-309-5	Sequence 5, Appl
36	101.5	9.1	3075	US-08-125-077-5	Sequence 5, Appl
37	98.5	8.8	21	US-08-445-135-7	Sequence 7, Appl
38	94.5	8.5	675	5258288-1	Patent No. 5258288
39	94.5	8.5	675	5258288-1	Patent No. 5258288
40	91	8.1	212	US-09-270-767-43408	Sequence 43408, A
41	89.5	8.0	1381	US-08-826-134-4	Sequence 4, Appl
42	84.5	7.6	1384	US-09-949-016-7814	Sequence 7814, Ap
43	84	7.5	814	US-09-486-072-1	Sequence 1, Appl
44	83.5	7.5	1331	US-09-949-016-6861	Sequence 6861, Ap
45	82	7.3	271	US-08-956-012-3	Sequence 3, Appl

ALIGNMENTS

```

RESULT 1
US-09-560-385A-12
; Sequence 12, Application US/09560385A
; Patent No. 6703363
; GENERAL INFORMATION:
; APPLICANT: Bouland, Ariel
; TITLE OF INVENTION: Recombinant Laminin 5
; FILE REFERENCE: 99-274-C
; CURRENT FILING DATE: 2000-04-28
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 12
; LENGTH: 1694
; TYPE: PRT
; ORGANISM: Rattus norvegicus
; US-09-560-385A-12

Query Match      100.0%; Score 1118; DB 4; Length 1694;
Best Local Similarity 100.0%; Pred. No. 56-124;
Matches 218; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MNKLKKTSGVRLNDTVGVTVTKKCEDEWKLVRITASFSRGGQMSFTNLDVPSDRPQLSFGF 60
DB 1098 MNKLKKTSGVRLNDTVGVTVTKKCEDEWKLVRITASFSRGGQMSFTNLDVPSDRPQLSFGF 1157
QY 61 QTRPQSGTLLNMQTRTSSLLVTEDEGHIELSTDSNIPFKSPGTWMDGLLHVSVISDT 120
DB 1158 QTRPQSGTLLNMQTRTSSLLVTEDEGHIELSTDSNIPFKSPGTWMDGLLHVSVISDT 1217
QY 121 SGRLILDDVLRNORLPFSNAOOSLRIGGHPFECISNVTVORPSQSPVYDLASKS 180
DB 1218 SGRLILDDVLRNORLPFSNAOOSLRIGGHPFECISNVTVORPSQSPVYDLASKS 1277
QY 181 TKTDASIGGCSLNKPFLMLFKSPKRFNKGRIFFVNVQL 218
DB 1278 TKTDASIGGCSLNKPFLMLFKSPKRFNKGRIFFVNVQL 1315

RESULT 2
US-09-560-385A-10
; Sequence 10, Application US/09560385A
; Patent No. 6703363
; GENERAL INFORMATION:
; APPLICANT: Bouland, Ariel
; TITLE OF INVENTION: Recombinant Laminin 5
; FILE REFERENCE: 99-274-C
; CURRENT FILING DATE: 2000-04-28
; NUMBER OF SEQ ID NOS: 36

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SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 10
LENGTH: 1725
TYPE: PRT
ORGANISM: Rattus norvegicus
US-09-560-385A-10

Query Match 100.0%; Score 1118; DB 4; Length 1725;
Best Local Similarity 100.0%; Pred. No. 5, 2e-124;
Matches 218; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKNLKTSGVRLNDVGVTKKCSBDMKLVRTASFSRGQMSFTNLDVPSIDRFGLSFGF 60
DB 1129 MKNLKTSGVRLNDVGVTKKCSBDMKLVRTASFSRGQMSFTNLDVPSIDRFGLSFGF 1188
QY 61 QTFPQSGTLLNHQRTSSLLVLTLEDGHIELSTDSNIPFKSPGYMDGLHHVSVISDT 120
DB 1189 QTFPQSGTLLNHQRTSSLLVLTLEDGHIELSTDSNIPFKSPGYMDGLHHVSVISDT 1248
QY 121 SGRLIIDQVLRNRQLPSFSNAQSLRLGGHFEFGCISNVLVQRFSGSPETLDLASKS 180
DB 1249 SGRLIIDQVLRNRQLPSFSNAQSLRLGGHFEFGCISNVLVQRFSGSPETLDLASKS 1308
QY 181 TKKDAISGGCSLNKPPFLMFKSPKRFNKGRIYNNQL 218
DB 1309 TKKDAISGGCSLNKPPFLMFKSPKRFNKGRIYNNQL 1346

RESULT 3
US-09-560-385A-4
Sequence 4, Application US/09560385A
Patent No. 6703363
GENERAL INFORMATION:
APPLICANT: Boutand, Ariel
TITLE OF INVENTION: Recombinant Laminin 5
FILE REFERENCE: 99-274-C
CURRENT APPLICATION NUMBER: US/09/560, 385A
CURRENT FILING DATE: 2000-04-28
NUMBER OF SEQ ID NOS: 36
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 4
LENGTH: 1693
TYPE: PRT
ORGANISM: Homo sapiens
US-09-560-385A-4

Query Match 76.0%; Score 850; DB 4; Length 1693;
Best Local Similarity 76.6%; Pred. No. 6, 5e-92;
Matches 167; Conservative 18; Mismatches 33; Indels 0; Gaps 0;

QY 1 MKNLKTSGVRLNDVGVTKKCSBDMKLVRTASFSRGQMSFTNLDVPSIDRFGLSFGF 60
DB 1098 MKNLKTSGVRLNDVGVTKKCSBDMKLVRSASFSRGQSLSTDGLPPTDHLQASFGF 1157
QY 61 QTFPQSGTLLNHQRTSSLLVLTLEDGHIELSTDSNIPFKSPGYMDGLHHVSVISDT 120
DB 1158 QTFPQSGTLLNHQRTSSLLVLTLEDGHIELSTDSNIPFKSPGYMDGLHHVSVISDT 1217
QY 121 SGRLIIDQVLRNRQLPSFSNAQSLRLGGHFEFGCISNVLVQRFSGSPETLDLASKS 180
DB 1218 SGRLIIDQVLRNRQLPSFSNAQSLRLGGHFEFGCISNVLVQRFSGSPETLDLASKS 1277
QY 181 TKKDAISGGCSLNKPPFLMFKSPKRFNKGRIYNNQL 218
DB 1278 LKRDVSLGGCSLNKPPFLMFKSPKRFNKGRIYNNQL 1315

RESULT 4
US-09-560-385A-8
Sequence 8, Application US/09560385A
Patent No. 6703363
GENERAL INFORMATION:
APPLICANT: Boutand, Ariel

TITLE OF INVENTION: Recombinant Laminin 5
FILE REFERENCE: 99-274-C
CURRENT APPLICATION NUMBER: US/09/560, 385A
CURRENT FILING DATE: 2000-04-28
NUMBER OF SEQ ID NOS: 36
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 8
LENGTH: 1693
TYPE: PRT
ORGANISM: Homo sapiens
US-09-560-385A-8

Query Match 76.0%; Score 850; DB 4; Length 1693;
Best Local Similarity 76.6%; Pred. No. 6, 5e-92;
Matches 167; Conservative 18; Mismatches 33; Indels 0; Gaps 0;

QY 1 MKNLKTSGVRLNDVGVTKKCSBDMKLVRTASFSRGQMSFTNLDVPSIDRFGLSFGF 60
DB 1098 MKNLKTSGVRLNDVGVTKKCSBDMKLVRSASFSRGQSLSTDGLPPTDHLQASFGF 1157
QY 61 QTFPQSGTLLNHQRTSSLLVLTLEDGHIELSTDSNIPFKSPGYMDGLHHVSVISDT 120
DB 1158 QTFPQSGTLLNHQRTSSLLVLTLEDGHIELSTDSNIPFKSPGYMDGLHHVSVISDT 1217
QY 121 SGRLIIDQVLRNRQLPSFSNAQSLRLGGHFEFGCISNVLVQRFSGSPETLDLASKS 180
DB 1218 SGRLIIDQVLRNRQLPSFSNAQSLRLGGHFEFGCISNVLVQRFSGSPETLDLASKS 1277
QY 181 TKKDAISGGCSLNKPPFLMFKSPKRFNKGRIYNNQL 218
DB 1278 LKRDVSLGGCSLNKPPFLMFKSPKRFNKGRIYNNQL 1315

RESULT 5
US-08-600-982-24
Sequence 24, Application US/08600982
Patent No. 6120991
GENERAL INFORMATION:
APPLICANT: Carter, William G.
APPLICANT: Gail, Susanna A.
APPLICANT: Ryan, Maureen C.
TITLE OF INVENTION: Epiligrin, an Epithelial ligand for
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
ADDRESSER: Christensen, O'Connor, Johnson, and Kindness
STREET: 1420 Fifth Avenue
CITY: Seattle
STATE: WA
COUNTRY: USA
ZIP: 98101-8100
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/600,982
FILING DATE: 02-SEP-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Shelton, Dennis K.
REGISTRATION NUMBER: 26,997
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 682-8100
TELEFAX: (206) 224-0779
INFORMATION FOR SEQ ID NO: 24:
SEQUENCE CHARACTERISTICS:
LENGTH: 1713 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
DESCRIPTION: B170 protein as translated from sequence

DESCRIPTION: OF FIGURES 15A-15F, and as shown also in FIGURES
; DESCRIPTION: 19A-19R
US-08-600-982-24

Query Match 76.0%; Score 850; DB 3; Length 1713;
Best Local Similarity 76.6%; Pred. No. 6.6e-92;
Matches 167; Conservative 18; Mismatches 33; Indels 0; Gaps 0;

QY 1 MKRLKTSGVRLNDVGVTKKCEBDMKLVRTASFSRGQMSFTNLDVPSDFOLSGF 60
DB 1118 MKRLKTSGVRLNDVGVTKKCEBDMKLVRSASFSGQLSFTDGLPPTDHLQASFGF 1177
QY 61 QTFQPSGTLNHOQRTSSLVLTLEDGHIELSTRDSNIPFKSPGTMDGLHHVSVISDT 120
DB 1178 QTFQPSGTLNHOQRTSSLVLTLEDGHIELSTRDSNIPFKSPGTMDGLHHVSVISDN 1237
QY 121 SGRLILIDQVLRNORLPSFSNAQSLRLGGHFGFCISNVLYVORFOSPEVLDLASKS 180
DB 1238 SGRLILIDQVLRNORLPSFSNAQSLRLGGHFGFCISNVLYVORFOSPEVLDLTSNS 1297
QY 181 TKKDAISGCSLNKPPFLMFKSPKRNKGRINYNOL 218
DB 1298 LKRDVSLGGCSLNKPPFLMLKSGTRFNKTKFRINOL 1335

RESULT 6
US-09-560-385A-6
; Sequence 6, Application US/09560385A
; Patent No. 6703363
; GENERAL INFORMATION:
; APPLICANT: Boutand, Ariel
; TITLE OF INVENTION: Recombinant Laminin 5
; FILE REFERENCE: 99-274-C
; CURRENT APPLICATION NUMBER: US/09/560.385A
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: Patent Ver. 2.0
; SEQ ID NO 6
; LENGTH: 1713
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-560-385A-6

Query Match 76.0%; Score 850; DB 4; Length 1713;
Best Local Similarity 76.6%; Pred. No. 6.6e-92;
Matches 167; Conservative 18; Mismatches 33; Indels 0; Gaps 0;

QY 1 MKRLKTSGVRLNDVGVTKKCEBDMKLVRTASFSRGQMSFTNLDVPSDFOLSGF 60
DB 1118 MKRLKTSGVRLNDVGVTKKCEBDMKLVRSASFSGQLSFTDGLPPTDHLQASFGF 1177
QY 61 QTFQPSGTLNHOQRTSSLVLTLEDGHIELSTRDSNIPFKSPGTMDGLHHVSVISDT 120
DB 1178 QTFQPSGTLNHOQRTSSLVLTLEDGHIELSTRDSNIPFKSPGTMDGLHHVSVISDN 1237
QY 121 SGRLILIDQVLRNORLPSFSNAQSLRLGGHFGFCISNVLYVORFOSPEVLDLASKS 180
DB 1238 SGRLILIDQVLRNORLPSFSNAQSLRLGGHFGFCISNVLYVORFOSPEVLDLTSNS 1297
QY 181 TKKDAISGCSLNKPPFLMFKSPKRNKGRINYNOL 218
DB 1298 LKRDVSLGGCSLNKPPFLMLKSGTRFNKTKFRINOL 1335

RESULT 7
US-09-538-092-1359
; Sequence 1359, Application US/09538092
; Patent No. 6753314
; GENERAL INFORMATION:
; APPLICANT: Giot, Loic
; APPLICANT: Mansfield, Traci A.
; TITLE OF INVENTION: Protein-Protein Complexes and Method of Using Same
; FILE REFERENCE: 15966-542

CURRENT APPLICATION NUMBER: US/09/538,092
; CURRENT FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: 60/127,352
; PRIOR FILING DATE: 1999-04-01
; PRIOR APPLICATION NUMBER: 60/178,965
; PRIOR FILING DATE: 2000-02-01
; NUMBER OF SEQ ID NOS: 1387
; SOFTWARE: CuraPatSegFormatter Version 0.9
; SEQ ID NO 1359
; LENGTH: 1713
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (0)..(0)
; OTHER INFORMATION: Polypeptide Accession Number Q16787
US-09-538-092-1359

Query Match 76.0%; Score 850; DB 4; Length 1713;
Best Local Similarity 76.6%; Pred. No. 6.6e-92;
Matches 167; Conservative 18; Mismatches 33; Indels 0; Gaps 0;

QY 1 MKRLKTSGVRLNDVGVTKKCEBDMKLVRTASFSRGQMSFTNLDVPSDFOLSGF 60
DB 1118 MKRLKTSGVRLNDVGVTKKCEBDMKLVRSASFSGQLSFTDGLPPTDHLQASFGF 1177
QY 61 QTFQPSGTLNHOQRTSSLVLTLEDGHIELSTRDSNIPFKSPGTMDGLHHVSVISDT 120
DB 1178 QTFQPSGTLNHOQRTSSLVLTLEDGHIELSTRDSNIPFKSPGTMDGLHHVSVISDN 1237
QY 121 SGRLILIDQVLRNORLPSFSNAQSLRLGGHFGFCISNVLYVORFOSPEVLDLASKS 180
DB 1238 SGRLILIDQVLRNORLPSFSNAQSLRLGGHFGFCISNVLYVORFOSPEVLDLTSNS 1297
QY 181 TKKDAISGCSLNKPPFLMFKSPKRNKGRINYNOL 218
DB 1298 LKRDVSLGGCSLNKPPFLMLKSGTRFNKTKFRINOL 1335

RESULT 8
PCT-US94-10261A-24
; Sequence 24, Application PC/TUS9410261A
; GENERAL INFORMATION:
; APPLICANT: Carter, William G.
; APPLICANT: Gil, Susana A.
; APPLICANT: Ryan, Maureen C.
; TITLE OF INVENTION: Epiligrin, an Epithelial Ligand for
; NUMBER OF SEQUENCES: 30
; CORRESPONDENCE ADDRESSES:
; ADDRESSER: Christensen, O'Connor, Johnson, and Kindness
; STREET: 1420 Fifth Avenue
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98101-8100
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/10261A
; FILING DATE: 02-SEP-1994
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Shelton, Dennis K.
; REGISTRATION NUMBER: 26,997
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 682-8100
; TELEFAX: (206) 224-0779
; INFORMATION FOR SEQ ID NO: 24:
; SEQUENCE CHARACTERISTICS:

RESULT 12

US-09-561-818A-4
; Sequence 4, Application US/09561818A
; Patent No. 6638907
; GENERAL INFORMATION:
; APPLICANT: Kortteamaa, Jarkko
; APPLICANT: Tytgvaason, Karl
; TITLE OF INVENTION: Laminin 8 and Methods For Its Use
; FILE REFERENCE: 99,274-D
; CURRENT APPLICATION NUMBER: US/09/561,818A
; CURRENT FILING DATE: 2000-04-28
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: Patentln Ver. 2.0
; SEQ ID NO 4
; LENGTH: 1792
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-561-818A-4

Query Match 16.7%; Score 187; DB 4; Length 1792;
Best Local Similarity 28.3%; Pred. No. 2e-12;
Matches 62; Conservative 34; Mismatches 103; Indels 20; Gaps 8;

QY 5 KKTSGVRLNDYGVTKKSEDMKLVRTASFSRGGMSTFNL-D-VSTDRFQLSFGQTF 63
DB 1178 KQPNLEQETELGVGCEPDSLSIRAYFN--GQSFASIQKISFFDFEGGFNRTL 1235
QY 64 QPGLTLNHOQRTSSLLVTLDEGHIELSTRDSNIPFKSPGTWMDGLHHVSVISDTSG 123
DB 1236 QPGLTLFYVASSGSDVFSISLNDGTVMYDK--GIKQVSDKQYNDGLSHF--VISSVSPT 1291
QY 124 R--LLID-DQVLRNORLPSPNAQOSLR---LGG-----GHFEGCISNVLVORFSQS 170
DB 1292 RYELIYDKSRVSGKNPTKGIETQASBKFFYGGSPISAQVNFQGCISNAFTVRD 1351
QY 171 PEVLDAKSTKQDASLGCGSLNKPPLMLFKSPKRNK 209
DB 1352 VEVEDFORYTEKHTSLYECPIESSPLFLHKKGNLSK 1390

RESULT 13

US-09-561-818A-8
; Sequence 8, Application US/09561818A
; Patent No. 6638907
; GENERAL INFORMATION:
; APPLICANT: Kortteamaa, Jarkko
; APPLICANT: Tytgvaason, Karl
; TITLE OF INVENTION: Laminin 8 and Methods For Its Use
; FILE REFERENCE: 99,274-D
; CURRENT APPLICATION NUMBER: US/09/561,818A
; CURRENT FILING DATE: 2000-04-28
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: Patentln Ver. 2.0
; SEQ ID NO 8
; LENGTH: 1800
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-561-818A-8

Query Match 16.7%; Score 187; DB 4; Length 1800;
Best Local Similarity 28.3%; Pred. No. 2e-12;
Matches 62; Conservative 34; Mismatches 103; Indels 20; Gaps 8;

QY 5 KKTSGVRLNDYGVTKKSEDMKLVRTASFSRGGMSTFNL-D-VSTDRFQLSFGQTF 63
DB 1178 KQPNLEQETELGVGCEPDSLSIRAYFN--GQSFASIQKISFFDFEGGFNRTL 1235
QY 64 QPGLTLNHOQRTSSLLVTLDEGHIELSTRDSNIPFKSPGTWMDGLHHVSVISDTSG 123
DB 1236 QPGLTLFYVASSGSDVFSISLNDGTVMYDK--GIKQVSDKQYNDGLSHF--VISSVSPT 1291

QY 124 R--LLID-DQVLRNORLPSPNAQOSLR---LGG-----GHFEGCISNVLVORFSQS 170
DB 1292 RYELIYDKSRVSGKNPTKGIETQASBKFFYGGSPISAQVNFQGCISNAFTVRD 1351
QY 171 PEVLDAKSTKQDASLGCGSLNKPPLMLFKSPKRNK 209
DB 1352 VEVEDFORYTEKHTSLYECPIESSPLFLHKKGNLSK 1390

RESULT 14

US-09-561-818A-2
; Sequence 2, Application US/09561818A
; Patent No. 6638907
; GENERAL INFORMATION:
; APPLICANT: Kortteamaa, Jarkko
; APPLICANT: Tytgvaason, Karl
; TITLE OF INVENTION: Laminin 8 and Methods For Its Use
; FILE REFERENCE: 99,274-D
; CURRENT APPLICATION NUMBER: US/09/561,818A
; CURRENT FILING DATE: 2000-04-28
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: Patentln Ver. 2.0
; SEQ ID NO 2
; LENGTH: 1816
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-561-818A-2

Query Match 16.7%; Score 187; DB 4; Length 1816;
Best Local Similarity 28.3%; Pred. No. 2e-12;
Matches 62; Conservative 34; Mismatches 103; Indels 20; Gaps 8;

QY 5 KKTSGVRLNDYGVTKKSEDMKLVRTASFSRGGMSTFNL-D-VSTDRFQLSFGQTF 63
DB 1202 KQPNLEQETELGVGCEPDSLSIRAYFN--GQSFASIQKISFFDFEGGFNRTL 1259
QY 64 QPGLTLNHOQRTSSLLVTLDEGHIELSTRDSNIPFKSPGTWMDGLHHVSVISDTSG 123
DB 1260 QPGLTLFYVASSGSDVFSISLNDGTVMYDK--GIKQVSDKQYNDGLSHF--VISSVSPT 1315
QY 124 R--LLID-DQVLRNORLPSPNAQOSLR---LGG-----GHFEGCISNVLVORFSQS 170
DB 1316 RYELIYDKSRVSGKNPTKGIETQASBKFFYGGSPISAQVNFQGCISNAFTVRD 1375
QY 171 PEVLDAKSTKQDASLGCGSLNKPPLMLFKSPKRNK 209
DB 1376 VEVEDFORYTEKHTSLYECPIESSPLFLHKKGNLSK 1414

RESULT 15

US-09-561-818A-6
; Sequence 6, Application US/09561818A
; Patent No. 6638907
; GENERAL INFORMATION:
; APPLICANT: Kortteamaa, Jarkko
; APPLICANT: Tytgvaason, Karl
; TITLE OF INVENTION: Laminin 8 and Methods For Its Use
; FILE REFERENCE: 99,274-D
; CURRENT APPLICATION NUMBER: US/09/561,818A
; CURRENT FILING DATE: 2000-04-28
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: Patentln Ver. 2.0
; SEQ ID NO 6
; LENGTH: 1824
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-561-818A-6

Query Match 16.7%; Score 187; DB 4; Length 1824;
Best Local Similarity 28.3%; Pred. No. 2e-12;
Matches 62; Conservative 34; Mismatches 103; Indels 20; Gaps 8;

QY 5 KKTSGVRLNDYGVTKKSEDMKLVRTASFSRGGMSTFNL-D-VSTDRFQLSFGQTF 63

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Db      1202 KDFNLLEQETETLGVGCGCPEDSLISRRAVFN--GQSFIASIOKISFFDGFEGGFNFRFL 1259
Qy      64  OPSGTLNHOQRTSSLLVTLBDOGHIELSTRDSNIPIFKSPGYMDGLLHVSVISDPSGL 123
Db      1260 QPENGILFYAAGSDVPSISLDNGTVMYK--GIKVQYVDKQYNDGLSHF--VISVSPT 1315
Qy      124  R--LLID-DQVLRNRQRLPSPFSAQOSLR---LGG-----GHFEGCISNVLVORFSQS 170
Db      1316 RYELIYDKSRVGSKNPTKGKIEQTOASEKKFYFGGSPISAOYANFTGCISNAVFTRVDRD 1375
Qy      171  PEVLDAASKSTKKDASLGCSLNKPPFLMLFKSPKRPNK 209
Db      1376 VEVEDFQRYTEKVTSTLYECPIESSPLFLHKKGKNLSK 1414
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Search completed: February 22, 2005, 08:40:56
Job time : 11.1795 secs